02-09-096-903B-10_COFY_194_416 10 taccataattataattatacatgaacacccaaactcgat 223 IDENTIY_NUC	11111111111111111111111111111111111111	1000 200.8 200.6 200.6 200.9 200.3 200.3 190.8 190.7		AX127757 Sequents and a sequents are a sequents as a sequent and a sequent as a seq
	44444444444444444444444444444444444444	20011111111111111111111111111111111111		AF2 AZ0 AZ0 AZ0 AZ0 AZ0 AZ0 AZ0 AZ0 AZ0 AZ0
	000000000000000000000000000000000000000	43 19.3 193996 48 19.3 203718 2.8 19.2 175014 2.8 19.2 175020 2.8 19.2 211316 2.4 19.0 60208 2.4 19.0 101584 2.4 19.0 152958 2.4 19.0 152958 2.4 19.0 152958 2.4 19.0 158671 2.4 19.0 168519 2.5 19.0 168519 2.7 19.0 168519 2.8 19.0 168519 2.8 19.0 188671 2.9 19.0 188671 2.1 19.0 188671 2.2 18.9 108880	2 AC068503 9 AC009486 2 AC0011854 9 AC022317 2 AC022317 2 AC022911 2 AC022911 9 AF222854 9 AF222854 9 AF222854 2 AC1022 2 AC1022 2 AC1162 2 AC1162 2 AC1162 2 AC01339 9 AC004878	AC06503 AC064153 AC01854 AC01854 AC02317 AP002063 AC022856 AF222856 AF222856 AF222856 AF35340 AC019247 AC019247 AC019247 AC019247 AC019247 AC073039 AC073039
22: em_pat:* 23: em_pat:* 24: em_ph:* 25: em_ro:* 25: em_ro:* 26: em_rsts:* 27: em_sy:* 28: em_lun:* 30: em_htgo_hum:* 31: em_htgo_lnv:* 32: em_htgo_lnv:* 33: em_htgo_lnv:* 34: em_htgo_lnv:* 35: em_htgo_lnv:* 36: em_htgo_lnv:* 37: em_htgo_lnv:* 38: em_htgo_lnv:* 39: em_htgo_lnv:* 30: em_htgo_lnv:* 31: em_htgo_lnv:* 32: em_htgo_lnv:* 33: em_htgo_lnv:* 34: em_htgo_lnv:* 35: em_htgo_lnv:* 36: em_htgo_lnv:* 36: em_htgo_lnv:* 37: em_htgo_lnv:* 38: em_htgo_lnv:* 38: em_htgo_lnv:* 39: em_htgo_lnv:* 39: em_htgo_lnv:* 39: em_htgo_lnv:* 30: em_htgo_lnv:* 31: em_htgo_lnv:* 32: em_htgo_lnv:* 33: em_htgo_lnv:* 34: em_htgo_lnv:* 35: em_htgo_lnv:* 36: em_htgo_lnv:* 36: em_htgo_lnv:* 37: em_htgo_lnv:* 38: em_htgo_lnv:* 39: em_htgo_lnv:* 3	RESULT 1 AX127757 LOCUGS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUICE	AX127757 416 bp Sequence 10 from Patent AX127757 AX127757 AX127757.1 GI:14134404 Synthetic construct. Synthetic construct. Synthetic construct. artificial sequence. 1 (bases 1 to 416) Weston, B. and de Beucke Male sterile brassica p Patent: WO 0131042-A 10 Aventis Cropscience N. V. Location/Quali 1. 416 /organism="syn /db_xref="taxo /note="ax' bord /note="ax' bord	AX127757 416 bp DNA PAT Sequence 10 from Patent W00131042. AX127757 AX127757.1 GI:14134404 synthetic construct. synthetic construct artificial sequence. I chases 1 to 416 Weston, B. and de Beuckeleer, M. Wale sterile brassica plants and methods for Patent: W0 0131042-A 10 03-MAY-2001; Aventis CropScience N.V. (BE) Location/Qualifiers 1. 416 /organism="synthetic construct" /db_xref="taxon:32630" /note="3" border flanking region of	PAT 15-MAY-2001 ods for producing same tt"

AX127757 Sequence
AX127755 Sequence
ACO008817 Homo sap1
U66722 Human chrom
ACO10801 Homo sap1
ACO91684 Homo sap1
ACO91684 Homo sap1
ACO91687 Trypanoso
ACO68887 Homo sap1
ACO3912 Sequence
AX033912 Sequence
ACO3391 Homo sap1
ACO2689 Homo sap1
ACO26089 Homo sap1
ACO301986 Oryza sat
ACO90578 Homo sap1
ACO48342 Homo sap1
ACO48342 Homo sap1
ACO48342 Homo sap1
ACO48343 Homo sap1
ACO4831 Homo sap1
ACO3311 Homo sap1
ACO331 Homo sap1
ACO3391 Homo sap1
ACO33039 Homo sap1

```
human
                                                                                           DEFINITION
                                                                                                    ACCESSION
VERSION
                                                                                                                                               ORGANISM
                                                                                                                                                                                                            JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                           RESULT
AC008817
                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
HSU66722
                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
       à
                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                â
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                    /organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' border flanking region of elite event MS-B2"
                                                                                                                                       121 tatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttccatatgtaat 180
                                                                                                                                                                                                                       114 TATATGAACAFGATTAATGCTTGTGAGTTGTTCTCATCCGTAAGAGTTTCAATATGTAAT 373
                                                                                                             Gaps
                                                                                                                           1 ctaccataattataattataattatatataatactgaaaccatggtgcccctgctgtta 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                       15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                       Male-sterile brassica plants and methods for producing same Patent: WO 0131042-A 8 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ctaccataattataattataattatatatatac-tgaaaccatggtgcccctgctgcttt
                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 415;
                                                                                       Length 416;
                                              others
                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                      181 ggtgaagagtcaaaacccaaaatcatgaacacccaaactcgat 223
                                                                                                                                                                                                                                                                                                                                       PAT
                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                    Score 223; DB 6
Pred. No. 1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 189.8; DB Pred. No. 9e-36;
                                                                                Query Match
100.0%; Score 223; D
Best Local Similarity 100.0%; Pred. No. 1e-
Matches 223; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ų
                                            152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                AX127755 415 bp DNA
Sequence 8 from Patent WO0131042.
AX127755
AX127755.1 GI:14134402
      /note="T-DNA"
194. 416
/note="plant DNA"
a 72 c 54 g
                                                                                                                                                                                                                                                                                                                                                                                                         artificial sequence.
1 (bases 1 to 415)
Weston, B. and de Beuckeleer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"plant DNA"
235. .415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235. .415
/note="T-DNA"
1 55 c 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.1%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                      synthetic construct. synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.29
Matches 213; Conservative
                                         137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
                     misc_feature
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                      AX127755/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                              g
                                                                                                                                                                   ò
                                                                                                                                                                                       음
                                                                                                                                                                                                            à
                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
Use John Canning and Carlot Submission Direct Creek, CA 94598, USA

Drive, Malnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14327774.

Draft Sequence Produced by DoE Joint Genome Institute
www.jgl.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 1.

Location/Qualifiers

Jurce
//organism="#homo sapiens"
//db.xref="maxon:9606"
//chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 186185)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (basea 1 to 18618)
Dice Johnt Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 186185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (07-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 186185)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 163975 CTTCAACAATCTCATATGGAGTTTCATACTACTGACTTAATAGAAGTAACTCCTCAGATG 164034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 164035 CATGGCCTTCTATACTTGCTTATATATTTGAGTATCTATACCATGTTAAATATCTTTAAT 164094
                                                                                                                                                                                    AC008817 186185 bp DNA PRI 21-JUL-2001
Homo saplens chromosome 5 clone CTD-2122P11, complete sequence.
AC008817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ctaccataattataattataattataatactgaaaccatggtgcccctgctgcttta 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
21.4%; Score 47.8; DB 9; Length 186185;
Best Local Similarity 54.2%; Pred. No. 0.059;
Matches 97; Conservative 0; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSUG6722 110434 bp DNA PRI
Human chromosome 3p14.2 fragile site FRA3B sequence.
/clone="CTD-2122P11"
36324 c 34624 g 59225
                                                                                                                                                                                                                                                                                  AC008817.8 GI:14993662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56012 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
```

```
AUTHORS
TITLE
                                                                      JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                   RFERENCE
                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC010801 138350 bp DNA HTG 30-MAR-2000
Homo sapiens clone RP11-2L13, WORKING DRAFT SEQUENCE, 19 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catggatttctccgctactatttgtatacgtgtatatataccgtataatgtacatatat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 tatatgeacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaat 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ctaccataattataattataattatatatatactgaaaccatggtgcccctgctgtta 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 110434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 others
                                                                                                                                                                          85341. .85493
/rpt_family="MER42"
85859. .85960
/note="HPV viral intergration site"
/note="LTR11"
                                                             /note="CC19 telomeric breakpoint"
78426. .78469
/note="LTR11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46.4; DB 9;
Pred. No. 0.13;
0; Mismatches 86;
                                                                                    old i. 81638

/rpt_famlly="MIR"

complement(82365. 82488)

/rpt_famlly="ALU"

complement(83558. 83843)

/rpt_famlly="ALU"

85341. 8540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20889 g 32500 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(108781. .110294)
            /rpt_family="ALU"
complement(75316, .75446)
/rpt_family="L1"
75959, .76959
                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="HSATI"
99834: 100410
/rpt_family="ALU"
101347: 101767
/rpt_family="THF1"
                                                                                                                                                                                                                                                                                                                         /rpt_family="HSATI"
96613. .96910
/rpt_family="ALU"
99040. .99081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC010801
AC010801.3 GI:7341823
HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                      /rpt_family="ALU"
90782. .91043
/rpt_family="L1"
96484. .96611
                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(108148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="L1"
22068 c 20889
                                                                                                                                                                                                                                                           88396. .88683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch
1 Similarity 53.3%;
98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34970 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43130 TGTG 43133
repeat_region
                        repeat_region
                                                                                                    repeat_region
                                                                                                                             repeat_region
                                                                                                                                                       repeat_region
                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ggtg 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                         LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                 LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AC010801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
ENERTY PLAS NEEDERS (COLOCIALS) CENTRALIALS (NETEBRARE): BICHARTYOLS (NEEDERS)

I (DASSES) 1 to 1383501

I (DASSES) 1 to 1383501

BITTON 31. LINTON, L. NUSINAMIC. and LANGER.E.

BITTON 31. LINTON, L. NUSINAMIC. and LANGER.E.

TOTHERS, L. LINTON, L. NUSINAMIC. and LANGER.E.

BITTON 3. LINTON, L. NUSINAMIC. and LANGER.E.

TOTHERS (LINTON). L. NUSINAMIC. and LANGER.E.

BITTON A. CASTELLA. (COLDINGS). COLDINGS, COLDI
```

Gaps

ö

80; Indels

Pred. No. 0.16; Mismatches

54.0%;

ö

ttataattataattatatataatactgaaaccatggtgccccctgctgctttacatggattt 69

2

```
Best Local Similarity 54.0
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                         δy
                                                                                                              44370 44369; gap of 100 bp 44370 51461: contig of 7092 bp in length 51462 51561: gap of 100 bp 51562 59216: contig of 7092 bp in length 51562 59216: contig of 7655 bp in length 59217 59316: gap of 100 bp 69985 69984: gap of 100 bp 69985 69984: gap of 100 bp 69985 80594: contig of 10610 bp in length 80595 80694: gap of 100 bp 80695 93129: contig of 13751 bp in length 93130 93229: gap of 100 bp 69320: gap of 100 bp 107080: gap of 107080: gap of 100 bp 107080: gap of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1810 others
                                             gap of 100 bp
69: contig of 6257 bp in length
gap of 100 hr
48: gap of 100 bp
37912: contig of 6364 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="Laxon:9606"
/clone="RP11-2L13"
/clone="RP1-2L13"
/clone=lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
25076 c 24703 g 44151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1270. .4174
/note-"assembly_fragment"
4275. .6879
/note-"assembly_fragment"
6980. .10304
/note-"assembly_fragment"
10405. .13133
/note-"assembly_fragment"
13234. .16716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
80695. .93129
/note="assembly_fragment"
93230. .106980
/note="assembly_fragment"
107081. .121789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assemily_fragment"
16817. 21929
/note="assembly_fragment"
22030. .26268
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31549. 37912
/note="assembly_fragment"
38013. .44269
/note="assembly_fragment
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44370. .51461
/note="assembly_fragment"
51562. .59216
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1169
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59317. .69884 ...
/note="assembly_fragment"
69985. .80594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26369. .31448
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
31549. .37912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector_side:right"
                                                             38012: gap of
44269: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121890. .138350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .138350
                                                             37913
38013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
```

```
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Joses 1 to 142126)
Mclay, K.
Direct Submission
Submitted (28-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jul 199, 2001 this sequence version replaced g1:15022382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 141907 bases at least 040
Consensus quality: 141961 bases at least 020
Insert size: 142026; sum-of-contigs
Insert size: 159858; 4.5% error; agarose-fp
Quality coverage: 12.33x in Q20 bases; sum-of-contigs Quality
coverage: 10.95x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                    29-JUL-2001
                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 1 clone RP11-2L13, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
                                                                                                                                 Db 131080 CTTCTTAATACTAGGFACATGTACACACCTATATCTATACCTATATCTACAGTT 131133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                         130 atgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggt 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 6452: contig of 6452 bp in length 6453 6552: gap of 100 bp 6553 142126: contig of 135574 bp in length. Location/Qualiffers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-2113"
/clone=11b="RPCI-11.1"
1. .6452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: bA2L13
                                                                                                                                                                                                                                                                                                                                                                                      AL596266.2 GI:15028804
                                                                                                                                                                                                                                                                                    142126 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
                                                                                                                                                                                                                                                                                  AL596266
                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                  RESULT
AL596266
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
```

misc_feature

DB 2; Length 138350;

Score 46;

20.68;

Query Match

ð

ð

```
length
                                                        bp in length
                                                                         bp in length
length
                                                                                           bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
length
                                                                                                                                                bp in length
                                                                                                                                                                    bp in length
                                                                                                                                                                                     bp in length
                                                                                                                                                                                                      in length
                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                           bp in length
                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                        length
bp in length
                                                                                                                                                                                                                                                                                                                                             length
bp in length
                                                                                                                                                                                                                                                                                                                                                                       bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                  length
bp in length
                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                                                                                                                                      bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                             length
                                              length
                                                               length
                                                                                                   length
                                                                                                                      length
                                                                                                                                        length
                                                                                                                                                           length
                                                                                                                                                                                               length
                                                                                                                                                                                                                length
                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                               pp in
                                                                                                                                                                                                                                                                                                                            ength
                                                                                                                                                                                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                                                                                                                                                                                                                                       ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 1194 bp in l
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pb tu
                                                                                                                            unknown of 2680 hunknown of 2288 h
                                                                                                                     unknown
of 2015
                            unknown
                                                      of 2532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 1433 k
unknown 1
of 2087 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown 1
of 2299 r
unknown 1
of 2473 r
unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown 1
of 1850 b
unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
of 1260 l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown of 1833 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown of 1379 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οį
        gap of
contig
gap of
                                  contig
gap of
contig
gap of
                                                                               gap of contig gap of contig gap of gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                11094:
11194:
13957:
14057:
16689:
18911:
                                                                                                                  24179:
26194:
                                                                                                                                     26294:
                                                                                       21691:
21791:
24079:
                                                                                                                                                                                                                                                                                      12269:
                                                                                                                                                                                                                                                                                                       13631:
                                                                                                                                                                                                                                                                                                                                             6484:
                                                                                                                                                                                                                                                                                                                                                             47867:
                                                                                                                                                                                                                                                                                                                                                                                                                     53394:
                                                                                                                                                                                                                                                                                                                                                                                                                                       5085:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61632:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63819:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63919:
                                                                                                                                                                                                                                                                   40976
                                                                                                                                                                                                                                                                                                                  14992:
                                                                                                                                                                                                                                                                             12169
                                                                                                                                                                                                                36497
     7333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65180
65280
6759
67679
70152
70253
772333
74266
774266
775945
775945
775945
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (17-MAY-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 81503) Waterston, R.H.
The Sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                AC091684 81503 bp DNA HTG 17-MAY-2001
Homo sapiens chromosome UNK clone RP13-581E15, *** SEQUENCING IN
PROGRESS ***, 41 unordered pieces.
                                                                                                                                                                                          70 ctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatatgaac 129
                                                                                                                                           Gaps
                                                                                                                                                       10 ttataattataattataataatactgaaaccatggtgccccctgctgctttacatggattt 69
                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                          ö
                                                                                                                  Query Match
20.6%; Score 46; DB 2; Length 142126;
Best Local Similarity 54.0%; Pred. No. 0.16;
Matches 94; Conservative 0; Mismatches 80; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center Web site:http://genome.wustl.edu/gsc/index.shtml Project Information .........
                                                                                   100 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1406: contig of 1406 bp in length
1506: gap of unknown length
3416: contig of 1910 bp in length
516: gap of unknown length
6161: contig of 2645 bp in length
5261: gap of unknown length
7972: contig of 1711 bp in length
/note="assembly_fragment:01221
fragment_chain:1
clone_end:SP6
                         vector_side:left"
6553. 142126
^/note-"assembly_fragment:01911
fragment_chain:1
clone_end:T7
                                                                       vector_side:right"
26793 c 24991 g 42846 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- Genome Center
                                                                                                                                                                                                                                                                                                                                  AC091684.1 GI:14140336
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 81503)
Waterston, R.H.
                                                                                                                                                                                                                                                                                               81503 bp
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                 ಪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1407
1507
3417
3517
6162
                                                                                                                                                                                                                                                                                               AC091684
                                                                                47396
                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                    human.
                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                          RESULT
AC091684
                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
```

Gaps

ö

Length 81503;

```
1 (bases 1 to 146349)
El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K., Peterson, J., Hou, L., Zhao, H., Mason, T., Militscher, J., Pai, G., Van Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Melville, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Trypanosoma brucei GUTatlo.1 RPC193-26G9 BAC genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC007863 146349 bp DNA HTG 17-JUL-2001
Trypanosoma brucei chromosome VI clone RPC193-26G9, *** SEQUENCING
IN PROGRESS ***, 1 ordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA On Jul 17, 2001 this sequence version replaced gi:12746518.

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pleces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                           6 ataattataattataattataatataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 146349; contig of 146349 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgt 177
                                                                                                                                                                                                                                                                            ch 20.4%; Score 45.6; DB 2; 1 Similarity 54.1%; Pred. No. 0.21; 93; Conservative 0; Mismatches 79;
                                                                                            /note="assembly_name:Contig94"
7233. 74165
700te="assembly_name:Contig95"
74266. 75644
/note="assembly_name:Contig96"
75454. 77594
/note="assembly_name:Contig97"
77695. 77898
65280. .67578
/note="assembly_name:Contig91"
(67679. .70151
/note="assembly_name:Contig93"
70252. .72232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Trypanosoma brucei"
/isolate="GUTatl0.1"
/db_xref="taxon:5691"
/chromosome="V1"
/clone="RPC193-2669"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 146349)
El-Sayed, N.M., Khalak, H. and Adams, M.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG: HTGS_PHASE2.
Trypanosoma brucei.
Trypanosoma brucei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .146349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma.
                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC007863
        misc_feature
                                                                                                                         misc_feature
                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                          misc_feature
                                              misc_feature
                                                                                  misc_feature
                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
AC007863/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                             ó
    81503: contig of 2515 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /notee"assembly_name:Contig109"
24180 . 26194
/notee"assembly_name:Contig110"
26295 . 29162
/notee"assembly_name:Contig111"
29263 . 33740
/notee"assembly_name:Contig111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43632. .44992

/note="assembly_name:Contigy7"

/note="assembly_name:Contigy7"

/note="assembly_name:Contigy0"

/note="assembly_name:Contigy0"

/note="assembly_name:Contigy0"

/note="assembly_name:Contigy1"

/note="assembly_name:Contigy1"

/note="assembly_name:Contigy1"

/note="assembly_name:Contigy3"

53395. .54985

/note="assembly_name:Contigy3"

53395. .54986
                                                                                                                                                                                                                                                                              8073. .11094
/note="assembly_name:Contigl04"
11195. .13957
/note="assembly_name:Contigl05"
14058. .16589
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19012. .21691
/note="assembly_name:Contig108"
21792. .24079
                                                                                                                                                                             1507. .3416
/note="assembly_name:Contig101"
                                                                                                                                                                                                     3517. .6161
/note="assembly_name:Contig102"
6262. .7972
                                                                                                                                                                                                                                                          5262. .7972
/note="assembly_name:Contig103"
                                                                                                                                                                                                                                                                                                                                                                       14058. .16589
/note="assembly_name:Contig106"
                                                                                                                                                                                                                                                                                                                                                                                                             16690, .18911
/note="assembly_name:Contig107"
                                                                                                                                                           'note="assembly_name:Contig100'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig69"
19147. .40876
/note="assembly_name:Contig71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40977. .42169 --
Anote="assembly_name:Contig73"
42270. .43531
/note="assembly_name:Contig75"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55086. .56463
/note="assembly_name:Contig85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56564. 58670
/note="assembly_name:Contig86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58771. .60099
/note="assembly_name:Contig87"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig88"
61733. .63819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig89"
63920. .65179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig90"
                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                  /chromosome="UNK"
/clone="RP13-581E15"
                    Location/Qualifiers
1. .81503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50200. .61632
                                                                                                                                         misc_feature
                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                      FEATURES
```

ð

ô

à

```
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                          JOURNAL
                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                  TITLE
                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS MURDAY, D.M. Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alisocoks, S.L., Amaretunge, H.C., Aed, J.R., Barks, T., Barbaria, J., Benton, J., Brager, R., Bondry, C., Caron, T.E., Bente, C., Escett, C., Briede, M., Bryan, C., Caron, T.E., Chen, R., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Douthwaite, K.J., Davis, C., Escettoli, L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Davis, C., Chen, R., Elhaj, C., Escettoli, L., Dadisi, Y., Garcia, A., Garce, T., Elhaj, C., Escettoli, L., Edaisi, A., Gao, J., Garcia, A., Garner, T., Elhaj, C., Escettoli, R., Gorcell, J.H., Guevara, W., Gunaratne, P., Hamelton, K., Harris, C., Harris, K., Harris, K., Harris, C., House, M., Holloway, C., Jackson, L.E., Jackson, E., Hand, M., Harris, C., Ludis, M., Harlak, J., Hume, J., Jackson, E., Kallak, C., Ludie, K., Judier, S., Ludie, K., Ludier, K., Ludier, K., Ludie, K., Marting, E., Mascon, M., Morgan, M., Morris, S., Moser, M., Neuten, R., Paraneris, R., Moser, M., Neuten, R., Paraneris, R., Martine, S., Moser, M., Neute, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shockers, M., Neuten, R., Wallen, M., Shockers, M., Neuten, R., Wallen, M., Stone, H., Sutcon, A., Savery, G., Scherer, S., Scott, G., Shen, R., Wallen, M., Stone, H., Sutcon, A., Savery, G., Taylor, P., Tamerisa, A., Tamerisa, A., Tangeris, R., Wall, R., Wall, R., Warlen, S., Warlen, A., Taylor, C., Taylor, Wall, R., Wall, R., Wall, R., Warlen, R., Warlen, R., Wall, R., Wall, R., Wall,
                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         Db 11970 TATTATTATATTACTGTTGTTTGGTATTCATCGACTTGTACTCCTTGTGGTTATT 11911
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                       2 taccataattataattataattatatatataatactgaaaccatggtgcccctgctgctttac 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO Sapiens chromosome 12 clone RP11-392G11, WORKING DRAFT SEQUENCE, 9 unordered pleces.
                                                                                                                              Score 45.2; DB 2; Length 146349;
Pred. No. 0.25;
0; Mismatches 73; Indels 0;
                                                                                                                                                                                                  ;
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 11850 GIGTGTACGTTTCGTTGTCGTGTTTTGTGCTGCTTTGTA 11809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 atatgaacatgattaatgcttgtgagttgttctcatccgtaa 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC06887.22 GI:15145500
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                      73;
   37892 a 34490 c 35232 g 38734 t
                                                                                                                              20.3%;
54.9%;
                                                                                                                                                 Best Local Similarity 54.9
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                     Query Match
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
AC068887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
```

```
Submitted (11-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Aug 9, 2001 this sequence Version replaced gi:14717197.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid, M77789
Sequencing vector: Plasmid, M77789
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990229
Consensus quality: 140201 bases at least Q40
Consensus quality: 147355 bases at least Q30
Consensus quality: 14737 bases at least Q30
Estimated insert size: 158898; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 5.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence it currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ataattataattataattatataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 149241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38028: contig of 38028 bp in length 38128: gap of unknown length 62053: gap of unknown length 62053: gap of unknown length 85448: contig of 23395 bp in length 85548: contig of 23395 bp in length 105441: contig of 20393 bp in length 105441: gap of unknown length 122066: contig of 16525 bp in length 123066: gap of unknown length 133065: gap of unknown length 133065: contig of 1659 bp in length 14226: contig of 8391 bp in length 14226: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            818 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown length
of 4417 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146873: gap of unknown length
149241: contig of 2368 bp in length.
                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45.2; DB
Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-392G11"
32275 c 31743 g 41487 t
                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: RP11-392G11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146773: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="12
                                            2 (bases 1 to 149241)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.3%;
54.1%;
Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .149241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.3
Best Local Similarity 54.1
Matches 92; Conservative
                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85549
105942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61954
62054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123067
133766
133866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142257
142357
146774
146874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42918 a
```

ò

ò

```
Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                           Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
Center project name: L2492
Center clone name: 1_1_20
                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11 Human Male BAC"
907. .1194
/rpt_family="AluSc"
2366. .2412
/rpt_family="AT_rich"
3023_.3045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Alusx" complement(21320, 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="MLflJ1"
17105. .17129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MLT2A2"
[1444. .1157:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="L1PA16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L1PA16"
23637. .23667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(17249. 17318)
/rpt_family="L1PA16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MIR"
5997, .6510
                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MIR"
16336. .16363
/rpt_family="AT_rich"
complement(16689. .1679
                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AT_rich" 3919. .4158
/rpt_family="MIR" 4705. .4762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'rpt_family="AT_rich"
.4381. .14697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
26266, .26355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'rpt_family="(TTTA)n"
.0455. .10480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(GGAA)n"
14215. .14253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7105. .17129
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'rpt_family="AT_rich"
15073. .25095
'rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="(TGAA)n"
27824. .28310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family="(CAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..._ric.
.o266. .26355
'rpt_family="(TA)n"
7347. .27400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="(TAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'rpt_family="(TA)n"
7438. .27800
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'rpt_family="MLT1D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="MER6"
27801. .27823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'rpt_family="L3"
5032. .15270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="L2"
294. .9340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (17323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .14697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .27823
                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                  source
                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barnta, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colange, M., Collins, S., Collymore, A., Colange, P., Dekrellano, K., Dewar, K., Domino, M., Domino, M., Domino, M., Domino, M., Domino, M., Denselan, L., Develle, J., Brown, C., Jonson, R., Gane, G., Gane, G., Gane, G., Rann, L., Karatas, A., Klein, J., Ital, C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Ital, C., McKernan, K., McLaughlin, J., Meddrim, J., McGurk, A., McGurk, R., McGenal, F., Marquis, N., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stanger, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wayn, J., Zhanger, H., Wo, A., Wheeler, J., Wu, X., Wayn, J., Zhanger, H., Wo, A., Wheeler, J., Wu, X., Wayn, J., Zhange, Street, Cambridge, MA 02141, USA

B. Stanger, M. Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Callins, S., Collins, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-MXY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAY 1, 2001 this sequence version replaced gi:11612361.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RW/RepeatWasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo. [ toases 1 to 158236]
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-1120
                                                66 atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                 01-MAY-2001
                                                                                                                                            Db 106745 ATATATTTTTTTTTTTTTTTTTTTTTTTGAGAGTTTCGCTCT 106794
                                                                                                                 126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatat 175
                                                                                                                                                                                                                                                           ACO11631 158236 bp DNA PRI
Homo sapiens, clone RP11-1120, complete sequence.
AC011631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                AC011631.6 GI:13899434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 158236)
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                              RESULT 10
AC011631
LOCUS
                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
```

```
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 18% of reads
Chemistry: Dye-terminator ET-amersham; 18% of reads
Consensus quality: 214865 bases at least Q40
Consensus quality: 215040 bases at least Q30
Consensus quality: 215040 bases at least Q30
Insert size: 186031; sum-of-contigs
Insert size: 183707; 12.3% error; agarose-fp
Coulity coverage: 6.62x in Q20 bases; sum-of-contigs Quality
Coverage: 8.28x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216431)
Mclay,K.
                                                                        atttotocgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                             126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (189-70N-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 2, 2001 this sequence version replaced g1:14586086.
                                                                                                                                                                                                                                                                                                                                                AL354771 216431 bp DNA HTG 29-JUN-2001
Homo sapiens chromosome 1 clone RPI1-545P21 map q25.1-31.1, **
SEQUENCING IN PROGRESS ***, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18610 18709: gap of 1000 bp 11 Length 18710 27338; contlg of 8629 bp in length 27339 27438; contlg of 8629 bp in length 27439 126572; contlg of 99134 bp in length 126573 206680; contlg of 90008 bp in length 206681 206780; gap of 100 bp 206781 216431; contig of 9651 bp in length 1. .216431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18609: contig of 18609 bp in length
                                                                                                                                                                                                                                    Db 47218 AAAGCCATCAATAAAATATATACACAGATATAATCAA 47254
                                                                                                                                                                                                        186 agagtcaaaacccaaaatcatgaacacccaaactcga 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL354771.11 GI:14586527
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: SC
                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                     AL354771
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                     g
                                                  ò
                                                                                                                             δy
                                                                                                                                                                  ద
                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ateattataattatatatatatactgaaaccatggtgcccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 158236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.8%; Score 44.2; DB 9; )
Best Local Similarity 50.2%; Pred. No. 0.43;
Matches 109; Conservative 0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                    36929. 37123
/rpt_family="L2"
complement(37520. 37534)
/note="<30 qual SNGL region"
//rrt 2. 38451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement (39691. 39921)
/rpt_family="LiPA4"
39922. 39986
40909. 41087
/rpt_family="AluSg/x"
41125. 41118
/rpt_family="AluSg/x"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_ram1,
44402. .44452
/rpt_family="AT_rich"
complement(45526. .45638)
                                                      complement(30740. .30982) /rpt_family="L2"
                                                                                             complement(31154. .31455)
/rpt_family="Alusx"
31918. .32085
                                                                                                                                                                    /rpt_family-"MLT1J1"
                                                                                                                                                                                                      complement(33566. 34050)
/rpt_family="MLTID"
34060. 34099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y="MIR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family-"AT_rich"
complement(36872. .39498)
/rpt_family="LiMB3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(42412. 43988)
/rpt_family="LiMA6"
complement(44170. 44263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(47306. .47892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="L3"
45882. 45938
45882. 45938
46055. 46114
/rpt_family="(TA)n"
46181. 46381
/rpt_family="Limc1"
/rpt_family="Limc1"
                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
36266. 36309
/rpt_family="(TA)n"
36929. 37123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46862. .47087
/rpt_family="LiMDa"
47088. .47218
/rpt_family="(TA)n"
47219. .47305
/rpt_family="LiMDa"
                    28491. .28904
/rpt_family="MSTA"
                                                                                                                                                                                                                                               34060 ...34099
/rpt_family="L2"
34504 ...34742
/rpt_family="MIR"
36212 ...36246
/rpt_family="MER6"
                                                                                                                                                   /rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47892, .48666
/rpt_family="L1P"
48667, .48913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family
14299. .443
                                                  repeat_region
                                                                                           repeat_region
                                                                                                                               repeat_region
                                                                                                                                                                      repeat_region
                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                         unsure
```

source

```
AF042484 80155 bp DNA PRI 22-JUN-2000 Milko sapiens sequence of the 80 kb core centromere protein binding region of the mar del(10) neocentromere corresponding to human chromosome 10q25.2, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 80155)
Barry, A.E., Howman, E.V., Cancilla, M.R., Saffery, R. and Choo, K.H.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                        Db 15314 CATAAATATATACATAAATATGTATATATGTGTATATAGACATAAATATGTATATGTG 15373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 41008)
Cancilla,M.R., Choo,K.H. and Du,S.D.
A novel nucleic acid molecule
Patent: WO 9851790-A 4 19-NOV-1998;
CANCILLA MICHAEL ROBERT (AU); CHOO KONG HONG ANDY (AU); SART
DESIREE DU (AU); ARRAD OPERATIONS PIY LTD (AU)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                     Gaps
                                                                      64
                                                                                                                                                                                                                                                                                                                                         21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 cataattataaattataattataatactgaaaccatggtgcccctgctgctttacatg
                                                                      5 cataattataattataattatatataatactgaaaccatggtgcccctgctgctttacatg
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
Score 44; DB 6; Length 40917;
Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 41008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Indels
                                                                                                                                                                                                                                                                                                                                         PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 6
Pred. No. 0.52;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11. 41008
/organism="unidentified"
/db_xref="taxon:32644"
a 8413 c 8415 g 12398 t
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                       AX033912 41008 bp DNA
Sequence 4 from Patent WO9851790.
AX033912
                                                                                                                                                                                                                                                                                                                                                                                           AX033912.1 GI:10280480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF042484
AF042484.1 GI:4205782
19.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 19.7%;
Best Local Similarity 58.3%;
Matches 77; Conservative
                                   77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 15699 TAGACATAAATA 15710
                                                                                                                                                                                                               125 tgaacatgatta 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 tgaacatgatta 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
Query Match
                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                      RESULT 1
AX033912
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF042484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                            g
                                                                                                                                                                                                                 ŏ
                                                                                                                                        δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 40917)
Cancilla,M.R., Choo,K.H. and Du,S.D.
A novel nucleic acid molecule
Patent: WO 9851790-A 3 19-NOV-1998;
CANCILLA MICHAEL ROBERT (AU); CHOO KONG HONG ANDY (AU); SART
DESIREE DU (AU); ARRAD OPERATIONS PIY LID (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 ataattataattataattataataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 216431;
                                                                                                                                                                                                                                                                                                                                                                                                                              421 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 108;
                                                                                                                                                                    18710. .27338
/note-"assembly_fragment:01738
/note-"assembly_fragment:01738
/note-"assembly_fragment:01150
/note-"assembly_fragment:01150
/note-"assembly_fragment:02306
/note-"assembly_fragment:02306
/note-"assembly_fragment:02306
/note-"assembly_fragment:02306
/note-"assembly_fragment:02306
/note-"assembly_fragment:00386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 19.8%; Score 44.2; DB 2; Local Similarity 50.2%; Pred. No. 0.42; hes 109; Conservative 0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGCCATCAATAAAATATACACAGATATAATCAA 55131
                                              /map="q25.1-31.1"
/clone="RP11-545P21"
/clone_lib="RPC1-11.2"
1. .18609
/note="assembly_fragment:02814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agagtcaaaaacccaaaatcatgaacacccaaactcga 222
                                                                                                                                                                                                                                                                                                                                                                                                        vector_side:right"
| 35565 c 36468 g 73389 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:32644"
8408 c 8383 g 12389 t
/organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX033911 40917 bp DNA
Sequence 3 from Patent WO9851790.
AX0333911
                                                                                                                                                     vector_side:left"
18710. .27338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX033911.1 GI:10280479
                                                                                                                                       clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                             clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .40917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11737 a
                                                                                                                                                                                                                                                                                                                                                                                                                              70588
                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
```

Best Loca Matches

ò

99

ò

g

BASE COUNT ORIGIN

LOCUS DEFINITION ACCESSION VERSION

RESULT 12

AX033911

186

ò

g

õ

55095

qq

ORGANISM

KEYWORDS

SOURCE

AUTHORS TITLE

JOURNAL

REFERENCE

BASE COUNT ORIGIN

source

FEATURES

ö

/rpt_family="MIR" /rpt_type=dispersed complement(88399124) /rpt_family="AluJb" /rpt_family="AluJb" /rpt_family="MIR" /	/standard_name="GAI" /note="82.5% homology" /rpt_type-direct /rpt_unit-(GAAGAAAGG)4 /rpt_type-disect /rpt_family="FRAM" /rpt_type-dispersed	repeat_region /db_xrer=dbEST:AA774571" /db_xrer=11996. /dbandard_name="AT4" /note="100% homology" /rpt_type=tandem	repeat_region complement(1394614235) /rpt_type=dispersed repeat_region /rpt_type=dispersed 1513015159 /rpt_family="Ar-rich" /rpt_family="Ar-rich" /rpt_family="Ar-rich" /rpt_family="Ar-rich" /rpt_family="Ar-rich" /rpt_family="Ar-rich" /rpt_type=direct	repeat_region 15577. 15731 repeat_region 15577. 15731 /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=milly="1.2" /rpt_type=dispersed	/rpt_type-dispersed /rpt_type-dispersed complement(1640716592) /rpt_family="L2" /rpt_family="L2" /rpt_family="MIR" /rpt_family="MIR" /rpt_type-dispersed region 1691416936 /rpt_family="Antrich" /rpt_family="Antrich" /rpt_family="Antrich" /rpt_family="Antrich" /rpt_family="Antrich" /rpt_family="Antrich" /rpt_family="Antrich" /rpt_family="Antrich"
repea repea repea	repea repea	repeat	repeat repeat repeat	repeat, repeat,	repeat_region repeat_region repeat_region
TITLE Sequence analysis of an 80 kb human neocentromere JOURNAL Hum. Mol. Genet. 8 (2), 217-227 (1999) MEDLINE 99135901 PUBBED 9931329 REFERENCE 2 (bases 1 to 80155) AUTHORS Barry, A.E., Howman, E.V., Cancilla, M.R., Saffery, R. and Choo, A. TITLE Direct Submission JOURNAL Submitted (13-JAN-1998) Chromosome Research Unit, The Murdoch Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd., Parkville, Melbourne, Victoria 3052, Australia Source 1. 80155 //organisme*Homo sapiens*	/chromosome="10" /chromosome="	repeat_region /rpt_type=dispersed repeat_region 2558. 2581 /rpt_type=dispersed /rote="100% homology" /rpt_type=direct /rpt_type=direct /rpt_type=direct /rpt_type=dispersed	/note="83.3% homology" /note="83.3% homology" /rpt_type=direct /rpt_unit=(rAACAAAGTG)3 /rpt_family="Alusx" /rpt_family="Alusx" /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_unit=(AAAAAAATAATT)3 repeat_region complement(4546.4848)	repeat_region /rpt_type=dispersed repeat_region complement(59096208) /rpt_tamily="Alusg" /rpt_type=dispersed repeat_region join(62326573,66386688) /rpt_type=dispersed repeat_region 65986645 /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed	repeat_region /rpt_unit=Ac 637 /rpt_unit=Ac 637 /rote="microsatellite" /rpt_type=tendem /rpt_type=tendem /rpt_type=dispersed /rpt_fym=12" /rpt_family="Mr" /rpt_family="La" /rpt

```
The 10q25 neocentromere and its inactive progenitor have identical primary nucleotide sequence: further evidence for epigenetic
                                                                                                                             Direct Submission
Submitted (11-JAN-2000) Chromosome Research Unit, The Murdoch
Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd.,
Parkville,, Melbourne, Victoria 3052, Australia
Genomic sequence from human 10q25.2, clonelib-HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MLT1"
complement(31817. .32352)
/rpt_family="MER1"
complement(32489. .32607)
/rpt_family="MER1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(12428. 12675)
/rpt_family="Alu"
complement(14304. 14583)
/rpt_family="Alu"
17503. 17794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33039. 33316
/rpt_family="Alu"
33469. 33760
/rpt_family="Alu"
complement(34527. 34590)
                                                                                                                                                                                                           Location/Qualifiers
1. 80622
Acganism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(9215. 9490)
/rpt_family="Alu"
complement(11280. 11565)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MLT1"
33039, .3331¢
                                            Genome Res. 10 (6), 832-838 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .20533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .23323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .26342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .24479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ly="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4920. .5181)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                            complement(3. .176)
/rpt_family="Alu"
complement(979. .3564)
                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Tiggerl"
2967. .3094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5625. .6966
/rpt_family="MLT2B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="MER2"
27538. 27814
/rpt_family="Alu"
27891. 28161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'rpt_family="THE1" 17097. .27335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
29063. .29334
                                                                                                                                                                                                                                                                                                                                                                                                                             3664. .3934
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Alu"
complement(31025.
                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family-"Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
complement(20250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alu"
complement(23031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(24301./rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4951. .25250
'rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (25987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (6287
                                                                                                                                                                                                                                                                                            /map="10q25.2"
                                                                                         2 (bases 1 to 80622)
Barry, A.E.
                                                                                                                                                                                                                                                                                                                                                                                             .3094
                                                                                                                                                                                                                                                                                                               /clone="HC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_famil
                                   modification
                                                                                 10854414
                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                 source
                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                              JOURNAL
                                                                MEDLINE
                                                                                   PUBMED
                                               JOURNAL
                                                                                                                                                                                               REMARK
FEATURES
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80622)
Barry,A.E., Bateman,M., Howman,E.V., Cancilla,M.R., Tainton,K.M., Irvine,D.V., Saffery,R. and Choo,K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF222855 80622 bp DNA PRI 17-JUL-2000
Homo sapiens clone HC chromosome 10 map 10q25.2 genomic sequence.
AF222855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.7%; Score 44; DB 9; Length 80155; llarity 58.3%; Pred. No. 0.5; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_type=direct
/rpt_unit=(AATATTACAATAATT)3
complement(22647. .22947)
                                                                                                                               17647. 17702

/rpt_family="MIR"

/rpt_type=dispersed

complement(19863. 20161)

/rpt_family="Alusx"

/rpt_type=dispersed

complement(20842. 20913)

/rpt_family="L2"

/rpt_type=dispersed

/rpt_type=dispersed

/rpt_type=dispersed

/rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                       /note="microsatellite"
/rpt_tvpe=tard...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="low complexity"
/rpt_family="purine-rich"
22409. .22646
/rpt_family="LiM4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(21524. .21646)
           /standard_name="GA2"
/note="81.8% homology"
/rpt_type=direct
17416. 17543
/note="microsatellite"
/rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                             /standard_name="CT1"
/note="75% homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="80% homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_type=dispersed
22560. .22604
                                                                                                                                                                                                                                                                                                                                                                                             /rpt_type=dispersed
complement(21415. ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name="T4"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_type=tandem
/rpt_unit=TGGAA
                                                                                                                                                                                                                                                                                                               /rpt_type=tandem
                                                                                                            /rpt_unit=GAAA
17647. .17702
                                                                                                                                                                                                                                                                                                                            /rpt_unit=GAAA
21375. .21639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF222855.1 GI:9246845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||| | ||
|DD 15343 TAGACATAAATA 15354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 tgaacatgatta 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 77; Conserv
repeat_region
                                                                                                                               repeat_region
                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
AF222855
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
Db
                   qq
                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region complement(73192. 73470)

repeat_region 74086. 74367

repeat_region 75916. 76183

repeat_region 75916. 76183

/rpt_family="Alu"

repeat_region 75916. 76183

/rpt_family="Alu"

/rpt_family="Alu"
/rpt_family="MIR"
34689. 34995
/rpt_family="Alu"
complement(36349. 36437)
/rpt_family="MIR"
complement(38796. 39079)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="LTR12"
59460. 60054
/rpt_family="LTR12"
60349. 60633
/rpt_family="NIR12"
complement(60669. 60801)
/rpt_family="MRR"
complement(6184. 61852)
frpt_family="MRR"
63466. 63753
frpt_family="MRRS"
63466. 63753
/rpt_family="MRRS"
65794. 65883
rpt_family="MRR"
65794. 65883
rpt_family="MRR"
65794. 65883
/rpt_family="MRR"
65794. 65883
/rpt_family="MRR"
65794. 66891
/rpt_family="MRRS"
66772. 66951
                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(50710, 50972)
/rpt_family="Alu"
complement(51031, 51192)
/rpt_family="Li"
complement(51450, 51739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MER41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Alu"
complement(53270, .53562)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family-"LTR12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54808
                          repeat_region
                                                                  repeat_region
                                                                                                          repeat_region
                                                                                                                                                  repeat_region
                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
```

```
15639 TATATATACATAAATATGTATATATGTGTATATAGACATAAATATGTATATGTGTGTATA 15698
                                                                                                                                                                                                                  Search completed: February 25, 2002, 18:02:29 Job time: 18557 sec
                                                                                      | ||||| ||||
|15699 TAGACATAAATA 15710
                                                   125 tgaacatgatta 136
```

0;

DD 15579 CATAAATATACATAAATATGTGTATATAGAGATAAATATGTGTATATGTG 15638

5 cataattataattataattatatatatactgaaaccatggtgccccctgctttacatg 64

ò

Query Match
Best Local Similarity 58.3%; Pred. No. 0.5;
Matches 77; Conservative 0; Mismatches 55; Indels

65 gattctccggctactatttgtatacgtgtatataccgtataatgtacatatttata 124

Oligonucleotide D2 Oligonucleotide D2 Oligonucleotide D1 Oligonucleotide D1 Oligonucleotide D1 Arabidopsis thalla NC-contly derived HC-contly derived Arabidopsis thalla Soybean 318013 reg Soybean 318013 reg

Human genomic DNA Plasmodium falcipa Nucleotide sequenc

Arabidopsis thalia SHOX gene prelimin Human SHOX (short Human CDNA sequenc P.falciparum GBP13 Human genomic DNA Plasmodium falcipa Arabidopsis thalia N. meningitidis pa Soybean 240017 reg Soybean 240017 reg

Human hypocretin r Human hypocretin r Human FSH-beta DNA Human FSH-beta DNA

/ascular endotheli

Human genomic DNA BAC containing rep Nucleotide sequenc

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

08

Minimum | Maximum |

Database

```
MS-B2 elite event; transgenic Brassica plant; transformation event; male-sterility gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Left (3') border flanking region of elite event MS-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to plant DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                 AAH03844
AAH15369
AAQ27886
                                                                                  AAC39525
AAV83940
AAV83939
AAC46330
AAI61373
AAN71222
AAI62927
AAI62927
AAI62937
AAH93297
                                                                                                                                                                                                                                                              AAV35616
AAV35620
                                                                                                                                                                                                                                                                                                                                                        AAI62932
AAH93300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH21613
AAZ43720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..193
/*tag= a
/note="Corresponds t
                                                                                                                                                                                                                                                                                                                                                                                         AAD05774
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS10873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH21613
                                                                                                                                                                                                                                                                                                                                                                                                          AAA81567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "Corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVET ) AVENTIS CROPSCIENCE NV
 AAD06999 standard; DNA; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Agrobacterium sp.
- Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194..416
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15418
168575
168575
                                                                                                                                                                                                                                                 426
15577
32367
                                                                                                                                                                                                                                                                                                                                                                                                                          335913
335913
                                                                                                                                                                                                                                                                                                                                                                                                                                                             41100
101786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6038
7622
2451
                                                                                                                                                          513445
                                                                                                                                                                                                                              50000
WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-2001
                                                                                                                                                                                                                                               40.8
38.8
38.2
37.4
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD06999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD06999
   υυυ
                                                                                                                                                                                                                                                              0000
                                                                                                                                                                                                                                                                                                                                                                                           Ö
                                                                                                                                                                                                                                                                                                                                                                                                                          000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Left (3') border f
Right (5') border
Oligonucleotide D1
Oligonucleotide D1
Oligonucleotide D1
Oligonucleotide D1
Oligonucleotide D1
Oligonucleotide D1
Oligonucleotide D2
Oligonucleotide D2
                                                                                                            February 25, 2002, 18:17:36 ; Search time 716.55 Seconds (Without alignments) 266.811 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                             1 ctaccataattataattata......catgaacacccaaactcgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **Contractory**

**Contractory**

**Contractory**

**SIDSZ/gcddata/geneseqn/Na1980.DAT:*

**SIDSZ/gcddata/geneseqn/Na1981.DAT:*

**SIDSZ/gcddata/geneseqn/Na1991.DAT:*

**SIDSZ/gcddata/geneseqn/Na1991.DAT:*

**SIDSZ/gcddata/geneseqn/Na1991.DAT:*

**SIDSZ/gcddata/geneseqn/Na1991.DAT:*

**SIDSZ/gcddata/geneseqn/geneseqn/Na1991.DAT:*

**SIDSZ/gcddata/geneseqn/geneseqn/geneseqn/Na1991.DAT:*

**SIDSZ/gcddata/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/geneseqn/ge
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                 930621 seqs, 428662619 residues
                                                                                                                                                                             US-09-698-903B-10_COPY_194_416
223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD06997
AAF58238
AAF58252
AAF58254
AAF58254
AAF58257
AAF58259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD06999
                                                                                                                                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1000.0
85.1
222.6
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
222.4
```

189.8 50.4 50.4 50.5 50 50 50 50 50 50 50

6 7 8 8 10 11

Score 223

. 9 Result

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF58238
                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                               The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
                                                                                   Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 tatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaat 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ctaccataattataattataattatatatatactgaaaccatggtgcccctgctgcttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Right (5') border flanking region of elite event MS-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ggtgaagagtcaaaacccaaaatcatgaacacccaaactcgat 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 223; DB 22;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 223; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /+tag- a
/note= "Corresponds to plant DNA"
235..415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/note= "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                        Claim 11; Page 52; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MS-B2 elite event; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD06997 standard; DNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Agrobacterium sp. Chimeric - Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
    De Beuckeleer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 male-sterility gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..234
                                         WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
  Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD06997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD06997/
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  吕
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A A C A A C A A C A A C A A C A A C A A C A A C A A C A A C A A C A A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A
```

```
The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is right (5') border flanking region of elite event
                                                                                                                               Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ctaccataattataattatatatatatac-tgaaaccatggtgccccctgctgcttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 189.8; DB 22; Length 415;
Pred. No. 1.1e-40;
0; Mismatches 2; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 tggtgaagagtcaaaacccaaaatcatgaacacccaa 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 51; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                               (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                              85.1%;
99US-0430497
                                                                   Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Standard; DNA; 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide D1250:D1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                 De Beuckeleer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200107665-A2.
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2001
                                                               Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF58238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF58238
```

'n

```
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                      The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                               Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF58252 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2000; 2000WO-US20476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                  monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                             a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200107665-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF58252;
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Umek RM;
                                                                                                                                                                                                                                                                                                                                                                        Matches
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                      Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                           The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atttctccgctactatttgtatacgtgtatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ataattataattataattatatataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 244 BP; 19 A; 9 C; 12 G; 10 T; 194 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.4; DB 22;
Pred. No. 0.0002;
6; Mismatches 62;
                                                                                                                                                                                                      Example 4; Page 120; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CLIN-) CLINICAL MICRO SENSORS INC.
(CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.6%; Soilarity 6.0%; Pre-
Conservative 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agagtcaaaacccaaaatca 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF58252 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                                                                      monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electron-transfer group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression; ss.
                                                                               WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-159728/16
                                                                                                                                                                 a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200107665-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF58252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jmek RM;
                                      Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AAF58252
```

g

셤

ð

8 ò

ò

```
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                              66 atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                        75 иничиничиничиничиничиничиничиничиничичичичичичичичичичичи 134
                                                                                                                                                                                                  126 gaacatgattaatgcttgttgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                            Gaps
                                                                                                                    74
                                                                                          6 ataattataattataattatatatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                    ö
                                      Length 936;
                                                                 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Electron-transfer group; ETM; mismatch; genotyping;
Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                       DB 22;
                                    22.4%; Score 50; DB 22;
illarity 1.0%; Pred. No. 0.00033;
Conservative 141; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 127; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                      186 agagtcaaaacccaaaatcatgaa 209
```

4

ö

Length 936;

) DB 22; 0.00033;

Score 50;

22.48;

Query Match

Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

x og

```
ö
                     two nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                      atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 gaacatgattaatgottgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 МИМИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИМИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИНИМИН
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) monitoring gene expression.
The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 6 ataattataattataattatataaatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                            Length 936;
                                                                                                                                                                                                                                                                                                                                                                61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                          Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                   Query Match 22.4%; Score 50; DB 22; Best Local Similarity 1.0%; Pred. No. 0.00033; Matches 2; Conservative 141; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 agagtcaaaacccaaaatcatgaa 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF58254 standard; DNA; 936 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         559 ИМИМИМИМИМИМИМИМИМИМИМИ
                                                                                                                                                   monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0145695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide D1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200107665-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF58254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF58254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
   88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

```
66 atttctccgctactatttgtatacgtgtatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                    126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggga 185
                  Gaps
                                                                                                                                                             The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nuclectide polymorphisms, e.g. for genotyping,
                                    6 ataattataattataattatataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 936;
               Indels
                                                                                                                                                                                                                                                                                                                                                                            ETM; mismatch; genotyping;
               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 22;
Pred. No. 0.00033;
 larity 1.0%; Pred. No. 0.000 Conservative 141; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                      186 agagtcaaaacccaaaatcatgaa 209
                                                                                                                                                                                                            195 WGWWWWWWWWWWWWWW 218
                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                       AAF58254 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.48;
1.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0145695
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monitoring gene expression
                                                                                                                                                                                                                                                                                                                                                                      Electron-transfer group;
                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide D1875
                                                                                                                                                                                                                                                                                                                                                                                      gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-159728/16
Local Similarity
tes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200107665-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2001
                                                                                                                                                                                                                                                                                                                       24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                 AAF58254:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Umek RM;
                                                                                                                                                                                                                                                              AAF58254/C
           Matches
                                                                                                                                                                                                                                                                       g
                                                                                                           g
                                     ð
                                                                                   á
                                                                                                                                  à
                                                                                                                                                          g
                                                                                                                                                                                    ŏ
                                                                                                                                                                                                           D
```

S

```
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    attrotcogotactatttgtatacgtgtatatatatacogtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
  66 atttetteegetaetatttgtataegtgtatatataecegtataatgtaeatatatttatat 125
                                                                     The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                     126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga
                           ataattataattataattataataatactgaaaaccatggtgccccctgctgctttacatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                           Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.4%; Score 50; DB 22; 1.0%; Pred. No. 0.00033; ive 141; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                         195 wgwwwwwwwwwwwwwwwwww 218
                                                                                                        186 agagtcaaaacccaaaatcatgaa 209
                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 141;
                                                                                                                                                                                                    AAF58257 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2000; 2000WO-US20476
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monitoring gene expression.
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                  Oligonucleotide D1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a single surface
                                                                                                                                                                                                                                                                                                                                                                            WO200107665-A2
                                                                                                                                                                                                                                                        24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                              AAF58257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                       AAF58257,
                          g
                                                                           Ω
                                                                                                       δλ
                                                                                                                                g
                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
  δ
                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         group, useful as labels in allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                              atttotocogotaotatttgtatacogtgtatatatatocogtataatgtacatatattttatat 125
                                                                                                                                126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ataattataaattataattatataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 ataattataattataattatataatactgaaaccatggtgccccctgctgctttacatgg
                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 936;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                        Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.4%; Score 50; DB 22;
1.0%; Pred. No. 0.00033;
tive 141; Mismatches 61
 Conservative 141; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                      WWWWWWWWWWWWW 536
                                                                                                                                                                                    186 agagtcaaaacccaaaatcatgaa 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 141;
                                                                                                                                                                                                                                                                               AAF58257 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide D1954
                                                                                                                                                                                                                                                                                                                                                                                                      gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 936 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200107665-A2
                                                                                                                                                                                                                                                                                                                                    24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2001
5
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                          AAF58257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Umek RM;
                                                                                                                                                                                                                                                        œ
                                                                                                                                                                                                               559
                                                                             99
                                                    739
Matches
                                                                                                                                                                                                                                                       RESULT
AAF58257
                                                                                                    Q
                                                                                                                                                                                                                                                                                               g
                                                                           ò
                                                                                                                                ò
                                                                                                                                                         a
                                                                                                                                                                                   ò
                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

ó

a à

```
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 gaacatgattaatgettgtgagttgtteteateegtaagagttteaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ataattataattataaattatataatactgaaaccatggtgccccctgctgctttacatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 atttotccgctactatttgtatacgtgtatatataccgtataatgtacatatttatat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.4%; Score 50; DB 22;
Best Local Similarity 1.0%; Pred. No. 0.00033;
Matches 2; Conservative 141; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 agagtcaaaacccaaaatcatgaa 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WWWWWWWWWWWWWWWW 536
                                                               AAF58259 standard; DNA; 936 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF58262 standard; DNA; 936 BP.
                                                                                                                                                                                                                                                                                                                                   26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monitoring gene expression.
                                                                                                                              (first entry)
                                                                                                                                                            Oligonucleotide D2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single surface
                                                                                                                                                                                                                                                                     WO200107665-A2.
                                                                                                                              24-APR-2001
                                                                                                                                                                                                                                                                                                   01-FEB-2001
                                                                                                                                                                                                                                         Synthetic.
                                                                                               AAF58259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF58262;
                                                AAF58259/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF58262
ID AAF5
XX
AC AAF5
                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 atttotocgotactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ataattataaattataattatatataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.4%; Score 50; DB 22; Length 936; Loarity 1.0%; Pred. No. 0.00033; Conservative 141; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                    Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CLIN-) CLINICAL MICRO SENSORS INC.
                               186 agagtcaaaacccaaaatcatgaa 209
                                                   559 WWWWWWWWWWWWWWWWWWWWW 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agagtcasascccasastcatgas 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                        AAF58259 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2000; 2000WO-US20476
                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                       Oligonucleotide D2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 2; Conserva
                                                                                                                                                                                                                                                                                                                                               WO200107665-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-1999;
                                                                                                                                                                                                      24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2001
                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                        AAF58259;
```

Umek RM;

à 8

g à

à 셤 à

RESULT 1
AAF58259
ID AAF58259
XX
XX
XX
DT 24-A
DT 24-A
DY 24-A

ö

Length 936; 61; Indels

```
Oligonucleotide D1876.
    gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-159728/16
                                                                                WO200107665-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200107665-A2
                                                                                                                         01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF58255;
                                                                                                                                                                                                                                                                                                                Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF58255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ataattataaattataattataataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Indels
                                                                                                    Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 50; DB 22; ilarity 1.0%; Pred. No. 0.00033; Conservative 141; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 128; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                               (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 wgwwwwwwwwwww 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 agagtcaaaacccaaaatcatqaa 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF58262/C
ID AAF58262 standard; DNA; 936 BP.
                                                                                                                                                                                                                                                                                        26-JUL-2000; 2000WO-US20476
                                                                                                                                                                                                                                                                                                                                  26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                          Oligonucleotide D2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide D2007
                                                                                                                         gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single surface
                                                                                                                                                                                                      WO200107665-A2.
                                                                                                                                                                                                                                                                                                                               26-JUL-1999;
                   24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-APR-2001
                                                                                                                                                                                                                                                 01-FEB-2001
                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF58262;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Umek RM;
NAME OF THE PROOF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
```

```
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 ataattataattataattatataatactgaaaccatggtgccccctgctgctttacatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 22; Length 936;
Pred. No. 0.00033;
11; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 128; 159pp; English.
                                                                                                                                                                    (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 agagtcaaaacccaaaatcatgaa 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ИМИМИМИМИМИМИМИМИМИМ 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.4%; Sc
Best Local Similarity 1.0%; Pre
Matches 2; Conservative 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF58255 standard; DNA; 938
26-JUL-2000; 2000WO-US20476
                                                                  26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2001 (first entry)
```

```
Search completed: February 25, 2002, 18:17:38 Job time: 16696 sec
                                        Umek RM;
                                                                                                                                                                                                                                                                                                                                 619
                                                                                                                                                                                                                                                                                                                                                    126
                                                                                                                                                                                                                                                                                                                                                                                         186
                                                                                                                                                                                                                                                                                                                                                                                                           559
            ð
                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                        Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
                                                                                                                                                                               The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nuclectide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                           66 atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                               126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttccaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                             6 ataattataaattataaattatatataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                       Length 938;
                                                                                                                                                                                                                                                                                                        61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                    Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                  22.4%; Score 50; DB 22; 1.0%; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                    Conservative 141; Mismatches
                                                                                                                                                              Example 6; Page 127; 159pp; English.
                                                                 (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    186 agagtcaaaacccaaaatcatgaa 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 Wgwwwwwwwwwwwww
                  26-JUL-2000; 2000WO-US20476.
                                    26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1255/c
AAF58255 standard; DNA; 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-1999; 99US-0145695,
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide D1876.
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Thes 2; Conserva
                                                                                                      WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200107665-A2.
 01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2001
                                                                                    Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF58255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
```

```
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                  The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 atttotocgotactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 ataattataattataattatataatactgaaaccatggtgcccctgctgctttacatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 22.4%; Score 50; DB 22; Best Local Similarity 1.0%; Pred. No. 0.00033; Matches 2; Conservative 141; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                     Example 6; Page 127; 159pp; English.
(CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agagtcaaaacccaaaatcatgaa 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-159728/16
                                                                                                                                                                                             a single surface
```

THIS PAGE BLANK (USP. L.

l, App Appli Appli Appli Appli Appli Appli

Appl

Appli Appli Appli Appli Appli Appli Appli Appli

OM nucleic

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result Š. 2002210084987658465846584

00000

000

0000

Searched:

```
Db 15314 cataaatatatacataaatatgtatatatgtgtatatagacataaatatgtatatatgtg 15373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 15374 tatatatacataaatatgtatatatgtgtatatagacataaatatgtatatatgtgtata 15433
                      sequence 14, Appsequence 7, Appsequence 9, Appsequence 9, Appsequence 113, Appsequence 11, Appsequence 30, Appsequence 30, Appsequence 6, Appsequence 5, Appsequence 5, Appsequence 11, Appsequence 5, Appsequence 11, Appsequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gattictccgctactatttgtatacgtgtatatataccgtataatgtacatatattata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 cataattataattataatatatataatactgaaaccatggtgcccctgctgctttacatg
      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 80246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-078-294-4

Sequence 4, Application US/09078294

Sequence 4, Application US/09078294

Patent No. 626211

GENERAL INFORMATION:

APPLICANT: Choo, Kong-Hong Andy

APPLICANT: Cancilla, Michael R.

TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE

FILE REFERENCE: Davies Col

CURRENT APPLICATION UNDER: US/09/078,294

CURRENT FILNG DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-078-294-3
Sequence 3, Application US/09078294
Fatent No. 6265211
GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFRENCES: Davies Col.
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 4; Ler
Pred. No. 0.0015;
US-08-874-563-5
US-08-577-483-14
US-08-577-483-14
US-08-480-604A-9
US-08-405-496A-9
US-08-947-823-1
US-08-947-823-1
US-08-947-823-1
US-08-947-823-1
US-08-947-823-1
US-08-947-823-1
US-08-947-823-1
US-08-947-823-1
US-08-947-823-1
US-08-120-629-9
US-08-031-538-5
US-08-916-5595-1
US-08-916-5595-1
US-08-916-5595-1
US-08-916-5595-1
US-08-916-5595-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
) ORGANISM: Nucleotide sequence of NC-contig
US-09-078-294-4
                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.7%;
nilarity 58.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
    125 tgaacatgatta 136
| | ||| | ||
15434 tagacataaata 15445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 80246
    SEQ ID NO 4
                                                                                                                                                                                                                   00000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
    Q
    000000 00
                                                                                                                                                                                                                                                                   Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                        (without alignments)
167.456 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1, Appli
12, Appl
3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2, Appli
4, Appli
4, Appli
5312912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                 1 ctaccataattataattata......catgaacacccaaactcgat 223
                                                                                                                                                    February 25, 2002, 18:05:29; Search time 301.6 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sednence sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-078-294-3
US-09-305-639-4
US-09-305-639-1
US-08-006-082A-4
US-08-006-082A-1
US-09-058-947A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-487-826B-13
US-09-383-630-1
US-09-383-630-2
US-08-282-581-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-383-756-3
US-08-460-898-3
US-09-058-947A-1
US-08-947-823-1
US-08-443-639-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-550-544-4
US-08-817-188-3
US-08-874-186-42
US-08-104-072B-6
US-08-351-413-7
US-09-025-583-7
                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-446-855A-1
US-09-150-741-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-550-544-4
5312912-3
                                                                                                                                                                                                                                                                                                                                                                                            351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-282-581-4
                                                                                                                                                                                                                                        US-09-698-903B-10_COPY_194_416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80246
80595
76238
76238
1160
11264
1951
1983
3725
4254
8920
8920
480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1601
2799
3627
3627
3627
3627
19124
5993
5993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322...8
322...8
322...8
322...8
322...8
323...8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                               Scoring table:
```

ö

Gaps

```
APPLICANT: Selden, Richard F
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REFERENCE: 07236/016001
CURRENT APPLICATION NUMBER: US/09/305,639
EARLIER APPLICATION NUMBER: 60/084,663
EARLIER FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 7622
                                                                                                                                                                                                                                                                                                                                                                               117 tatttatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatg 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPINITY: USAN
ZUP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 7.0.
SOFTWARE: Microsoft Word Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/006,082A
FILING DATE: 19-TAN-1993
CLASSIFICATION: 800
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

14.9%; Score 33.2; DB

Best Local Similarity 55.1%; Pred. No. 0.65;

Matches 65; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                              Score 34.6; DE
Pred. No. 0.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROBINSON ET AL.
TITLE OF INVENTION: TRANSGENIC MAMMALS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: Amgen Center
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08006082A Patent No. 5489743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1160 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single stranded
                                                                                                                                                                                                                                                                                                       Query Match 15.5%;
Best Local Similarity 53.3%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 taatggtgaagagtcaa 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 TATTTTTGAGACAGAA 346
                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-08-006-082A-4
                                                                                                                                                                                                                                        ; ORGANISM: HC
US-09-305-639-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                 á
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-305-639-4/c

i Sequence 4, Application US/09305639

patent No. 6200778

GENERAL INFORMATION:
APPLICANT: Traco, Douglas A.
APPLICANT: Selden, Richard F.
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
CURRENT APPLICATION NUMBER: US/09/305,639

CURRENT APPLICATION NUMBER: 05/084,663

EARLIER APPLICATION NUMBER: 60/084,663

EARLIER PILING DATE: 1998-05-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FASTEEQ for Windows Version 3.0
                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                         Db 15579 catamatmatmacatmamatmatgtmatmatmagacmamamatmatgtmatmatmagacmamamatmatgtg 15638
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 cataattataattataattatataatactgaaaccatggtgccccctgctgcttacatg 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tatttatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatg 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.5%; Score 34.6; DB 4; Length 6038; 53.3%; Pred. No. 0.38; tive 0; Mismatches 64; Indels 0
                                                                                                                                                              Query Match
Best Local Similarity 58.3%; Pred. No. 0.0015;
Matches 77; Conservative 0; Mismatches 55; Indels
                                                                                         ; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09305639
Patent No. 6200778
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 taatggtgaagagtcaa 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATTTTTGAGACAGAA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.5
Best Local Similarity 53.3
Matches 73; Conservative
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2,
SEQ ID NO 3
LENGTH: 80595
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                   Db 15699 tagacataaata 15710
                                                                                                                                                                                                                                                                                                                                                                                   125 tgaacatgatta 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-305-639-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-305-639-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 6038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362
                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

ó

```
121 tatatgaacatga--ttaatgcttgtgagttgttctcatccgtaagagtttcaatatgta 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 catggatttctccgctactatttgtatacgtgtatataccgtataatgtacatatatt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            892 CGTGAAAATCAGAGAAATTATAGGTATACATATATATTCGGGTTTAAATGTCGATACATG 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08383756
Patent No. 5654495
GENERAL INFORMATION:
APPLICANT: Dehesh, Katayoon
APPLICANT: Hawkins, Deborah
APPLICANT: Hawkins, Deborah
APPLICANT: Davies, Huw Maelor
TITLE OF INVENTION: Production of Myristate in Plant Cells
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32.8; DB 4;
Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh 7.0
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,756
FILING DATE: 02-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 5493-50032/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
MEDIUM TYPE: Disk, 3.5-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Word97 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,947A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/043,831
FILING DATE: APFLI 14, 1997
ATTORNEY/AGENT INFORMATION:
NAME: DAVID J. EARP, Ph.D.
REGISTRATION NUMBER: 41,401
PRESENTATION NUMBER: 41,401
PRESENTATION NUMBER: 41,401
PRESENTATION NUMBER: 41,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 atggtgaagagtcaaaacccaaaatc 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/261,695
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Calgene, Inc.
1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.23
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1920
CITY: Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-383-756-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-058-947A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09058947A
Patent No. 6274790
GENERAL INFORMATION:
APPLICANT: Kunst et al.
TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
TITLE OF INVENTION: Involved in Very Long Chain Fatty Acid Synthesis
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston, LLP
STREET: One World Trade Center, Suite
STREET: 1600, 121 S.W. Salmon Street
  49 cotgotgotttacatggatttotcogotactatttgtatacgtgtatatatacgtataa 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 tgtacatatatttatatgaacatgattaatgcttgtgagttgttctcatccgtaagag 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 tgtacatatatttatatgaacatgattaatgcttgtgagttgttctcatccgtaagag 166
                                                                     14.9%; Score 33.2; DB 1; Length 1264; 55.1%; Pred. No. 0.66; Live 0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Macintosh OS 7.0. SOFTWARE: Microsoft Word Version 5.1a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               APPLICANT: ROBINSON ET AL.
TITLE OF INVENTION: TRANSGENIC MAMMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/006,082A FILING DATE: 19-JAN-1993
                                                                                                                                                                                                 Sequence 1, Application US/08006082A Patent No. 5489743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                STREET: Amgen Center
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1264 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-JAN-1993
CLASSIFICATION: 800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 55.1
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
2IP: 97204-2988
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LITY: Portland STATE: OP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-058-947A-12/C
                                                                                                                                                                          US-08-006-082A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
```

ï

Length 1951;

62; Indels

```
109 igtacatatatttatatgaacatgattaatgctigtgagtigtictcatccgtaagagti 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Kunst et al.

APPLICANT: Kunst et al.

TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis

TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis

TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis

NUMBER OF SEQUENCES: 12

CORRESPEDINGE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell

ADDRESSEE: Leigh & Whinston, LLP

STREET: One World Trade Center, Suite

STREET: 1600, 121 S.W. Salmon Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32.8; DB 2; Length 1983;
Pred. No. 0.95;
0; Mismatches 57; Indels n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Indels
                                                                                                                                                  CLASSIFLCATION: 4.5.

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/261,695

CLASSIFICATION DATA:
FILING DATE: 16-JUN-94

CLASSIFICATION DATA:
FILING DATE: 29-CAT-93

CLASSIFICATION DATA:
FILING DATE: 30-CAT-92

ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,845

ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,845

NAME: Elizabeth Lassen

REGISTRATION NUMBER: 34,719

NAME: Carl J. Schwedler

REGISTRATION NUMBER: 34,719

NAME: Carl J. Schwedler

REGISTRATION NUMBER: 36,924

REGISTRATION NUMBER: 36,924

REGISTRATION NUMBER: 36,924

REGISTRATION NUMBER: 36,924

RELEPRONCE/DOCKET NUMBER: 36,924

RELEPRONCE/DOCKET NUMBER: 36,924

RELEPRONCE/DOCKET NUMBER: 36,924

RELEPRONCE/POCKET NUMBER: 36,924

REGISTRATION NUMBER: 36,924

RELEPRONCE/POCKET NUMBER: 36,924

REGISTRATION NUMBER: 36,934

REGISTRATION NUMBER: 36,934

REGISTRATION NUMBER: 36,934

REGISTRATION NUMBER: 36,934

REGISTRATION NUMBER: 37,719
                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,756
FILING DATE: 02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-058-947A-1/c
; Sequence 1, Application US/09058947A
; Patent No. 6274790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
US-08-460-898-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.7%;
Best Local Similarity 54.0%;
Matches 67; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Portland
SPATE: OR
COUNTR: USA
ZIP: 97204-2988
COMPUTER READABLE FORM:
                                                                                                                   FILING DATE: 02 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1598 TCAA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 tcaa 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 tgtacatatatttatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtt 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08460898
Patent No. 5850022
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Debesh, Katayoon
APPLICANT: Uoalker, Toni Alois
APPLICANT: Bavkins, Deborah
APPLICANT: Bavkins, Deborah
APPLICANT: Bavies, Huw Maelor
TITLE OF INVENTION: Production of Myristate in Plant Cells
CORRESSONDENCES: 17
CORRESSONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

14.7%; Score 32.8; DB 1; Length 1983;
Best Local Similarity 54.0%; Pred. No. 0.95;
Matches 67; Conservative 0; Mismatches 57; Indels 0;
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10814
FILING DATE: 29-OCT-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-OCT-92
ATTORNEY/ACENT INFORMATION:
RABEISTRATION NUMBER: 31,845
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 36,924
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
ELNGTH: 1983 base pairs
TUDES: TELEGISTRATICS:
LENGTH: 1983 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB COMPUTER: Apple Macintosh OPREATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1(a) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,898 FILING DATE: 05-UJN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
HOLECULE TYPE: CDNA to mRNA
US-08-383-756-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1598 TCAA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 tcaa 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-460-898-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

Gaps

```
APPLICATION NUMBER: PCT/US97/18802 FILING DATE: 09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 aagagtcaaaacccaaaatcat 206
      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-443-639-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 tatatgaacatga--ttaatgcttgtgagttgttctcatccgtaagagtttcaatatgta 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832 TATATCTACAAGAGTTACATGTTTTGTTATTTACATTCGCAATTAATGTTTCTTTTTTGC 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08947823
Fatent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isgouhi
APPLICANT: Kaloshian, Jafar
APPLICANT: Radoobi, Jafar
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.7%; Score 32.8; DB 4; Length 3722; 56.2%; Pred. No. 1.1; tive 0; Mismatches 62; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/043,831
FILING DATE: APTIL 14, 1997
ATTORNEY/AGENT INFORMATION:
NAME: David J. Earp, Ph.D.
REGISTRATION NUMBER: 41,403
REFERENCE/DOCKET NUMBER: 5493-50032/DJE
TELEFONDWINICATION INFORMATION:
TELEFOND: (503) 228-9446
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
MEDIUM TYPE: Disk, 3.5-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Word97 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,947A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/947,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-947-823-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 13606 CATTCTAACGTATCTATAAAATTCACATGAAACACACGGGTGTGAAGGGCATCCTCAGAAA 13665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 13726 TATATATATATATATATATATATTCTTATTAAAAAAGAATGTCCTTATTTCATTTT 13785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 gattteteegetaetatttgtataegtgtatatatataecgtataaatgtaeatatatttata 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 tgaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtg 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 cataattataattataattataataatactgaaaccatggtgcccctgctgctttacatg 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08443639

Batent No. 5981843

GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Yin, Shaohui
APPLICANT: Carnett, Catherine A.G.
TITLE OF INVENTION: Transcriptional Control Sequences and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.5%; Score 32.4; DB 3; Length 5
Best Local Similarity 47.5%; Pred. No. 2.6;
Matches 96; Conservative 0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,639
FILING DATE: 18-MAY-1995
CLASSIFICATION: 800
                                                                                                                     REGISTRATION NUMBER: 34.774
REGISTRATION NUMBER: 34.774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMULICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 31952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WILECULE TYPE: DNA (genomic)
US-08-947-823-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13786 AATCTGGTTAAAAAAAAATAAT 13807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
```

```
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-150-741-1/c
                                                                                                                                                                              ; MOLECULE IN
US-08-446-855A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 8920
                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ctccgctactatttgtatacgtgtatatataccgtataatgtacatatttatatgaac 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 ttataattataattatataatactgaaaccatggtgccccctgctgctttacatggattt 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 atgattaatgettgtgagttgtteteategtaagagttteaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stewart, Thomas S
APPLICANT: Stewart, Thomas S
APPLICANT: Stewart, Thomas S
APPLICANT: Stewart, Thomas S
APPLICANT: COSULIVAN, WILLIAM J
TITLE OF INVENTION: WILLIAM J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: Nosphate Synthetase II
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 NO. 5849573th Glebe Road, 8th Floor
GITY: Arlington
STATE: Virginia
COMPUTR: USA
ZIP: 22201-4714
COMPUTR: IBM PC COMPATION
SOPTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: OS-DOS/MS-DOS
SOFTWARE: PATENTING NATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
GLASSIFICANTON: 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 2; Length 4254;
Pred. No. 1.9;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                           Join(1217..1327, 1455..1718, 1806..2182,
2259
...2477, 2609..2747, 2903..3148, 3262..3558)
            REFERENCE/DOCKET NUMBER: 69-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
VS-08-446-855A-1/C
VS-08-446-855A-1/C
Sequence 1, Application US/08446855A
Patent No. 5849573
CENERAL INFORMATION
APPLICANT: Stewart, Thomas S
                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Nicotiana tabacum
REGISTRATION NUMBER: 33878
                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
HYBOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 48.9%;
Matches 86; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
; LOCATION:
; LOCATION:
US-08-443-639-7
                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                  8484 TACTITICATGITGITATGGAATGAAGTTAATAATACATAATAATAAGTAATGITAAATC 8425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 actatttgtatacgtgtatatataccgtataatgtacatatatttatatgaacatgatta 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 atgettgtgagttgtteteatecgtaagagttteaatatgtaatggtgaagagteaaae 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8484 TACTITICATGITGITATGGAATGAAAGTTAATAATACATAAATAAGTAAGTAATGTTAAATC 8425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 actatttgtatacgtgtatatataccgtataatgtacatatatttatatgaacatgatta 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 atgottgtgagttgttotcatccgtaagagtttcaatatgtaatggtgaagagtcaaaac 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                              DB 2; Length 8920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 8920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-282-581-4
Sequence 4, Application US/08282581
Sequence 4, Application US/08282581
Sequence 4, Application US/08282581
SERENT NO INFORMATION:
APPLICANT: Cramer, Carole L.
APPLICANT: Weissenborn, Deborah L.
TITLE OF INVENTION: HMG2 PROMOTER EXPRESSION SYSTEM AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Indels
                                                                                                                                                                                                                                                                      Score 32; DB 2
Pred. No. 2.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 4; Pred. No. 2.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-05
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09150741
Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
                                                                                                                                                                                                                                                                 Query Match 14.3%;
Best Local Similarity 54.2%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
14.3%;
Best Local Similarity 54.2%;
Matches 65; Conservative (
                                                                    LENGTH: 8920 base pair:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
TITLE OF INVENTION: POST-HARVEST PRODUCTION OF GENE PRODUCTS
TITLE OF INVENTION: IN PLANTS AND PLANT CELL CULTURES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: 1155 Avenue of the Americas
TITY: New York
COUNTRY: 10.36.2711
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAPCICATION NATA:
COMPUTER: PATENTION ROPES: 129.40.69.60
FILING DATE: 29-JUL-1994
CLASSIFTCATION: 800
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 7956-009
TELECOMMUNICATION INFORMATION:
TELEBANS: 212-86-8864/9741
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 base pairs
TTPE: Nucleic acid
STRANDENDESS: double
TYPE: Nucleic acid
STRANDENDESS: double
TYPE: Nucleic acid
STRANDENDESS: double
TYPE: Name/KEV: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
14.1%; Score 31.4; DB 1; Length 480;
Best Local Similarity 61.7%; Pred. No. 1.7;
Matches 50; Conservative 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: modified_base
LOCATION: 162
OTHER INFORMATION: /label= n
OTHER INFORMATION: /note= "n=x=Unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /label- n
CTHER INFORMATION: /note= "n=x=Unknown nucleotide"
US-08-282-581-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: modified_base
LOCATION: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

g

110 gtacatatattatatgaaca 130 || || || || || || || || 286 ATATATATATATAAAAA 306

ò

Search completed: February 25, 2002, 18:05:49 Job time: 18597 sec

THIS PAGE BLANK (USPTO)

HS_2272_A UI-M-CG0p

AQ745537 BF460992

AA394343

1M0181L12

BG836222 BH040914

3086_A

RPCI-11-3 GM02540.3 038PbG10 nbeb0056M

BG633595 BF296565 AQ915359

AW941790 BH126294

AL069970 AQ542682

Tetraodon RPCI-23-2

AL268414 AZ698385

Tetraodon Drosophi] BARC-Sat_ HS_5268_A BARC-Sat_ AU087788

AQ818698 BH126267

HS_5342_B MB3D6V1G0

AU087788 AZ013131 AQ561057 AA547848

BARC-Satt ws10a07.x 2M0181N19

AZ640886 AQ367613 BH126635 AI991410 AZ869448

HS_3154_A 1M0503E11

1M0084E22

OM nucleic

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

0 0

000000

U

Searched:

```
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[ (pases 1 to 507)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA605352 507 bp mRNA EST 29-SEP-1997
30388 Lambda-PRLZ Arabidopsis thaliana cDNA clone 269H8T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Thomas Newman
MSU-DOB Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.

    .507
        — Arabidopsis thaliana"
        /strain="var columbia"
        /db_xref="taxon:3702"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                           AU087788
AO5613131
AO561057
AA547848
AZ060650
AZ347990
AZ34790
AZ3470
AZ3470
AZ3470
AZ3470
AZ
                                                                                                                                                                                  CNSOODGO
AQ542682
BG633595
BF296565
AQ915359
AW941790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualiflers
                              AQ745537
BF460992
                                                                                                                                                                                                                                                                                              18698
                                                                                                                                                                                                                                                                                              A081
BH12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:2445880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thale cress.
Arabidopsis thaliana
   Tel: 517-353-0854
                                                                                                                                                                                                                  511
610
7640
834
834
453
596
596
563
604
514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA605352.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lansing, Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sednence
44.00.4
44.00.2
44.00.2
339.8
339.8
339.6
339.2
339.2
339.2
339.2
339.2
                                                                                                                                                                                                                                                                              338.0
338.0
338.0
338.0
388.0
388.0
388.0
388.0
388.0
388.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.8
37.8
37.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA605352/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU087926
AU088152
HS_3179_B
nbxb0030P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPCI-23-1
OSJNBD007
HS_2161_B
2M0282F21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UI-M-BH3-
Tetraodon
                                                                                                    February 25, 2002, 17:21:10 ; Search time 8261.74 Seconds (without alignments) 290.049 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA605352 30388 Lam
AU088482 AU088482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                  ctaccataattataattata......catgaacacccaaactcgat 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU088482
BE948306
AL222093
AU088152
AQ172252
AQ172252
AQ172252
AQ172252
AQ172572
AZ126726
AZ126726
AZ126726
AZ126726
                                                                                                                                                                                                                                                                                                             22703874
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                              11351937 segs, 5372889281 residues
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                     US-09-698-903B-10_COPY_194_416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE948306
CNS030D0
AU087926
AU088152
AQ172252
AQ273686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ126726
AQ797772
AZ996260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA605352
AU088482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ119444
                                                                                                                                                                                                                             IDENTITY_NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Π
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_gss_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_gss_hum:*
em_gss_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_gss_fun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_estfun:*
em_esthum:*
em_estin:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est1:*
gb_est2:*
gb_htc:*
gb_gss:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_estom:*
em_estpl:*
em_estba:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_estov:*
em_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368
465
1024
487
500
527
599
711
789
605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.4
119.9
118.8
118.7
118.7
118.7
118.7
118.7
118.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112.
112.
112.
112.
113.
113.
113.
113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                Scoring table:
```

```
Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                      BE948306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                               q
                                                                                                                                                                                                                                                          셤
                                                                                                                                         à
                                                                                                                                                                            a
                                                                                                                                                                                                                  οy
                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                     g
Colone_1b="Leanbda-PRL2"

/clone_1lb="Leanbda-PRL2"

/clone_1lb="Leanbda-PRL2"

/clone_1lb="Leanbda Zip-Lox; Site_1: Sal; Site_2: Not;

Lanbda PRL2 is a cDNA library derived from equal

day germinated etiolated seedlings; 2) tissue culture

grown roots; 3) staged plants half with 24 hour light

grown roots; 3) staged plants half with 24 hour light

grobe, half on 16 hr light, 8 hour dark-rosettes; 4)

same plants as 3 but aerial tissue (stems, flowers and

slilques. The vector is BRL's lambda Zip-Lox. The cDNA

lisserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria parasite P. falciparum.

SM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

E (bases 1 to 368)

SWatanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.

FULL-malaria: a database for a full-length enriched cDNA library

E 70574754

LOCOLEC Acids Res. 29 (1), 70-71 (2001)

E 20574754

CONTACT: Junich! Watanabe

Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan

Fax: 81-3-5449-5378

Fax: 81-3-5449-5410
                                                                                                                                                                                                                                                                                                                                                         ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: jwatenabdenage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU088482 368 bp mRNA EST 27-JAN-2001
AU088482 Sugano Malaria cDNA library Plasmodium falciparum cDNA
clone XPFn7177, mRNA seguence.
                                                                                                                                                                                                                                                                                                                                                                                  93 tatatataccgtataatgtacatatatttatatgaacatgattaatgcttgtgagttgtt 152
                                                                                                                                                                                                                                                                                                                                                                                                           276 ATCTCCATAGAGTTGCCAATATGTCAATGGTGAACAGTCAAAACCCAAAATCATGAACAC 217
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 ctcatccgtaagagtttcaatatgtaatggtgaagagtcaaaacccaaaatcatgaacac
                                                                                                                                                                                                                                                                                                                  Length 507;
                                                                                                                                                                                                                                   19 others
                                                                                                                                                                                                                                                                                                                                                     49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lone_lib="Sugano Malaria cDNA library"
                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .368
/organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="erythrocytic stage"
28 c 37 g 152 t
                                                                                                                                                                                                                                                                                                            Score 45.6; DB
Pred. No. 0.23;
0; Mismatches
                                                                                                                                                                                                                              144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5833"
/clone="XPFn7177"
                                                                                                                                                                                                                            112 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU088482.
AU088482.1 GI:12390623
                                                                                                                                                                                                                                                                                                         20.4%;
1 Similarity 60.5%;
75; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="3D7"
                                                                                                                                                                                                                            94 C
                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                              138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 ccaa 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAA 213
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU088482/c
LOCUS
DEFINITION
                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

DB 10; Length 368;

Score 44.4;

Query Match

```
Email: mESTemail.nih.gov
The Sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand CDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the Notl site and the oligo-dr track served to identify it as a clone from the cerebellum tissue CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BNAP CDNA clones from RESEANCH SENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BNAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive
                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UI-W-BH3-awp-b-11-0-UI"
/clone="UI-M-BH3-awp-b-11-0-UI"
/dev_stage="10"-10"
/dev_stage="10"-10"-10"
/dev_stage="10"-10"
/dev_stage="10"-10"
/dev_stage="10"-10"
/dev_stage="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases 1 to 465)

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE948306 465 bp mRNA EST 03-OCT-2000 UI-M-BH3-awp-b-11-0-UI.sl NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-awp-b-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 tttatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttccatatgta 178
                                                                                                                                                                                                                                           62 atggatttctccgctactatttgtatacgtgtatatataccgtata---atgtacatata 118
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                            2 taccataattataattataattatatataatactgaaaccatggtgccccctgctgctttac 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TITITIAAAATTTTTAATTTTTTTATGTTTTCGTACCCTATATTTTAT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                   .,
m
                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 atggtgaagagtcaaaacccaaaatcatgaacaccc 214
Pred. No. 0.44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 TTCAATAGATATAAACNCAANATCATATATATCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE948306.1 GI:10526065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13 Forward
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        discovery
```

```
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jwatanab@nanage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 487)
Watanabe,J., Sasaki,M., Suzuki,Y. and Sugano,S.
FULL-malaria: a database for a full-length enriched cDNA library from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
                                                                                                                                                                                                                                                                                                                                /clone_lib="G"
/rote="Genoscope sequence ID : COAG184BH01LP1-end : T7"
/ note="Genoscope sequence ID : T0 c 174 g 333 t 101 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU087926 Sugano Malaria cDNA library Plasmodium falciparum cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 ataattataattataattataatactgaaaccatggtgccccctgctgctttacatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="184002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 13;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 agagtcaaaacccaaaatcatgaacacccaaact 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone XPFn6146, mRNA sequence. AU087926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Junichi Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU087926.1 GI:12390067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 bp
                               3 (bases 1 to 1024)
Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 81-3-5449-5378
Fax: 81-3-5449-5410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88; Conservative
                                                                                                                                                                                                                                                1. .1024
                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20574754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU087926
                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
AU087926/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
(cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTS had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1, and NIH_BMAP_M_S3.1, and NIH_BMAP_M_S3.1, and NIH_BMAP_M_S3.1, and NIH_BMAP_M_S3.1, and NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1, and NIH_BMAP_M_S3.1, and NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1, libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 1024)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene number estimate provided by genome wide analysis using Tetraodon nigrovíridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1024)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Welssenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSO30D0 1024 bp DNA GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 184002 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 ttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatatga 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 aattataattataattataataatactgaaaccatggtgccccctgctgctttacatggat 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.6%; Score 43.6; DB 11; Length 465; 53.5%; Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 acatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgt 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                freshwater pufferfish Tetraodon nigroviridis
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6:791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _TISSUE=cerebellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS; genome survey sequence. Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_SEQ=GACTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL222093.1 GI:7880912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sedneuce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT,
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
CNS030D0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
```

27-JAN-2001

ö

Gaps

ö

```
203 tcatgaacacccaaact 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195
                                                                                                                                                                                                                                                                                                                                                              Hood, L.
                                                                                                                                                                                                                                                         human.
                                                                                                                             RESULT 7
AQ172252/c
                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ273686/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                     SOURCE
                        셤
                                                                               pp
                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                              AU088152 Sugano Malaria cDNA library Plasmodium falciparum cDNA clone XPFn6606 similar to Plasmodium falciparum microsatellite TA61 AU088152 AU088152. I GI:12390293
                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Fax: 81-3-5449-5410
Email: Jwatenabémanage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (bases 1 to 500)
Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.
FULL-malaria: a database for a full-length enriched cDNA library from human malaria parasite, Plasmodium falciparum
205/4754
                                                                                                                                                                                           168 AAATATTATGAAATATATTATGAAATATATATTATGAGTATTTTTCTTCATGCTGAT 109
                                                                                                                                                                                                                           ttctccgctactatttgtatacgtgtatatatacgtataatgtacatatatttatatga 127
                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                     108 TIGIATTANCCIATATATATATATATATATATATTATGTAATTAAAATATGTAGAAAC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 mattatmattatmattatatmatmatgatgamaccatggtgccccctgctgctttacmtggmt 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 igiatacgigiatatataccgiataaaigiacatatatitatatgaacaigaitaaigcii 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 gtgagttgttctcatccgtaagagtttcaatatgtaatggtgaagagtcaaaaacccaaaa 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                             Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41.8; DB 10; Length 500;
                                               6 others
                                                                                                                                                                                                                                                                                      128 acatgattaatgcttgtgagttgttctcatccgtaagagtttcaatat 175
                                                                                                                                          Indels
             19 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Indels
                                                                                                                                                                                                                                                                                                         /clone_lib="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
37 c 38 g 182 t 19 other
                                                                                                                                     80;
                                                                                                      /organism="Plasmodium falciparum"
/strain="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malaria parasite P. falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:5833"
/clone="XPFn6606"
/clone="XPFn6146"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Junichi Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.5%;
Matches 76; Conservative
                                                                                                                                       Conservative
                                                                                                                     Local Similarity
es 88; Conserv
                                          213
                                                                                                    Query Match
Best Local S:
Matches 88
                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
AU088152
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Source
                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                       ORIGIN
                                                                                                                                                                                           8
                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 527)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3179 Col=22 Row=D"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ172252 527 bp DNA GSS 17-OCT-1998 HS_3179_B2_B11_T7 CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=3179 Col=22 Row=D, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 03-NOV-1998
Library Oryza sativa genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: Jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3179 row: D column: 22
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.7%; Score 41.6; DF 70.0%; Pred. No. 2.1; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 527.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ273686 599 bp DNA nbxb0030P21f CUGI Rice BAC Lin nbxb0030P21f, DNA sequence. AQ273686 AQ273686.1 GI:3827001 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 g
                                                                                                                                                                        AQ172252
AQ172252.1 GI:3569619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 tatttatatgaacatgatta 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AAATTTAAANGCAAATT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Conservative
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
```

```
AZ119444.1 GI:7784375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
    sednence.
                                                                                                           Mus musculus
                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
AZ126726/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                          VERSION
KEYWORDS
                                                                                                                                                                         REFERENCE
                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //Olone="inba0009021"
//clone="lb="CuGI Rice BAC Library"
//clone="lb="CuGI Rice BAC Library"
//tlsbubost="Leaf"
//lab.host="E. coli DH10B"
//note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a happloid genome equivalent of 431 Mbp
(Arunganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from oryza sativa, Nipponbare variety. The
library contains 36.864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9%. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
               Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS AZ119444 711 bp DNA GSS 12-MAY-2000
DEFINITION RPCI-23-11A20.TJ RPCI-23 Mus musculus genomic clone RPCI-23-11A20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 tttctccgctactatttgtatacgtgtatatataccgtataaatgtacatatatttatatg 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 taattataattataattataataatactgaaaccatggtgccccctgcttcacatgga 66
                                                                                                1 (bases 1 to 599)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.6; DB 13; Length 599;
Pred. No. 2.1;
0; Mismatches 69; Indels 0
                                                                                                                                                                                                                                 Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 aacatgattaatgcttgtgagttgttctcatc 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 TATATATGGGATGAGTATGAATGGTACTCAAC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 394.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Japonica"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.6'
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                              BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ119444/C
                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                   JOURNAL
COMMENT
                                                                                                                          AUTHORS
                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                              TITLE
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ם
```

```
selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into BH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                   Zhao,S., Nierman,W., Feldblyum,T.; Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhaoftigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 11 row: A column: 20
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="OHIOB"
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A2126726 789 bp DNA GSS 02-JUN-2000 OSJNBb0079C19f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone OSJNBb0079C19f, DNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tggatttctccgctactatttgtatacgtgtatatataccgtataaatgtacatatattta 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 accataattataattataattataatactgaaaccatggtgccccctgctgctttaca 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 tatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttc 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                  Unpublished (1999)
Other GSSs: RPCI-23-11A20.TV
Contact: Shaying Jao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Far: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41.6; DB 13;
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="RPCI-23-11A20"
/clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.78;
53.08;
```

Homo

```
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 571)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High Throughput Sequencing Center

10 Jouen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Tex: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
Plate: 2161 row: J column: 20
Seg primer: T
Class: BAC ends
                                                                                                    AQ797772 571 bp DNA GSS 09-AUG-1999 HS_2161_B2_E10_T7C CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=2161 Col=20 Row=J, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: E
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 g
                                                                                                                                                                                                                                                                                                                                                                                                                               scanning the human genome
                                                                                                                                                                                          AQ797772.1 GI:5715030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.0%
The 70; Conservative
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
                                                                                                                                                                                                                                       human.
                                                              RESULT 11
AQ797772/c
LOCUS
                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
COMMENT
                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
AZ996260/c
                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_tipe="Lucal knice bac Library (ECORI)"
/tissue_tipe="Leaf"
/lab_host="E. coli DH108"
/notea" vector: pBACInd190; Site_1: ECORI; Site_2: ECORI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
on rice as their primary source of carbohydrate.
Nonocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 41 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
whyponbare variety using ECORI as the isolation
of 121 Kb providing approximatley is haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                 Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enratroldeae; Oryzeae; Oryza.

Entatroldeae; Oryzeae; Oryza.

Entatroldeae; Oryzeae; Oryza.

Rabac End Sequencing Framework to Sequence the Rice Genome Contact: Wing RA.

Unpublished (1998)

Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 7288

Fax: 864 656 7288

Fax: 864 656 7288

Fax: B64 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 totocgotactatttgtatacgtgtatatataccgtataatgtacatatattatatgaa 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 attataattataattatataatactgaaaccatggtgccccctgcttcacatggatt 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="05JNBD0079C19f"
/clone=lb="CUGI Rice BAC Library (EcoRI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 catgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgt 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.6; DB
Pred. No. 2.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 21
High quality sequence stop: 683.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Japonica"
    AZ126726
AZ126726.1 GI:8201718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 18.7%;
1 Similarity 50.9%;
86; Conservative
                                                                  Oryza sativa.
                                                                                      Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                    ORGANISM
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ996260 605 bp DNA GSS 27-APR-2001
ZM0282F21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0282F21F, DNA sequence.
AZ996260 GI:13867487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
/clone="Plate=2161 Col=20 Row=J"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                          /note="Organ: sperm: Vector: pBeloBAC11; BAC clones in E-Coli DH10B"
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                          120 ttatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgta 178
                                                                                                                                                                                                                                                                                                                                                    Length 571;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                            18.2%; Score 40.6; DB 13; 58.8%; Pred. No. 3.7;
                                                                                                                                                                                                                    49;
                                                                                                 241 t
                                                                                                                                                                                                                0; Mismatches
```

```
AA394343
AA394343.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sednence
                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 taa 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAA 277
                   AQ774291/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA394343/c
LOCUS
                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide Kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (q1!4732114) q19 hAPL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
                                                                                                                                                                                                         308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female" // Ab host="E. coli strain XLIO-Gold, Tl-resistant, F-" // Ab host="E. coli strain XLIO-Gold, Tl-resistant, F-" // Anote="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
1 (bases 1 to 605)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Slam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 atttctccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatat 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 ataattataattataattatatataatactgaaaccatggtgccccctgctgctttacatgg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon=10090"
/db_cre="UGC2M0282F1"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 18.2%; Score 40.6; DB 13; Length 605; Best Local Similarity 51.4%; Pred. No. 3.7; Matches 94; Conservative 0; Mismatches 89; Indels 0
                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0282 row: F column: 21
                                                                                                                                                                                                                                                                                                                                                                        Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                        plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 605.
Location/Qualifiers
                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 aga 188
                                                                                                                                                                                                                              쪖.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                       AUTHORS
                                                                                                                                           JOURNAL
  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                    TITLE
                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
```

```
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 583)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
AQ774291 583 bp DNA GSS 29-JUL-1999
HS_3086_Al_H04_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3086 Col=7 Row=O, DNA sequence.
AQ774291
AQ774291.1 GI:5654019
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
0 niversity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3086 row: O column: 7
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="texon:5606"
/clone="plate=3086 Col=7 Row=O"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA394343 595 bp mRNA EST 30-OCT-1997
26024 Lambda-PRL2 Arabidopsis thaliana cDNA clone 310A7T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 TATATATAAATATATANAATATAATTTATATATTTTATATATATATAAATATAAGTGTATATA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tatttatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatg 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 TATTTATATATAAAATATAATGTATATATATTATTATATATAACAATATATAAAATATATA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
Proc. Natl. Acad. Scl. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40.4; DB 13; Length 583;
Pred. No. 4.1;
0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 583.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:2047652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.1%;
Best Local Similarity 57.7%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
thale cress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
```

```
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360
                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
              JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Lambda-PRL2"
/clone_lib="Lambda Zip-Lox; Site_l: Sal; Site_2: Not;
/note="Wector: lambda Zip-Lox; Site_l: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated eticlated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA. " 11 others
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnollophyta; eudlcotyledons; core eudlcots; Rosidae; eurosida II Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 595)
Newman,T., deBrullin,F.J., Green,P., Keegstra,K., Kende,H., McIntosh.L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
                                                                                                                                                                               denes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
95148729
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MacU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (basa 1 to 84.5)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ745537 16-JUL-1999 DNA GSS 16-JUL-1999 HS_2272_A2_B12_T7C CIT Approved Human Genomic Sperm Library D Homo spatiens genomic clone Plate=2272 Col=24 Row=C, DNA sequence. AQ745537.1 GI:5523059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 tttatatgaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgta 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 TATGTATAAACATGACAACTCAATGCTTGTGTTCATCTCCATAGAGTTGCCAATATGTCA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40.4; DB 10; Length 595;
Pred. No. 4.1;
0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 atggtgaagagtcaaaacccaaatcatgaacacccaa 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="310A7T7
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 18.1%;
1 Similarity 63.3%;
62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ins.
oligo a.
107 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Source
  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                             MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
AQ745537/c
                                                                                     REFERENCE
                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250
                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

. .

```
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate 2 row: C column: 24
Seg primer: 77
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" 278 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 totocgctactatttgtatacgtgtatatataccgtataatgtacatatatttatatggaa 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 attataaattataattatataatactgaaaccatggtgccccctgctgctttacatggatt 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 catgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgta 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                          High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40.4; DB 13;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                          /clone="Plate=2272 Col=24 Row=C"
                                        Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: February 25, 2002, 17:21:13
Job time: 16166 sec
                                                                                                                                                                                                                                                                                              845.
                                                                                                                                                                                                                                                                                       High quality sequence stop: { Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.18;
52.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.1'
Best Local Similarity 52.4
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                  .845
```

ö

Description

AX127758 Sequence AX12775 Sequence AX12775 Sequence AX12775 Sequence AX12775 Sequence AX12757 Sequence AC021635 Arabidops AC072947 Homo sapi AK161557 Arabidops AC072048 Mus muscu AC040920 Homo sapi AK118429 Fal.co per AC040920 Homo sapi AC072147 Homo sapi AC072147 Homo sapi AC072147 Homo sapi AC072147 Homo sapi AC07294 Arabidops U29377 Caenorhabdi

Scoring table:

Searched:

Database

Perfect score: Sequence:

Run on:

AL049575 Human DNA AC013597 Homo sapi 284484 Human DNA s

```
synthetic construct.

SM synthetic construct
artificial sequence.

I (base 1 to 23)
S Weston, B. and de Beuckeleer, M.

Male-sterile brassica plants and methods for producing same
L Patent: WO 0131042-A 11 03-MAY-2001;
Aventis Cropscience N.V. (BE)
Location/Qualifiers
1. 23
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer MDB371"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AX127758 23 bp DNA
Sequence 11 from Patent W00131042.
AX127758 GI:14134405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AP003796
HSU95738
AL359697
AL592440
AE006464
HSPE53806
RCABCRYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS357116
HSDJ448H8
AC078902
CJ11168X6
                                                                                                        AC022947
ATCHRIV57
AC072048
AC046148
AC046020
AF118429
AC055083
AC055083
AC023167
AC023167
                                                                                                                                                                                                                                                               HSDJ316D7
AC013597
                                     AX127758
AX127755
AX127757
AC090679
ATT12H17
                                                                                                                                                                                                                                                                                                                                                 AC010246
AC090071
AC013461
AC008930
HS380A1
AC022667
AC007316
                                                                                                                                                                                                                                                                                                                                      AC019046
                                                                                                                                                                                                                                                                                                                       AC008573
                                                                                                                                                                                                                                                                                            HS50J22
             Ωī
             DB
                                                                                                                                   208684
168524
172650
535
146285
                                                                                                                                                                                                                                                               94835
139959
                                                                                                                                                                                                                                                                                                                                                                             213890
253038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155932
           Length
                                                                                                                                                                                                        183634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194873
256073
                                                                                                                                                                                                                                      23486
                                                                                                                                                                                                                                                                                                                                                                                                          25042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171368
171868
                                                                                                                                                                                                                                                                                            146746
                                                                                                                                                                                                                                                                                                                                                   179665
                                                                                                                                                                                                                                                                                                                                                                                                                                                 113033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36497
                                                                                                                                                                                                                                                                                                            149755
                                                                                                                                                                                                                                                                                                                       168749
                                                                                                                                                                                                                                                                                                                                                                   188537
Query
                                                                                                         Score
                                                                                                                                                                                                                                                                                                                      711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
711177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
71177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
7177.8
717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
AX127758
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                         ě
                                                                    000000 0 000
                                                                                                                                                                                                                                                                                                                         O
                                                                                                                                                                                                                                                                                                                                                                                                                                       ט ט
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000
                                                                                     February 25, 2002, 18:02:29; Search time 2331.3 Seconds (Without alignments) 162.757 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                1472140 segs, 8248589755 residues
                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                            1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                      IDENTITY_NUC Gapox 10.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_vi:*
em_htgo_hum:*
em_htgo_inv:*
em_htgo_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_htg_other:*
                                                                                                                                               US-09-698-903B-11
23
                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_htg_inv:*
em_htg_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                  9b_ba:*
9b_ln:*
9b_on:*
9b_on:*
9b_pat:*
9b_pi:*
9b_pi:*
9b_pr:*
9b_ro:*
9b_ro:*
9b_vr:*
9b_vr:*
9b_vr:*
9b_vr:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_ov:*
em_pat:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_om:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_ph:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_sts:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_in:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_ro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_sy:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_un:*
                                                                                                                                                                                                                                                                                                                                                                                                        GenEmbl:*
```

AC092795 Homo sapi AC019046 Homo sapi AC010246 Homo sapi AC010346 Homo sapi AC013461 Homo sapi AC00830 Homo sapi AC022667 Homo sapi AC022667 Homo sapi AC022667 Homo sapi AC022281 Homo sapi AC07316 Homo sapi AC07316 Homo sapi AC07318 Homo sapi AC07318 Homo sapi AC073902 Homo sapi AC078902 Homo sapi AC078902 Homo sapi AC078902 Homo sapi AC078902 Homo sapi

AL033919 H.sapiens X87114 R.catesbeia

AL359697 Human DNA AL592440 Homo sapi AE006464 Homo sapi AB002187 Epilachna AB002188 Epilachna AB002189 Epilachna

15-MAY-2001

SUMMARIES

```
Unpublished
                      137 a
                                                                                                                                                                                                                            AC090679
                                                                                                                                                                                                 RESULT 4
AC090679/c
LOCUS
DEFINITION
                     BASE COUNT
                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                   ORIGIN
                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                       Q
                                                                                                                               ò
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' border flanking region of elite event MS-B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:32630"
/note="3' border flanking region of elite event MS-B2"
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                           15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-2001
                                                                                                                                                                                                                                                                                 Synthetic construct
artificial sequence.
1 (bases 1 to 415)
Weston, B. and de Beuckeleer, M.
Wale-sterile brasica plants and methods for producing same
Patent: WO 0131042-A 8 03-MAY-2001;
Aventis CropScience N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 416)
Weston, B. and de Beuckeleer, M.
Wale-sterile brassica plants and methods for producing same Patent: WO 0131042.A 10 03.4MA1-2001;
Aventis CropScience N.V. (BE)
                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 6; Length 415; 100.0%; Pred. No. 0.35; Live 0; Mismatches 0; Indels
                                                         Length 23;
                                                   100.0%; Score 23; DB 6; Length 23
100.0%; Pred. No. 0.26;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                           PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .416
/organism="synthetic_construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX127757 416 bp DNA
Sequence 10 from Patent WO0131042.
AX127757
                                                                                                                                                                                                     AX127755 415 bp DNA
Sequence 8 from Patent WO0131042.
AX127755
    б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            б
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .234
/note-"plant DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 GAAATCCATGTAAAGCAGGG 174
                                                                                                                                1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                         1 gamatccatgtmaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                             AX127755.1 GI:14134402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX127757.1 GI:14134404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235. .415
/note="T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="T-DNA"
194. .416
                                                                                                                                                                                                                                                                        synthetic construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 c
                                                  Query Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1, .193
  Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
AX127757/c
LOCUS
BASE COUNT
ORIGIN
                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                          RESULT
AX127755
                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                         à
                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases I to 4176)

Muzuy, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Alian, C., Alabrocks, S.L., Amaratunog, H.C., Arej, R., Banka, T., Banka, J., Bubay, C., Blancon, J., Bimage, K., Blankenburg, K., Bonnin, D., Boudek, J., Burkett, C., Blankenburg, K., Bonnin, D., Chan, G., Burkett, C., Burkell, K.L., Byrd, N.C., Carron, T.B., Bubay, C., Burkett, C., Burkell, K.L., Byrd, N.C., Carron, T.B., Bubay, C., Burkett, C., Burkell, K.L., Byrd, N.C., Carron, T.B., Coyle, M.D., Dathorne, S.R., David, R., David, N., Davila, M.L., Davis, C., Chen, G., Chen, R., Carroll, J., Bederich, D.A., Delanay, K.R., Delagdo, O., Davy, Carroll, J., Dathorne, S.R., David, R., Douthwalte, K.J., Draper, H. Dugar, Cohe, S., Ourbin, K.J., Barnhart, C., Edgar, D., Erdwards, C., Elbaj, C., Escotto, M., Falls, T., Ferraquoto, D., Flago, N., Ford, J., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Harnandez, J., Harris, C., Harris, C., Harris, C., Harris, K., Hart, M., Havlak, P., Humes, J., Jackson, E., Jacobson, B., Jai, X., Johnson, R., Lu, J., Lu, J., Lu, J., Lu, J., Lu, J., Lucier, A., Lucier, A., Lucier, R., Luna, R., Martindale, A., Martinga, R., Martingale, A., Martinga, R., Marting, R.
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 41760)
Worley.K.C.
Direct Submission
Submitted (08-MAR-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC090679 41760 bp DNA HTG 27-JUN-2001
Homo sapiens chromosome 12q clone RP11-8003, *** SEQUENCING IN
PROCRESS ***, 14 unordered pieces.
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                        Length 416
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                        .
9
                                                                                                                                                                         Ouery Match

Ouery Match

Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 23; Conservative 0; Mismatches
                                          ų
                                          152
                                      б
/note="plant DNA"
72 c 54 g
                                                                                                                                                                                                                                                                                                                                                                                                263 GAAATCCATGTAAAGCAGCAGGG 241
                                                                                                                                                                                                                                                                                                                       1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC090679.3 GI:14190581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1
```

m

```
/product-"predicted protein"

/protein_id-"CAA16548.1"

/db_xref-"GI:3827540"

/db_xref-"SPTREMBL:049644"

/db_xref-"SPTREMBL:049644"

/db_xref-"SPTREMBL:0ATMVANAVGAAVVFLAVVMNPRWTEAQTYPKLDRLCVMMIP

/Itanslation-"MAYTMKNANAVGAAVVFLAVVMNPRWTEAQTYPKLDRLCVMMIP

/Itanslation-"MAYTMKNANAVGAAVVLKDP

// OVSHKYMCQAAKNRGEAKGGRNSTTTCDNSITNTSVGGKNKVATSMSAFGLVAILLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSLARRCLRRGANRLCGGMKPGQTRLGNEPKTPTVPRGHLVVHVGESGEDTRRVVVPV
IYFNHPLFGELLEQAERVYGFEQPGRIMIPCRVSDFEKVQMRIAAWDHCRRKSTFKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'translation-"MKRLRGFKIGHRFVKIFKWIIRSRRNQTGKRQCLTGILNPVTKI
                                                                                                                                                                                                                                                                                                                                                                                  Bevan,M., Hilbert,H., Braun,M., Holzer,E., Brandt,A.,
Duesterhoeft,A., Bancroft,I., Mewes,H.W., Mayer,K. and Schueller,C.
                                                                                                                                                                                                                                                                               Arabidopsis thaliana Eukaryota; Embryophyta; Tracheophyta; Ekaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing, project.

Direct Submission
Submitted (03-FEB-1998) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similarity to auxin-induced protein 10A, Glycine max., PIR2:JQ1099"
                                                                                                                                              ATT12H17 89350 bp DNA PLN 03-FEB-1998 Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"similarity to predicted proteins, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organisme"hrabidopsis thaliana"
/variety="Columbia"
/db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2406. . . 2983
/gene="T12H17.20"
join(2406. . . 2754, 2844. . . 2983)
/gene="T12H17.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="predicted protein"
/protein_id="CAALS547.1"
/db_xref="G1:2827539"
/db_xref="SPTREMBL:049643"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                            19612 GAATTCCATGTAAAGCTGCAGG 19591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="T12H17.10"
669. .1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="T12H17.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2406. .2754
/gene="T12H17.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="T12H17.10"
          1 gaaatccatgtaaagcagcagg 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                            AL021635.1 GI:2827538
                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 89350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2755. .2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .89350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                       AL021635
                                                                                                                                                                                     project
                                                                                                                                                                                                                                                                   thale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intron
                                                                                                      RESULT 5
ATT12H17/c
                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                             g
          ò
                                                                                                                                                          Center project name: HCGK
Center clone name: RP11-8003
Center clone name: RP11-8003
Sequencing vector: M13; LO8821
Chemistry: Dye-primer Bodipy: 50% of reads
Chemistry: Dye-terminator Big Dye: 50% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 91506 bases at least 040
Consensus quality: 101714 bases at least 030
Consensus quality: 106393 bases at least 020
Estimated insert size: 81455; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; sum-of-contigs estimation
Quality coverage: 1.1x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Baylor Plaza, Houston, TX 77030, USA
On May 23, 2001 this sequence version replaced gi:13470121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 41760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1355: contig of 2562 bp in length
1355: contig of 2562 bp in length
13655: gap of unknown length
17634: contig of 3979 bp in length
17734: gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1320 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39704: gap of unknown length 41760: contig of 2056 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6354: contig of 6354 bp in length 6454: gap of unknown length 10893: contig of 4439 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 2209 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                               Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7257 g 13504 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.8; DP
Pred. No. 88;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown 1
of 2666 k
unknown 1
of 2193 k
unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown of 2408 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 2059 l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
of 2339 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
of 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown
contig of 3029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of gap of unki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contiq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-8003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contiq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39604: contiq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="12q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37395:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20863:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32798:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32698:
                                                                                  code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7423 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 81.7
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32799
35138
35238
37296
37396
39605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6355
6455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20764
20864
23530
23630
25823
25923
28032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28132
30540
30640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10994
13556
13656
17635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                        COMMENT
```

```
jóin(9990. 10023,10239. 10535,10564. 10664,10910. 11292,
11755. 11809,11898. 12053,12143. 12311,12391. 124455,
12534. 12574,12769. 12885,13024. 13096,13244. 13380,
13468. 13525,13512. 13709)
                                                                                                                                                                                                                                                                                                     Product = "HSP associated protein like"

| Protein_id="CAA1652.1" |
| Protein_id="CAA16552.1" |
| Protein_id="CAA16552.1" |
| Ab_xref="G1:2827544" |
| Ab_xref="SPTEMBL:049648" |
| Ab_xref="SPTEMBL:049648" |
| ArmsylpeDccTDLKSATSYQVICLONITANPAVSNITGPSRATTHRCGFRATSYQVICTONITANPAVSNITGPSRATTHRCGFRATSYGVICTONITANPAVSNITGPSRATTHRCGFRATSYGVICTONITANPAVSNITGPSRATTHRCGFRATSYGVICTONITANPAVSNITGPSRATTHRCGFRATSYGVICTONITANPAVSNITGPSRATTHRCGFRATSYGVICTONITANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHRCTANPAVSNITGPSRATTHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similarity to p48, Homo sapiens, PATCHX:G904032 contains E3T gb:Aa605571, H76919, H76638, R30271, Z25650" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8; Length 89350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
(7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 81.7%; Score 18.8; D
Best Local Similarity 90.9%; Pred. No. 95;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=1
10239. 10535
/gene="rr2H17.60"
/number=2
10536. 10563
/gene="rr2H17.60"
                                                        9990. .13709
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /number=3
10665. .10909
/gene="T12H17.60"
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number-1
10024. .10238
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9990. .10023
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=2
10564. .10664
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=5
11898. .12053
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10910. .11292
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11293. .11754
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11755. .11809
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11810. .11897
/gene="T12H17.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D 15674 AAATCCATGTAAAGCAGTAAGG 15653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 agatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number=6
12054. .12142
                                                                                                   Join(9990.
11755. .11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
AC022947/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
                                                                                                                                                                                                                                                                                                                                /product="putative protein"
/product="putative protein"
/protein_id="CAA16549.1"
/db_xref="c1:2827541"
/db_xref="SPTRME1:049645"
/translation="MAYTNKVTISAAVATMMLFLAVTIVDAQSMPPMPKFNPVCALAD LPNIVQLCYFNLDLTPSEECCNDLKSSSTIQVNCLCDNFIAHPSNGNISQARYDLVNS CGVADKFRKGGDASGGSTNKIAASMVLLGLVASLFF"
/gene="T12117:30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Craislation="Meknonpytwsdlpldlinlupekrlsfanfroaksvcsswysas
kosveknoldwilepkdknnnknssctifenpedkdoliogolgyrodlgyereksyclaty
Spalladdskynlytinppfyeriglearisesogygwkydotidddelfddhnykl
Fkgnnyvdrpypwiddektkeyialmgigywcyvyrakodkimydipelidsidwyyk
DHKLYSFSYRNLFILDFSGEIPRRAPOCFWHYYRSBWLSPRSQLSNSWCVAETKLY
VTYTGDVLLYBRMIRHWSRIQSFNYKRYSSGTFLDKYELADSIGDBAMILLDGITTLA
ANBVEGLHRNTIYFSDSHDTTTKDLFLENYETREMEPLHKFDFDCSLLELSARWFLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(8019. .9209)

Gene="T12H17.50"

complement(8019. .9209)

/gene="T12H17.50"

/note="similarity to predicted protein, Arabidopsis
                                                                                                                                                                                                                                                                             /note-"contains EST gb:N38564"
                                                                                                                                                                            4696. .5489
/gene="T12H17.30"
join(4696. .5035,5407. .5489)
/gene="T12H17.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(6595. .6940,7035. .7105)
/gene⇔"T12H17.40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="predicted protein"
/protein_id="CAA1651.1"
/db_xref="GI:2827543"
/db_xref="SPTREMBL:049647"
                                                                                                                           3327. .3400
/note="Asn-tRNA_(GTT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(8019, .9209)
/gene="T12H17.50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="T12H17.40"
/941. 703
                                                        2844. .2983
/gene="T12H17.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6941. .7034
/gene="T12H17.40"
/number=1
7035. .7105
/gene="T12H17.40"
'gene-"T12H17.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5036. .5406
/gene="T12H17.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5407. .5489
/gene="T12H17.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5595. .6940
/gene="T12H17.40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8019. .9209
/gene="T12H17.50"
complement(8019. .
                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                /number=
                                                                                                           /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=1
6595...71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                   exon
                                                                                                                           trna
                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
```

us-09-698-903b-11.rge

```
ø
                                                                                                                                                                                                                                                                                                                                50352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCHRIV57/c
LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. Z. (bases 1 to 15515)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Bandan, N., Beckerly, R., Beda, F., Boyslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Horton, L., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGluk, J., McKennan, K., McPheeters, R., Maddrim, J., McEwan, P., McGluk, J., Narylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Triell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Zummer, A. and Zody, M., Zhamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Chander, A., Dillact, Subnission
ACO22947 156515 bp DNA HTG 12-MAR-2000
Homo sapiens clone RP11-8003, WORKING DRAFT SEQUENCE, 13 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced 91:6921807. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156515)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research Center code: Wile State: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center Close name: 80_0.3

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 115128 bases at least Q40
Consensus quality: 115128 bases at least Q30
Consensus quality: 153939 bases at least Q20
Insert size: 150000; agarose-fp
Insert size: 155315; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 4.8 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L6397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1027 1126: gap of 100 bp 1127 5787: contig of 4661 bp in length 5788 5887: gap of 100 bp 11595: contig of 5708 bp in length 11596 11695: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1026: contig of 1026 bp in length
                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-8003
Unpublished
                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                AC022947
AC022947.2 GI:7229879
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 156515)
                                                                                                                                                                                                                               Homo sapiens
   LOCUS
DEFINITION
                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
```

```
ATCHRIV57 199577 bp DNA PLN 16-MAR-2000
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57,
AL161557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 156515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1205 others
                                                                                                                                                                                                     60664 60763: gap of 100 bp 60764 75537: contig of 14774 bp in length 75538 75637: gap of 100 bp 100 bp 93139: contig of 17502 bp in length 93140 93239: gap of 100 bp 93240 114372: contig of 21133 bp in length
                                                                                                                              87: gap of 100 bp
50251: contig of 12064 bp in length
513: gap of 100 bp
60663: contig of 10312 bp in length
                                                                                                                                                                                                                                                                                                                                         contig of 42043 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                 14531: gap of 100 bp 20088: contig of 5557 bp in length 20188: gap of 100 bp 29619: contig of 9431 bp in length
                                                                                          29620 29719: gap of 100 bp 29720 38087: contig of 8368 bp in length
14431: contig of 2736 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-11 Human Male BAC"
1. .1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.8; DB 2
Pred. No. 1e+02;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93240. .114372
/note="assembly_fragment"
114473. .156515
/note="assembly_fragment"
27072 c 27170 g 51430 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75638. 93139 --
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
60764. 75537
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1127. .5787
/note="assembly_fragment"
5888. .11595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
11696. .14431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14532..20088
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector_side:left"
29720. .38087
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38188. .50251
/note="assembly_fragment"
50352. .60663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11696. .14431
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20189. .29619
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-8003"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114373 114472: gap of 114473 156515: conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                               .156515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                              38187:
                                                                                                                                                                   50351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 20; Conserve
```

ö

```
/godon_start=1
//number=1
//numbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MATNGSSEHLLPETTRESAIINKQOPEFPASRFTFMSLVLMFDQ
SNFGISFVSLSIWSRKFGMRRFLFLDKLWDVSDKVRIEYEAETQRSLKRLMIFVLPSL
TLEATYRIWWYISGFNQIPYIINPILSHVVACTLQLSSWLYRNSLFIIVCILYKITCH
LQTLRLDDFARCFASEITDVRSALGERQKIRRNLRIVSHRERRFILLSLILVTATQFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLTTRASVAVNIYEVGELALCSLSLVTGVFICLRSATKITHKAQSYTSLAAKWNVC
YOYDSFWLGSTPTGSIIESQVSLRGNAIETSDDEEGEGDDDLDNTKIHPIYANTIS
YQKQALVTYLENNKAGITVYGFLVDRSWLNTIFGIELALLLWLLNKTIGILA"
10245. 10394
/gene-"A14922270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"hypothetical protein"
/protein_id="CAB79182.1"
/db_xref="GI:7269073"
                             complement(7340. .7506)
                                                                           complement(7507, 7575)
/gene="AT4g22260"
                                                                                                                                                                                                        /gene="AT4922260"
/number=
                                                                                                                                                                                                                                                                                                                             complement(7863. .7978)
/gene="AT4g22260"
/number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AT4922260"
/number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(8588. .8777)
/gene="AT4g22260"
/number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene-"AT4g22260"
/number-0
                                                                                                                                                          complement(7576. .7666)
                                                                                                                                                                                                                                                                                    complement(7776. .7862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8455. .8587)
                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7979. .8360)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(8778. .8908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11168 ...11253
/gene="AT4922270"
/note="Tyr-tRNA_(GTA)"
11327 ...1179
/gene="AT4922270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10103. .10244
/gene="AT4g22270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10395. .10516
/gene="AT4g22270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10517. .11326
/gene="Ar4g22270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11868. .12174
/gene-"AT4g22270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11780. .11867
/gene="AT4g22270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12175. .12253
/gene="AT4g22270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (8909
                                                                                                                                                                                                                                                                                                                  /numper=4
                                                                                                                                                                                                                                                                                                                                                                                                                                              /numper=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number=6
                                                                                                                                    /numper=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /numper=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number=1
10395. .10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'number-4
                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                           exon
                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(6674. .6882,7268. .7339,7507. .7575,
7667. .7775,7863. .7978,8361. .8454,8588. .8777,8909. .9057))
/gene="AT4g22260"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(6674. .6882,7268. .7339,7507. .7575,
7667. .7775,7863. .7978,8361. .8454,8588. .8777,8909. .9057))
/gene="AT4g22260"
                                                                   Arabidopsis thallana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 64578 to 155510)
Wedler, H., Wambutt, R., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RILLIRNNHRVQATILQDDEEKVVVEESFKAETSTGTEPLEEPNMSSSSTSAFETWII
KLEQGVNVFETDSVIKILDTLYRDGTYARFPVLETIARVPYFAFMSVLHMYETFGWWR
RADYLKVHFAESWNEMHHLLIMEELGGNSWWFDRFLAQHIAFTYYFWYFVYFY
AYHFSECVESHAY FYFVEKIKASGEELKNMPARDIAVKYYTGGDLYLFENLYDVFVNI
RDDEAEHCKTWRACGTLGSLRSPHSILEDDDTEEESGCVVPEEAHCEGIVDCLKKSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative protein"
/protein_id="CAB79181.1"
/db_xref="G1:7269072"
/translation="MAAISGISSGTLTISRPLVTLRRSRAAVSYSSSHRLLHHLPLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 (bases 48809 to 64829)
Robben,J., Grymonprez,B., Volckaert,G, Mewes,H.W., Lemcke,K. and
Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similarity to alternative oxidase, Mangifera indica, PIR2:845035 Contains EST 9D:142793, A1994896.1, A1997645.1, R30022, AA395166"
                                                                                                                                                                                                                                   2 (bases 141638 to 141797)
Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Mewes,H.W.,
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                      Brandt, A., Duesterhoeft, A.
                                                                                                                                                                                                                                                                                                                                             3 (bases 143670 to 199577)
Hilbert,H., Braun,M., Holzer,E., Brand Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7268, .7339)
/gene="AT4922260"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(6883. .7267)
  AL161557.2 GI:7269071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                           AUTHORS
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
```

us-09-698-903b-11.rge

```
Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Bouffard, G., Dietrich, N.L., Eagle, M.O., Gupta, J., Ho, S.-L.,
Huang, M.C., Idol, J., Lee-Lin, S.-Q., Maduro, O.L., Maduro, V.B.,
Mastrian, S.D., McCloskey, J.C., Morse, E., Ojodu, M.A., Pearson, R.,
Stantripop, S., Summers, T.J., Thomas, J.W., Thomas, P.J.,
Tiongson, E.B., Touchman, J.W., Tran, J.T., Vogt, J.L., Walker, M.A.,
Wetherby, K.D. and Green, E.D.
                                                                                                                                                                                                                                                 Direct Submission
Submitted (07-JUN-2000) NIH Intramural Sequencing Center, 8717
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: 189215

Center clone name: 189215

Sequencing vector: plasmid; n/s; 100% of reads
Sequencing vector: plasmid; n/s; 100% of reads
Sequencing vector: plasmid; n/s; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 195465 bases at least Q40
Consensus quality: 197464 bases at least Q20
Consensus quality: 198446 bases at least Q20
Insert size: 209000; agarose-fp
Insert size: 209000; pulse-field-gel
Insert size: 206084; sum-of-contigs
Quality coverage: 6.43x in Q20 bases; agarose-fp
Quality coverage: 6.51x in Q20 bases; sun-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in length
                                                                                                                                                                                                                                                                                           Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                     Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 2209 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ф
                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
of 2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
of 5101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 9020
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 3853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 8485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: wp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of contig gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                    Unpublished
2 (bases 1 to 208684)
Green, E.D.
                                                                                                                                                                                                                                                                                                                                                           Center code: NISC
(bases 1 to 208684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22099: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62209: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82147:
82247:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39449:
39549:
48515:
48615:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55023:
55123:
64442:
64542:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7024
7124
9506
9506
14707
118607
11860
25425
25525
33330
33400
33450
48516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64543
73028
73128
82148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2210
2310
4737
4837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55024
55124
REFERENCE
AUTHORS
                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(12761. .13015,13081. .13227,13379. .14157,
14209. .14314,14995. .15111))
/gene="AT4g22280"
                                                                                                                                                                                                                                           complement(join(12761. .13015,13081. .13227,13379. .14157, 14209. .14314,14995. .15111))
//gene="Afriq2280"
//note="similarity to hypothetical protein, chr.4, Arabidopsis thaliana, PATCHX:G2392763
contains EST gb:A1998861.1, A1993240.1"
                                                                                                                                                                                                                                                                                                                                                                                           /product="putative protein"
/protein_id="CaB79183.1"
/db_xref="G1:7269074"
/translation="MEKDVMTDETCIVGRNPATIVNVNGLNISHQCMISLKLKCVIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGVVDAGDLLFRLITPERFIRIWQRMDRINEATSTSVLSMRWRYLFAFRPNLCLDDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGGGDSFIDFVDRVLVVTGNFPIRRISIKCRMSIDTGHVTRWMVDVLEHGVSYLDIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA HTG 07-JUN-2000 6 clone RP23-189E15 strain C57BL6/J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Length 199577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.8; DB 8
Pred. No. 1e+02;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(13016. .13080)
                                                                                                                        complement(12761, .13015)
/gene="AT4g22280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(13081, .13227)
/gene="AT4g22280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .13378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(14158. .14208)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .14314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(14315. .14994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(14209.
/gene="AT4g22280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(13228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(14995.
/gene="AT4g22280"
/number=5
                                                                            12761. .15111
/gene="AT4g22280"
                 12254. .12393
/gene="AT4g22270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AT4g22280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC072048 208684 bp DN
Mus musculus chromosome 6
WORKING DRAFT SEQUENCE, 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(13379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC072048
AC072048.1 GI:8313202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number-4
                                                                                                                                                                  'number-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number=3
                                                           'number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC072048/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                 gene
                                                                                                                        exon
                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
```

```
93854: contig of 11607 bp in length 103236: contig of 9282 bp in length 10336: gap of unknown length 117502: contig of 1242 bp in length 117502: contig of 14166 bp in length 130162: gap of unknown length 130162: contig of 12560 bp in length 130262: gap of unknown length 140708: contig of 10446 bp in length 140808: gap of unknown length 151652: contig of 10446 bp in length 151652: contig of 10844 bp in length 151852: contig of 10844 bp in length 163923: gap of unknown length 163923: gap of unknown length 163923: gap of unknown length 178730: contig of 12670 bp in length 178730: contig of 14807 bp in length 193099: contig of 16779 bp in length 194009: gap of unknown length 194009: contig of 15679 bp in length 208684: contig of 14675 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP23-189E15"
/clone_lib="RPCI mouse BAC library 23"
1. .200
/note="assembly_fragment"
2310. .4736
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /4837. 7023
//note-"assembly_fragment"
/124. 9505
//note-"assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64543. 73027

/note="assembly_fragment"

/3128 .82147

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // note="assembly_fragment"
130263. .140708_fragment"
// note="assembly_fragment"
140809. .151652.
// note="assembly_fragment"
15173. .163823
// note="assembly_fragment"
163924. .118730
// note="assembly_fragment"
// note="assembly_fragment"
// note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL6/J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_end:T7
                                                                     103237
103337
117503
117603
130163
140709
1151653
151753
                                                                                                                                                                                                                                                                                                                                                          178831
193910
194010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
```

```
H. (Cases I to Lebs.)

By Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
Dederich, D., Thomas, S., Okuvonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunz, C., Delgado, O., Ding, Y., Dugan-Rochs, S.,
Fernandez, C., Ferraguto, D., Forcum Tansey, J., Glal, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Harnandez, J., Martin, R.,
Rovar, C., Liu, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Wigupen, R., Nguyen, N., Oquh, M., Parish, B.,
Williamson, A., Wensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Direct Submission

A. Unpublished

On Nov 4, 2000 this sequence Version replaced gi:9929612.

Center: Baylor clalege of Medicine

Center: Baylor clalege of Medicine
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 168524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC046148 168524 bp DNA HTG 06-NOV-2000
Mus musculus chromosome 14 clone RP23-265D21, *** SEQUENCING IN
PROGRESS ***, 45 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: MARB
Center clone name: RP23-265D21
Center clone name: RP23-265D21
Sequencing vector: M13; L088210
Chenistry: Dye-primer Bodipy: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 13230 bases at least 040
Consensus quality: 14933 bases at least 030
Consensus quality: 156096 bases at least 020
Estimated insert size: 153798; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                            Query Match 81.7%; Score 18.8; DB 2; Length 208684; Best Local Similarity 90.9%; Pred. No. 1e+02; Matches 20; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                        2323 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                      ture 194010. 208684 / note" assembly fragment" 54390 a 48824 c 48605 g 54542 t
178831. .193909
/note="assembly_fragment
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                             Db 135605 AAATCCCTGTAAACCAGGG 135584
                                                                                                                                                                                                                                                                                                                                             2 aaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC046148.5 GI:11094639
HTG; HTGS_PHASE1.
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                 misc_feature
  misc_feature
                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
AC046148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                δ
```

gap of unknown length contig of 2143 bp in length gap of unknown length contig of 2448 bp in length gap of unknown length contig of 1365 bp in length gap of unknown length

150388: 150488:

length

gap of

145597: 145697: 147840: 147940:

bp in length bp in length in length bp in length bp in length

of 1606

contig

.56600: 156700:

gap of

unknown length unknown length of 1435 bp in l unknown length

2941 bp

oţ

contig gap of

151853: 151953: 154894: 154994:

in length

```
45461 a 36455 c 36516 g 45685 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP23-265D21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                      150389
150489
151854
151954
                                                                                                                                                                   154895
154995
156601
156701
                                                                                                                                                                                                                                                                                                                            161529
162994
                                                                                                                                                                                                                                                                                                                                                                                                                                  165951
167365
                 143205
145598
145698
                                                                                                                                                                                                                                                                                           159368
                                                                                                                                                                                                                                                                                                                                                                                                164487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167465
                                                                                                                                                                                                                                           .58136
                                                                                                                                                                                                                                                                             59268
                                                                                                                                                                                                                                                                                                                                                                                164387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC040920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC040920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC040920/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Quality coverage: 2.6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                  g of 10853 bp in length f unknown length of 9393 bp in length f unknown length g of 9945 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in length
                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                     contig of 10853
gap of unknown 1
gap of unknown 1
gap of unknown 1
contig of 9445 b
gap of unknown 1
contig of 8858 b
gap of unknown 1
contig of 7734 b
gap of unknown 1
contig of 6479 b
gap of unknown 1
contig of 6479 b
gap of unknown 1
contig of 6479 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 6289 b
gap of unknown l
contig of 4672 b
gap of unknown l
contig of 3980 b
gap of unknown l
contig of 4559 b
gap of unknown l
contig of 4406 b
gap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 5051 by contig of 4000m loonting of unknown loonting of unknown loonting of 3337 by contig of 33515 by contig of 3338 by contig of 3338 by contig of 3338 by contig of 3388 by contig of 2887 by contig of 2886 by contig of 2886 by contig of unknown loonting of 2886 by contig of unknown loonting of 2886 by contig of unknown loonting of all by contig of all by contig of all by contig of 3415 by contig of 2477 by contigued by continue of 2477 by contigued by continue of 2477 by 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 2015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 4127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
                                                                                                                                                                                                       10853:
10953:
                                                                                                                                                                                                                                                         20446:
30391:
                                                                                                                                                                                                                                                                                                                                            47183:
                                                                                                                                                                                                                                                                                                            39349:
39449:
                                                                                                                                                                                                                                                                                           30491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78684:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83343:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73910:74010:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87849:
87949:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118648:
                                                                                                                                                                                                                                                                                                                                                                                                                    58669:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11847
                                                                                                                                                                                                                                                                                                                                                                                                                                      58769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37507
                                                                                                                                                                                                                                                                                                                                                                                                  53862
                                                                                                                                                                                                                                                                                                                                                                                                                                                        65058
                                                                                                                                                                   as soon as it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118549
118649
121540
121640
124527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83444
87850
92077
92177
97228
101357
101457
104694
108133
111748
111148
111148
111144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127513
127613
                                                                                                                                                                                                                                                                                                          30492
39350
39350
47184
47284
47284
47284
53363
58670
65059
65159
665159
66931
73911
73911
73911
73911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133705
                                                                                                                                                                                                                                                       20347
20447
30392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139623
141183
141283
                                                                                                                                                                                                                       10854
                                                                                                                                                                                                                                         10954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137408
```

4407 others

contig of 1060 bp in length

unknown length

gap of

168524:

of 1293 bp in length

of 1465 unknown contig of 2061 gap of unknown

contig

gap of contig

163093; 164386: 164486:

length length length

of 1032

unknown

contig gap of

gap of

gap of unknown length

contig of 1364 bp in length gap of unknown length contig of 1414 bp in length

165850:

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Upubblished

2 (bases I to 17250)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Birren, S., Landavin, J. Barna, N., Bastien, V., Beda, F.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S.,

Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Gardy Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  clone RP11-509M23 map 5, WORKING DRAFT
                                                              Gaps
                                                                                                                                                                                                                                                                                                                               11-APR-2000
Length 168524;
                                                              ö
                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 172650)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo saplens chromosome 5, clone RP11-509M23
80.0%; Score 18.4; DB 2;
95.0%; Pred. No. 1.6e+02;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 5 clon
SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                       AC040920.1 GI:7534094
                                                                                                                                                                                                                                                                                                                               172650 bp
                                                           Conservative
   Query Match
Best Local Similarity
Matches 19; Conserva
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 172650
                              82866 82955; gap of 100 bp 82966 97230; contig of 14265 bp in length 97231 9730; gap of 100 bp 97331 114682; contig of 17352 bp in length 114683 113289; contig of 17357 bp in length 113290 132289; contig of 17357 bp in length 132390 13289; gap of 100 bp 132390 15164; contig of 19275 bp in length 151665 157744; gap of 100 bp 151665 1577445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 157445 15744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1804 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match

80.0%; Score 18.4; DB 2;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /"51765, .172650
/hote="assembly_fragment"
..., 19488 c 29466 g 55635 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"assembly_fragment"
9888. 13694
/note-"assembly_fragment"
13795. 18482
/note-"assembly_fragment"
18583. 24380
/note-"assembly_fragment"
24481. 30597
/note-"assembly_fragment"
24481. 30597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65944. .82865 /note="assembly_fragment"
82966. .97330
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523. .2269
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2370. 4946
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5047. .7162
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 422
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43987. 53642
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53743, .65843 /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9731. ,114682
/note="assembly_fragment"
114783. ,132289
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132390, .151664
'note="assembly_fragment"
:51765, .172650
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens'/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone-"RP11-509M23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_end:T7
vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector_side:left"
132390, 151664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 142729 AAAGCCATGTAAAGCAGCAG 142710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_end: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 aaatccatgtaaagcagcag 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McBwan, P., McGurk, A., McKernan, K., McDheeters, R.,
Maldrim, J., Maneus, L., Mihova, T., Miranda, C., Minordy, V., Morrow, J.,
O'Neil, D., Ollvar, T.M., Ollver, J., Peterson, K., Plerre, N.,
Pisani, C., Pollara, Y., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Tesfape, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J.,
Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Voung, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (11-ARP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, Ma 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ttp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: 18533

Center clone name: 509_M_23

Center clone name: 509_M_23

Center clone name: 509_M_23

Sequencing vector: M13: M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 163069 bases at least Q40

Consensus quality: 167976 bases at least Q20

Insert size: 170000; agarose-fp

Insert size: 170000; agarose-fp

Insert size: 170805; sum-of-contigs

Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 422: contig of 422 bp in length
423 522: gap of 100 bp
523 529: contig of 1747 bp in length
2270 2369: gap of 100 bp
2370 4946: contig of 2577 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
of 2577 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 bp
of 2116 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7262: gap of 100 bp 9787: contig of 2525 bp in length 9887: gap of 100 bp 13648: contig of 3807 bp in length 13794: gap of 100 bp 13794: gap of 100 bp 18882: contig of 4688 bp in length 1883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18582: gap of 100 bp 24380: contig of 5798 bp in length 24480: gap of 100 bp 30597: contig of 6117 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41: gap of 100 bp
43886: contig of 7545 bp in length
86: gap of 100 bp
53642: contig of 9656 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53742: gap of 100 bp 65843: contig of 12101 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43: gap of 100 bp
82865: contig of 16922 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97: gap of 100 bp
36241: contig of 5544 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13795 18482: conti
18483 18582: gap of
18583 24380: conti
24381 24480: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30698 36241 Conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43986:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65943:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24481
30598
                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
```

ó

```
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NIGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 12, 1999 this sequence version replaced gi:3212908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE INFORMATION:
Clone CTA-281G5 is from a release of the human BAC library
CITB-HS-A. The library contains cloned DNA from human sperm. See:
Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J.
Kim et al., Genomics 34:213-8 (1996). The clone is available from
Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC CTA-281G5 contains an E. coli transposon from 10982 to 12345 that is not represented in the submitted sequence.
Location/Qualifiers
1. .146285
//organism="Homo sapiens"
//db_xref="taxon:9606"
//chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actual start of this clone is at base position 1 of CTA-281G5; actual end is at 146285 of CTA-281G5
                                                               Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                       Center project name: H_RG281G05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CTA-281G5"
/clone_lib="CITB-HS-A"
322. .358
/rpt_family="(TAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   808. . 952
/rpt_family="MER1_type"
1172. .1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AT_rich"
4794. .4826
/rpt_family="AT_rich"
5764. .6034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
1264. .1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family~"AT_rich"
1882. .2171
                                              ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chloramphenicol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1"
1848. .1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map-"7p15-p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Selection:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-JAN-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 4 (bases I to 146285) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC005083 146285 bp DNA PRI 21-DEC-1999 (Indoo sapiens BAC clone CTA-281G5 from 7p15-p21, complete sequence. AC005083.1 GI:4150930
                                                                                                                                                                                                         Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Awes; Neognathae; Falconiformes; Falconidae; Falco. 1 (bases 1 to 535)
Nesje,M., Roed,K.H., Lifjeld,J.T., Lindberg,P. and Steen,O.F. Genetic relationships in the peregrine falcon (Falco peregrinus) and ysed by microsatellite DNA markers
Mol. Ecol. 9 (1), 53-60 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146285)
Madsen,C. and Blair,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                 10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-JAN-1999) MGA, Genetics, Norwegian College of Veterinary Medicine, P.O. Box 8146 Dep., Oslo 0033, Norway Location/Qualifiers
1. 535
/organism="Falco peregrinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 535,
                                              AFI18429 535 bp DNA VRT 10
Falco peregrinus microsatellite NVH Fp86-2 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of Homo sapiens BAC clone CTA-281G5 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:8954" |
1. .535
/note="microsatellite NVH Fp86-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.2; DB 5;
Pred. No. 1.2e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_type=tandem
110 c 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 GGAATCCATGACAAGCAGCAGGG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 535)
Nesje,M. and Roed,K.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 146285)
Waterston, R.H.
                                                                                                                AF118429.1 GI:6840932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 146285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.1%;
Best Local Similarity 87.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                                                                                                                                                               Falco peregrinus.
                                                                                                                                                                                          Falco peregrinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                                                                                                   10652075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                               DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
AC005083/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
PUBMED
RESULT 1
AF118429
                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFERENCE
                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rocus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
```

us-09-698-903b-11.rge

rpt_family=" 8917126	rpt_family="L1 1337263	rpt_family="L1" 4557481	/rpt_family="AT_rich" 75047554	_family=	/rpt_family~"(CA)n" 84668533	[am1]	amily .1017	amily=	amily="(CA)n" .10681	amily="(T	amily 1123	amily=" .11526	amily .1187	amily="(CATTA)n .12110	family 1216	family="(TA)n" 12490	family="(CAATA)n 12680	tamily= .1336	family="L2" 13540	[amily="	amily-	amily= 1461	Lly=" 16548	amily="L1" .18692	amily="MER119422	amily= .2013	amily. 205	amily- .2160	amily- .2249	amily=". 22523	amily= .2285	/rpt_family="MER4-group?" 2320323380	ყ დ	rpt_family="Al: 364424770	11y="L1 25846	rpt.
repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region		repeat_region	repeat_region	

Louse muscaluse.

Eskaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmusculus and Mammallai Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Barkaryota; Matzker, M. L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Cox, C., Burac, C., Burkett, C., Chacko, J., Chen, G., Chen, G., Cox, C., Davis, C., Delagado, O., Ding, Y., Dugan-Rocchs, S., Fernaque, D., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M., Houx, K., Huber, J., Jackson, L., Marin, R., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R. J., Martin, S., Nelson, A., Nguyen, R., Nguyen, R. ö AC023167 183634 bp DNA HTG 04-NOV-2000 Mus musculus clone RP23-361K18, *** SEQUENCING IN PROGRESS ***, 61 2 (bases 1 to 183034)
Morley, K.C.

Bullect Submission
Submitted (09-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 3, 2000 this sequence version replaced gi:8248589. Gaps Length 146285; ö 3; Indels Query Match
79.1%; Score 18.2; DB 9;
Best Local Similarity 87.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 3; /rpt_family="L2"
36476. 37873
/rpt_family="L1"
38324. 38899
/rpt_family="Retroviral" /rpt_family="AT_rich" 35261. 35288 /rpt_family="(CATTT)n" 35571. 35598 /rpt_family="(CA)n" 35924. 36007 26130. .26254 /rpt_family="MIR" 26792. .26563 /rpt_family="AT_rich" 26792. .27116 /rpt_family="Alu" 30744. 30982 /rpt_family="MIR" 31032, 31739 /rpt_family="L1" 32332, 32448 32536, 32730 /rpt_family="MIR" 32536, 32730 /rpt_family="MIR" Db 20614 GACATCCATGTAAGGAAGCAGGG 20592 1 gaaatccatgtaaagcagcaggg 23 AC023167 AC023167.8 GI:11079356 HTG; HTGS_PHASE1. house mouse. (bases 1 to 183634) Unpublished repeat_region RESULT 13 AC023167/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS δ

COMMENT

```
Jp i.
length
in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
bp in length
                                                                                                             in length
                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in length
                  in length
                                                in length
                                                                                                                                                                           in length
                                                                                                                                                                                                           in length
                                                                                                                                                                                                                                             in length
                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                            in length
                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                          in length
                                                                                                                                                                                                                                                                                                                                                                                                          in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                              length
                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in l
length
                                                                                              length
                                                                                                                                                                                            length
                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                           ength
                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ength.
                                                                                                                              length
                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ength
                                                of 2424
unknown
                                                                                                                                                                           of 2940
                                                                                                                                                                                                                                                                             2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                             2806
                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                        of 2591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                             οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οĮ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oŧ
                                             contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                         gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
contig
gap of
                                                                                                                                                            gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                           gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                              gap of
                                                                                                                                             contig
                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                            contig
                                                                                                                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
                                                                                                                                                                                              gap of
                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                            gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
               107522:
107622:
110046:
                                                            110146:
113098:
113198:
                                                                                                           116570:
116670:
119013:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179834:
179934:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178509:
178609:
                                                                                                                                                                           122053:
                                                                                                                                                                                                                                                                          29604:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44911:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64664:
                                                                                                                                                                                                           .24959:
                                                                                                                                                                                                                           .25059:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57973:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62823:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167971:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170694:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73563:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74902:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .76926:
                                                                                                                                                                                                                                                                                                                                          36608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70795
               103958
107523
1107623
110047
110147
113099
113199
116571
116671
                                                                                                                                                                                                           122154
124960
                                                                                                                                                                                                                                            125060
127169
127269
129605
129705
                                                                                                                                                                                                                                                                                                                         133156
133256
136609
136709
138128
138228
                                                                                                                                                                                                                                                                                                                                                                                                                                       41104
43695
43795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45012
46361
46461
48991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152303
154395
154495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161112
161212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164565
164665
166096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178510
178610
179835
                                                                                                                                                                           119114
122054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150493
152203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173564
174903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75003
                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                  Center course nate: National Center Course nate: Course nate: National Center Course National Center Course Sequencing vector: National Center Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 10583 bp in length
unknown length
of 9744 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
           ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown |
r of 8536 }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
of 7048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
of 4413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 2929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 2196 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
of 3583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
of 4067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 3041
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 3599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
of 3745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10583: contig of 1
10683: gap of unkn
20427: contig of 9
20527: gap of unkn
29063: contig of 8
29163: gap of unkn
36211: contig of 3
36311: gap of unkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
contig
gap of
contig
gap of
.----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93018:
93118:
96993:
97093:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100112:
103857:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29164
36212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36312
42255
42355
47693
47793
51860
51960
55001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59767
59867
59867
602758
67171
67271
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
70300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96994
97094
100013
100113
```

```
Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18673
18773
22304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. (bases 1 to 228809)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwhid, J., Barna, N., Beckerly, R., Beda, F., Baddar, T., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collina, S., Collymore, A., Cooke, P., Ferreitar, R., Tatzhugh, W., Portest, C., Gage, D., Galagan, J., Ferreitar, P., Filzhugh, W., Portest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Landers, T., Lehoczky, J., Levine, P., Macura, A., McKernan, K., Macdonald, P., Marquis, N., Meswan, C., Liu, G., Locke, K., Morman, C.H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Severy, P., Spencer, P., Stange-Thomann, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Lepeats were identified using Repeatmasker:

Nay 31, 2001 this sequence version replaced gi:11560245.

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/Repeatmasker:html
                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO Sapiens chromosome 11 clone RP11-692M12 map 11, WORKING DRAFT SEQUENCE, 25 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                    79.1%; Score 18.2; DB 2; Length 183634; 87.0%; Pred. No. 2.1e+02; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6058 others
181235: contig of 1301 bp in length 181335: gap of unknown length 182487: contig of 1152 bp in length 1818587: gap of unknown length 183634: contig of 1047 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 228809)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo saplens chromosome 11, clone RP11-692M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC021443.8 GI:14269788
HTG; HTGS_PHASE1; HTGS_FULLTOP.
                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-361K18"
a 38982 c 39763 g 49962 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: 692_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 60779 GAAATCCTTGCTAAGCAGGG 60757
                                                                                                                                                                                                                                                                                                                                                                                                         1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 228809)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228809 bp
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.0
Matches 20; Conservative
                   181236
181336
182488
182588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                           48869 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC021443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AC021443/c
LOCUS
                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
```

à

```
Sequencing vector: Mass, mirrors, as on treaus Sequencing vector: Plasmid; n/a; 56% of reads Sequencing vector: Plasmid; n/a; 56% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 214728 bases at least Q30 Consensus quality: 219470 bases at least Q30 Consensus quality: 22925 bases at least Q30 Insert size: 226409; sum-of-contigs Quality coverage: 10.4 in Q20.

* NOTE: This is a "working draft' sequence. It currently consists of 25 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                       of 100 bp contig of 1222 bp in length of 100 bp contig of 1168 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 100 bp contig of 1076 bp in length of 100 bp contig of 1495 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11470: contig of 100 bp
100 gap of 1074 bp in length
100 gap of 100 bp
12684: contig of 1114 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p of 100 bp
contig of 11618 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p of 100 bp contig of 12802 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p of 100 bp contig of 15290 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp contig of 15617 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ontig of 11055 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  up of 100 bp contig of 16876 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55392: contig of 17167 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179217: contig of 23725 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00 bp
3388 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 26004 bp in length.
                                                                                                                                                                                                                                                                                                                                3785: contig of 3785 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                               of 100 bp
contig of 1050 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18772: gap of 100 bp 22303: contig of 3531 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p of 100 bp contig of 2215 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p of 100 bp contig of 3573 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p of 100 bp contig of 9005 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p of 100 bp contig of 6122 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p of 100 bp contig of 7468 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p of 100 bp contig of 8969 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .228809
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Just gap of 28525:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45299 56916; continuous 56917 57016; gap of 55985; contri 65985; contri 66086 78887; contri 78888 78987; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cont
; u: gap of
56916: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109995 110094: gap of 110095 121149: cont.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121150 121249: gap of
121250 138125: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8802 10296; cont
10297 10396; gap of
10397 11470; cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15099; gap of
18672; conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36093; cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9317: gap of
202705: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2805: gap of 228809: cont.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36193; gap of
45198: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25: gap of
8701: con
11: gap of
10296: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94278 94377; gap of
94378 109994; cont
                                                                                                                                                                                                                                                                                                                                                3786 3885; gap of 51886 5107; cor
                                                                                                                                                                                                                                                                                                                                                                                                                 5200
6376 6475; gap c
6476 7525; c
                                                                                                                                                                                                                                                                                                                                                                                        5108 5207: gap
5208 6375:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14999:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179218 179317: 179318 202705 202706 202805: 208099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11570:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138126 138225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155393 155492:
155493 17921
                                                                                                                                                                                                                                                                                                                                                                                                                                              6476 75
7526 7625:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12784:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22403:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28526 28625:
28626 360
36094 36193:
36194 451
45199 45298:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8801:
```

Human gene signatu EST clone EY281. Human saccharide-t Human stomach canc

Selective marker g Human brain Expres

Drosophila melanog

Human TANGO 183 co Primer specific fo Human olfactory re Human ORFX ORF2101

```
PCR primer B01, to recognise foreign DNA and flanking sequence of MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MS-B2 elite event; transgenic Brassica plant; transformation event; male-sterility gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                       AAF93749
AAF29357
AAV49584
AAH64828
                                                                                                                                                                                                                                                                                                  AAF21831
AAC51418
AAC51029
AAC85075
AAF33128
                                                                 AAV88563
AA246937
                                                                                                                                                                                                                                                                                                                                                                                                                        AAS22844
AAZ33327
                                                                                                                                                                                                                                                                                      AAZ41983
                                                                                                                     AAF93941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-2000; 2000WO-EP10680.
 99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (4.00 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD07000 standard; DNA;
WO200131042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD07000;
 RESULT
AAD07000
(without alignments)
27.519 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                         February 25, 2002, 18:17:38; Search time 716.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SIDS2/gcgdata/geneseq/Nat1999.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1990.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1990.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1991.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1992.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1994.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1994.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1996.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1996.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1998.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1999.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1999.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1999.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1999.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1999.DAT:#
| SIDS2/gcgdata/geneseq/geneseqr/Nat1090.DAT:#
                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                     Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                             930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 nucleic search, using sw model
                                                                                                                                                                           gaaatccatgtaaagcagcaggg
                                                                                                                                                                                                     IDENTITY_NUC Gapor 1.0
                                                                                                                                           US-09-698-903B-11
23
                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
```

sed

Minimum DB Maximum DB

Database

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

cDNA encodin secreted pro organic cati

by of

Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -

(AVET) AVENTIS CROPSCIENCE NV

De Beuckeleer M;

Weston B,

PCR primer B01, to Right (5') border Left (3') border f Arabidopsis thalia

Human secreted pro Arabidopsis thalia Human cDNA sequenc polynucieoti polynucleoti

Human

AAD06997 AAD06999 AAC46330 AAC39525 AAL158467 AAI58467 AAI60253 AAT74989

416 1152 11567 1153 2857 4495 4775 8826

100.0 100.0 100.0 81.7 75.7 74.8 74.8 74.8 74.8

23 23 18.8 17.4 17.2 17.2 17.2 17.2

5 7 11 11 11

ပပ

Score

Result МО МО WPI; 2001-300517/31.

Claim 1; Page 33; 53pp; English

Saccharomyces cere Mutant YLR087c gen

Human secreted pro Human PRO1248 (UNQ DNA encoding prote Human TANGO 183 cD Human endometrium Human breast and o

Arabidopsis thalia Arabidopsis thalia Human secreted pro

Atherosclerosis-as cancer assoc ORFX ORF2413 cDNA encodin EST-derived

Human Human Human Human Human

Human cDNA encodin Amyloid-beta prote Human stomach canc

Arabidopsis thalia Arabidopsis thalia

70 G; 136 T; 0 other

us-09-698-903b-11.rng

```
hybrid seed from the transgenic Brassica plant.
The present sequence is right (5') border flanking region of elite event
MS-B2.
                                                           Sequence 415 BP; 154 A; 55 C;
                                                                                                                                                                                                                   RESULT
         888888
                                                                                                                                                                           οp
                                                                                                                                                    ò
                                                                                                                                                                                                                 ö
                     seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is PCR primer which is used to recognise foreign DNA and a flanking sequence of elite event MS-B2.
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by
of
             present invention relates to a transgenic Brassica plant or its
                                                                                                                                                                                                                                                                                                                                                                                                                               MS-B2 elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                               ö
                                                                                                                                                                                100.0%; Score 23; DB 22; Length 23; Larity 100.0%; Pred. No. 0.088; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "Corresponds to plant DNA"
235..415
                                                                                                                                           Sequence 23 BP; 9 A; 4 C; 7 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 51; 53pp; English
                                                                                                                                                                                                                                      gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AVET ) AVENTIS CROPSCIENCE NV.

    Agrobacterium sp.
    Brassica sp.

                                                                                                                                                                                                                                                                                                                         AAD06997 standard; DNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               male-sterility gene; ds
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-300517/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200131042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                              06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weston B,
                                                                                                                                                                                                                                                                                                                                                    AAD06997;
*888888888888
                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                           g
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elite event
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is left (3') border flanking region of elite event MS-B2.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by
of
                                                                                                                                                                                                                                              event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                             ö
    Length 415;
                             Indels
                                                                                                                                                                                                                  Left (3') border flanking region of elite event MS-B2.
                            ö
                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "Corresponds to plant DNA"
  Score 23; DB 22;
Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..193
/*tag= a
/note= "Corresponds to T-DNA"
                            Mismatches
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 52; 53pp; English.
                                                   1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AVET ) AVENTIS CROPSCIENCE NV.
 100.0%;
100.0%;
                                                                                                                             AAD06999/c
ID AAD06999 standard; DNA; 416
                                                                                                                                                                                                                                                                                    - Agrobacterium sp.
- Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0430497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Beuckeleer M;
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                          194..416
/*tag= b
                          Conservative
                                                                                                                                                                                                                                                           male-sterility gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-300517/31.
Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             WO200131042-A2
                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                           06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1999;
                                                                                                                                                                                                                                              MS-B2 elite
                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weston B,
                                                                                                                                                                    AAD06999
                                                                                                                                                                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                                                                Chimeric
```

Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;

The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the

```
990S - 0139452
990S - 0139453
990S - 0139454
990S - 0139455
990S - 0139456
990S - 0139456
990S - 0139459
990S - 0139461
990S - 0139461
990S - 0139461
990S - 0139462
990S - 0139462
990S - 0139462
990S - 0139463
990S - 0139463
990S - 0139899
                                                                                                                                                                                                                                                                                                  99US-0141287.
99US-0141287.
99US-0142055.
99US-0142390.
99US-0142803.
99US-0142803.
99US-0142877.
                                                                                                                                                                                                                                                                                                                                                                                                                    990S-0143624.
990S-0144005.
990S-0144085.
990S-0144086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990S-0145089.
990S-0145192.
990S-0145145.
990S-0145218.
990S-0145274.
990S-0145276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  990S-0145918.
990S-0145919.
990S-0145951.
990S-0146386.
990S-0146389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0147204.
990S-0147302.
990S-0147192.
990S-0147260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0144333.
99US-0144334.
99US-0144335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0144352.
99US-0144632.
99US-0144884.
99US-0144814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0145086.
99US-0145088.
99US-0145085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0147416.
99US-0147493.
99US-0147935.
99US-0148171.
                                                                                                                                                                                                                                                                          99US-0140823
99US-0140991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144331
99US-0144332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0145087
 14 - JUN - 1999;

16 - JUN - 1999;

17 - JUN - 1999;

18 - JUN - 1999;

22 - JUN - 1999;

23 - JUN - 1999;

23 - JUN - 1999;

24 - JUN - 1999;

24 - JUN - 1999;

26 - JUN - 1999;

27 - JUN - 1999;

28 - JUN - 1999;

29 - JUN - 1999;

20 - JUN - 1999;

21 - JUN - 1999;

21 - JUN - 1999;

22 - JUN - 1999;

23 - JUN - 1999;

24 - JUN - 1999;

27 - JUN - 1999;

28 - JUN - 1999;

29 - JUN - 1999;

20 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                           01-JUL-1999;
02-JUL-1999;
06-JUL-1999;
08-JUL-1999;
12-JUL-1999;
13-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1999;
15-JUL-1999;
16-JUL-1999;
16-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1999;
21-JUL-1999;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-1999;
09-AUG-1999;
10-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1999;
23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-1999;
23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1999;
27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 - JUL - 1
    ö
                             Gaps
                            .
0
                                                                                                                                                                                                                                             Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
 Score 23; DB 22; Length 416;
Pred. No. 0.14;
Mismatches 0; Indels
                                                                                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 49743.
                                                                 Query Match 100.0%; So
Best Local Similarity 100.0%; Pr
Matches 23; Conservative 0;
                                                   1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                             ВР
                                                                                                                                          AAC46330 standard; DNA; 1152
                                                                                                                                                                                                                                                                                                                                                                                                       9905-0121825.
9905-0123180.
9905-0125788.
9905-0126784.
9905-01267462.
9905-0127462.
9905-0128714.
9905-0128714.
9905-013049.
9905-013248.
9905-013248.
9905-013248.
9905-013248.
9905-013248.
9905-013248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0134221.
99US-0134370.
99US-0134768.
99US-0134941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0135124.
99US-0135353.
99US-0135629.
99US-0136021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0136392.
990S-0136782.
990S-0137528.
990S-0137528.
990S-0137724.
990S-0138540.
                                                                                                                                                                                                                                                                                                                                                                                 2000EP-0301439
                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 MAX - 1999;
19 MAX - 1999;
20 MAX - 1999;
21 - MAX - 1999;
24 - MAX - 1999;
27 - MAX - 1999;
28 - MAX - 1999;
01 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999, 05-MAR-1999, 23-MAR-1999, 23-MAR-1999, 25-MAR-1999, 01-APR-1999, 06-APR-1999, 23-APR-1999, 23-APR-1999, 05-MAY-1999, 05-MAY-1999, 05-MAY-1999, 14-MAY-1999, 14-MA
                                                                                                                                                                                                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MAY-1999;
-MAY-1999;
-MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
                                                                                                                                                                                              18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAY-1999;
                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                     AAC46330;
                                                                                                                   RESULT A
                                                    ò
                                                                            q
```

immunosuppressive, antiarterioscierotic; antiinflammatory; nootropic; neuroprotective; antidiabetic; tranquiliser; vulnerary; antibacterial; antipsoriatic; antiarrhythmic; antimematic; cardiant; anti-HIV; autoimmune disorder; allergic condition; cardiovascular disorder; cancer; neurological disease; tissue repair; ss.

secreted protein; cytostatic; antiarthritic; antiasthmatic;

Human secreted protein encoding cDNA for gene 41.

(first entry)

09-FEB-2001

AAC79889;

AAC79889 standard; cDNA; 1567 BP

AAC79889

```
DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.8; D)
Pred. No. 15;
0; Mismatches
                    9905-0148684
9905-0149368
9905-0149426
9905-0149426
9905-0149722
9905-0149929
9905-0149902
9905-0149930
                                                                                                                                          99US-0152363.
99US-0153070.
99US-0153758.
                                                                                                                                                                                   9908-0155139
9908-0155486
9908-0155486
9908-0156596
9908-0157117
9908-0157753
9908-0158029
9908-0158029
9908-015823
9908-015823
9908-0158369
                                                                                          99US-0150884.
99US-0151065.
99US-0151066.
99US-0151080.
                                                                                                                                                              99US-0154018.
99US-0154039.
99US-0154779.
        99US-0148341
99US-0148565
                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161359.
99US-0161360.
99US-0161361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.7%;
90.9%;
                                                                                                                                                                                                                                                                                    99US-0159329
99US-0159330
                                                                                                                                                                                                                                                                                                               99US-0159638
                                                                                                                                                                                                                                                                                                                                           99US-0160768
                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0161993
99US-0162142
                                                                                                                                                                                                                                                                                                  99US-0159331
                                                                                                                                                                                                                                                                                                                                                               99US-0160815
                                                                                                                                                                                                                                                                                                                                                                                                99US-0161405
                                                                                                                                                                                                                                                                                                                                   990S-0160767
                                                                                                                                                                                                                                                                                                                                                        99US-0160814
                                                                                                                      99US-015
99US-015
99US-015
                                                                                                                            31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
                                                                                                                                                                                                                                                       12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
                                                                                                                                                                                                                                                                           13 - OCT - 1999;
14 - OCT - 1999;
14 - OCT - 1999;
14 - OCT - 1999;
16 - OCT - 1999;
21 - OCT - 1999;
21 - OCT - 1999;
22 - OCT - 1999;
25 - OCT - 1999;
26 - OCT - 1999;
26 - OCT - 1999;
27 - OCT - 1999;
28 - OCT - 1999;
                            16-AUG-1999;
                                                                                                                                                                                                                      04-0CT-1999
                                                                                                                                                                                                                            -OCT-1999
                                                                                                                                                                                                                                                08-OCT-1999
                                                       20-AUG-19
20-AUG-19
23-AUG-19
23-AUG-19
25-AUG-19
26-AUG-19
```

Novel 49 human secreted proteins useful for diagnosis, prevention and treatment of disorders including neurological, cell proliferative, cardiovascular, and autoimmune/inflammatory disorders and microbial

Rosen CA, Ruben SM, Komatsoulis G;

WPI; 2000-638176/61. P-PSDB; AAB44870.

(HUMA-) HUMAN GENOME SCI INC

99US-0124142. 99US-0138597. 99US-0168666.

12-MAR-1999; 11-JUN-1999; 03-DEC-1999;

09-MAR-2000; 2000WO-US06057.

WO200055176-A2.

21-SEP-2000

Homo sapiens.

Claim la; Page 356-357; 405pp; English.

Infections

```
regeneration, cancer, neovascular glaucoma, diabetic retinopathy, rheumatoid arthritis, psoriasis, diseases associated with increased appproasis that include acquired immunodeficiency syndrome (AIDS), neurological diseases such as Parkinson's disease, viral, bacterial, fungal or parasitic diseases. They are also used to repair, replace or protect tissue damage by congenital defects, to treat trauma, in surgery, including cosmetic plastic surgery, to treat fibrosis, reperfusion injury
```

ö Gaps ; Length 1152; Indels

3

ö 23

20; Conservative

Similarity

Local Matches 1088

g à

2 aaatccatgtaaagcagcaggg

```
990S-0137222.
990S-0137222.
990S-013724.
990S-0138894.
990S-0138847.
                                                                                                                                                                                                                                                                           9905 - 0139454
9905 - 0139455
9905 - 0139456
9905 - 0139456
9905 - 0139459
9905 - 0139460
9905 - 0139461
9905 - 0139462
                    99US-0135124.
99US-0135353.
99US-0135629.
                                                             99US-0136021.
99US-0136392.
99US-0136782.
                                                                                                                                                                                                               990S-0139119.
990S-0139452.
990S-0139453.
990S-0139492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0144814.
99US-0145086.
99US-0145088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0145276.
99US-0145913.
99US-0145918.
99US-0145919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0140354.
99US-0140695.
99US-0140823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0144335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0145145.
99US-0145218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139763
99US-0139817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0142055
99US-0142390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0142803
99US-0142920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0142977
99US-0143542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144086
99US-0144325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0145085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0145089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0139899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0140353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0140991
99US-0141287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0141842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0142154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0143624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0144005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0144085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0144333
99US-0144334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0144632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0144884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0145087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0145192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0145224
    19-MAY-1999, 20-MAY-1999, 24-MAX-1999, 24-MAX-1999, 27-MAY-1999, 27-MAY-1999, 21-MAY-1999, 21-MAY-1999, 21-MAY-1999, 21-MAY-1999, 21-MAY-1999, 21-MAY-1999, 21-MAY-1999, 21-MAY-1999, 21-MAY-1999, 21-MAY-20N-1999, 21-MAY-20N-1999
                                                                                                                                                                                                                                                                                                          18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-1999;
23-JUL-1999;
23-JUL-1999;
23-JUL-1999;
                                                                                                                                                                                                                                                                            18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1999;
21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 - JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1999
       ö
or systemic cytokine damage, to stimulate chondrocyte growth, to prevent skin aging due to sunburn, to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression, memory, stress and for accelerating wound healing. (1), (11) and/Or their agonist or antagonist are useful as food additives or preservatives to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamin, mineral or other nutritional components. (1) is useful for screening therapeutic compounds. (II) is useful in forensic biology for detecting DNA sequences and as diagnostic probes for detecting the presence of specific mRNA in a particular cell type.
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                             75.7%; Score 17.4; DB 21; Length 1567; ilarity 94.7%; Pred. No. 71; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                    Sequence 1567 BP; 303 A; 510 C; 463 G; 291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 24952.
                                                                                                                                                                                                                                                                                                                                                                                  AAC39525 standard; DNA; 1153 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990S - 0121825
990S - 0123180
990S - 0125788
990S - 0125788
990S - 0126785
990S - 0126785
990S - 0128234
990S - 0128234
990S - 0130077
990S - 0130891
990S - 0130891
990S - 0132484
990S - 0132484
990S - 0132486
                                                                                                                                                                                                                                                                                            99US-0134219.
99US-0134221.
99US-0134370.
99US-0134768.
                                                                                                                                                                                                                                                                           4 atccatgtaaagcagcagg 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 - APR - 1999;
23 - APR - 1999;
28 - APR - 1999;
30 - APR - 1999;
30 - APR - 1999;
65 - MAY - 1999;
66 - MAY - 1999;
07 - MAY - 1999;
07 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                AAC39525;
                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                   AAC39525
                                                                                                                                                                                                                                                                                                       g
```

```
990S - 0147036
990S - 0147304
990S - 0147304
990S - 0147305
990S - 0147305
990S - 0147416
990S - 0147416
990S - 0147935
990S - 0148171
990S - 0148171
990S - 0148171
990S - 0148171
990S - 0149723
990S - 0149902
990S - 0149902
990S - 015966
990S - 015966
990S - 015966
990S - 015966
990S - 015973
                                                                                                                                                                                                                                                                                                                                           99US-0155139.
99US-0155486.
99US-0155659.
                                                                                                                                                                                                                                                                                                                                                                   99US-0156458.
99US-0156596.
99US-0157117.
  99US-0145951
                                                                                                                                                                                                                                                                                                                                                                                                    99US-0157865
99US-0158029
                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0158232
                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0158369
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0159295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0160768
99US-0160770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0160980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0161359
                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0159294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0159330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0159331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0159638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0159584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0160741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161406
                                                                                                                                                                                                                                                                                                                                                                                             99US-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0159
28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
                                                                                                                                                                     18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                      25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                          05-007-1999

06-007-1999

08-007-1999

13-007-1999

13-007-1999

13-007-1999

14-007-1999

14-007-1999

14-007-1999

14-007-1999

18-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999

21-007-1999
                                                                                                                                                                                                                                                                                                                                                   23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
                                                                                                                                                                                                      23-AUG-1999;
                                                                                                                                                             17-AUG-1999,
                                                                                                                                                                                                                                                                                                                                            22-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-0CT-1999
26-0CT-1999
                                                                                                            10-AUG-1
```

```
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises of comprises; to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprisising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises as 1'-end sequence complementary to a polynucleotide comprises as 1'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in each the primers are useful for synthesisaring polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length
                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                         ó
                                                                                                                       Length 1153;
                                                                                                                                                         Indels
                                                                                                                                                       ٠.
۳
                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID 17809; 2537pp + CD ROM; English.
                                                                                                                                                       0; Mismatches
                                                                                                                       Score 17.2;
                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence SEQ ID NO:17809.
                                                                                                                                                                                  AAH18005 standard; cDNA; 2857 BP
                                                                                                                 74.8%;
86.4%;
              990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999; 99JP-0248036.
27-AUG-1999; 9JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-02418999.
 99US-0161360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2001 (first entry)
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-318749/34.
                                                                                                                                     Best Local Similarity
Matches 19; Conserv
            26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2001
                                                                                                                                                                                                                                                                                                                                          AAH18005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T, Is
Ishii S,
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                       AAH18005
                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                     QD
PR
PR
PR
                                                                                                                                                                                                                                                                                                                        δλ
```

^

```
Tang YT,
                                                                                                                                                                                                                                                                        AAI60253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang
                                                                                                                                                                                                                                           AA160253
                                                                                                                                                                                                  Вp
   88888888888%8
                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAHH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang D;
                                                                                                                                                                                                                                                                                              nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                       peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease, Hauntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ren F, War Zhang J;
                                                                                                                 ;
0
                                                                                            Length 2857;
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qian XB,
Yang Y,
                                                              Sequence 2857 BP; 859 A; 564 C; 576 G; 858 T; 0 other;
                                                                                             22;
                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen R, Ma Y, (
Xu C, Xue AJ,
, Drmanac RT;
                                                                                               DB
                                                                                                                  Mismatches
                                                                                            Score 17.2;
Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 670; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen R,
                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 670.
                                                                                                                                                1659 aactccttgtaaagcagcagag 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                 ö
                                                                                                                                     23
                                                                                                                                                                                                            AAI58467 standard; cDNA; 4495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-048B725.
2000US-0552317.
2000US-0598042.
                                                                                            74.8%;
86.4%;
                                                                                                                                    2 aaatccatgtaaagcagcaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                     (first entry)
                                           the present invention.
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-442253/47.
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Z, V
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
Wang 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAM39311
                                                                                                                                                                                                                                                                                                                                                                                         WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                 leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2000;
                                                                                                                19;
                                                                                                                                                                                                                                                    22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
Wang J, V
Zhao QA,
                                                                                                                                                                                                                                AAI58467;
                                                                                                                                                                                                                                                                                              Human:
                                                                                                                                                                                       œ
                                                                                                                Matches
                                                                                                                                                                                                  AAI584
                                                                                                                                                         a
 ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic thateral scalerosls, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang D;
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                  4495;
                                                                                                                                                                                                                                             Sequence 4495 BP; 1401 A; 945 C; 1040 G; 1109 T; 0 other;
                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                Score 17.2; DB : Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4242; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 4242.
                                                                                                                                                                                                                                                                                                                                                                                                                                        3034 aactccttgtaaagcagcagag 3055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA; 4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
                                                                                                                                                                                                                                                                                                                  74.8%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                 2 aaatccatgtaaagcagcaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                Query Match 74.8
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442253/47.
P-PSDB; AAM41097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI60253 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QA,
```

æ

ö

Gaps

ó

Indels

Pred. No. 1.1e+02;

ö

Conservative

86.48;

Best Local Similarity

19;

Matches

23

2 aaatccatgtaaagcagcaggg

7504 AAATTAATGTAAAGCACCAGGG 7483

g à

11

```
ö
in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral solerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer dispnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This novel genomic DNA CSF-1 (cold sensitivity of fermentability) encodes by protein capable of complementing a mutation showing low temperature sensitivity in fermentation. The Saccharonayces cerevisiae YHK 1243 has an inactivated gene encoding the new protein or has the novel DNA sequence contained in its chromosome. The protein can be used in dough to produce
                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae; cold sensitivity of fermentability; CSF-1; low temperature sensitivity; yeast; bread; ethanol; fermentation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein for complementing low temperature sensitivity in fermentation - can be inactivated in yeast and used for producing
                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                      Score 17.2; DB 22; Length 4775; Pred. No. 1e+02; 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8826 BP; 2903 A; 1551 C; 1760 G; 2612 T; 0 other;
                                                                                                                                                                                                                                   Sequence 4775 BP; 1494 A; 999 C; 1122 G; 1160 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae YHK1243 encoding CSF-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tokai M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Pages 21-40; 48pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X,
                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contained in its chromosome. The bread, and to produce ethanol.
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
AAT74989/c
ID AAT74989 standard; DNA; 8826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                        ch
1 Similarity 86.4%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                    2 asstccstgtssagcagcaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95JP-0343700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-JP03862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawasaki H, Kikuchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-363678/33.
                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bread and ethanol
                                                                                                                                                                      disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW22050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9724442-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT74989;
                                                                                                                                                                                                                                                                                     Query Match
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated from a cold sensitive strain of Saccharomyces cerevisiae. The sequence was isolated from the clone YCp50-10.39 which was able to complement the cold sensitive strain Hil3.2.30. This gene contains a TCA to TGA mutation which encodes a truncated protein. The wild type gene contains an open reading frame of 8814 bases encoding a protein of 2958 amino acids, whereas this mutant gene contains an open reading frame of 7488 bases encoding a protein of 2496 amino acids. Weast strains containing the YLK087C gene are used, fresh or dried, in modified breadmaking processes, i.e. in processes where the delay between mixing the dough and baking exceeds 6 hr. Particularly they are used to make
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the dough and baking exceeds 6 hr. Particularly they are used to make French-style bread (no added sugar) or breads with sugar content below 5%. The strains can also be used to make mixed yeast/bacteria acidic leavening agents. The strains can also be used in brewing and winemaking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of a mutant gene (designated YLR087c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                     Mutant; cold sensitive; yeast; complementation; breadmaking; dough; sugar; leavening agent; brewing; winemaking; truncation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New strains of bread-making yeast with low fermentative activity low temperature - allows production of doughs that can be stored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9621 BP; 3126 A; 1679 C; 1903 G; 2907 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                  Mutant YLR087c gene from cold sensitive yeast strain.
                                                                                                                                                                                                                                                                                       /product= "mutant YLR087c protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.2; DB 18;
Pred. No. 1.2e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cold for many hours before final baking
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 56-59; 76pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wadoux I;
                 AAT94548 standard; DNA; 9621 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leavening agents. The strains as a cold-sensitive phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.8%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                               97WO-FR00254.
                                                                                                                                                                                                                                                                                                                                                                                                                               96FR-0001562
                                                                                     25-MAR-1998 (first entry)
                                                                                                                                                                                                                                                           376..7866
/*tag= a
                                                                                                                                                                                                       Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.4'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loiez A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LESA ) LESAFFRE & CIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-414988/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW36093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colavizza D,
                                                                                                                                                                                                                                                                                                                       WO9728693-A1
                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                             14-AUG-1997.
                                                     AAT94548;
AAT94548/c
```

23

2 aaatccatgtaaagcagcaggg

δλ

DB 18; Length 8826;

74.8%; Score 17.2;

Query Match

```
The invention relates to the use of effectors/regulators for Rab and Rho substances useful as pharmaceutical agents for the prophylaxis or treatment of cancer and other proliferative, invasive or cell migration treatment of cancer and other proliferative, invasive or cell migration disorders such as endometriosis, atherosclerosis, inflammatory and allergic diseases uch as poorlasis. The infectious diseases and skin repair diseases such as psoriasis. The infectious diseases include skin repair diseases such as psoriasis. The infectious diseases include they tuberculosis, pseudotuberculosis, cholera, gastroenteritis, enteric fever, malaria, typhus, diseases caused by pathogens such as Listeria, Mycobacterium, Staphylococcus, Toxoplasma, Trypanosoma, Salmonella, Destinania, Coxiella, Shigella, Yersinia, Nelsseria, Vibrio, Bartonella, The cancer includes benign tumor, malignant tumor, carcinoma, leukemia, glioma or a neuroblastoma, in particular lung carcinoma, brain, prostate, liver and every tumor, that invades other tissues and corgans distinct from its site of origin. The assay is highly sensitive and advantageous in the selectivity of the targets. The present sequence crepresents the DNA encoding a human p95 protein. A multiprotein complex including p100, p95, p60, p45, p25 (sequences AAF57404-408) acts as a creams and an an analysis of the function of endocytic trafficking.
antipsoriatic; antiinflammatory; antiallergic; antipyretic; cytostatic; antibacterial; gynecological; antiatherosclerotic; gene therapy; human; p100; p95; p60; p45; p25; endocytic trafficking; GTPase effector; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of effectors of GTPase as target in a in vitro/vivo assay for detecting substances for prophylaxis, treatment of cancer, cell migration disorders, e.g. Alzheimer's, infectious diseases, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1752 BP; 496 A; 425 C; 444 G; 387 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                            Murphy C, Zerial M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.0%; Score 16.8; DB 22;
90.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                         (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 70-71; 76pp; English.
                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT60073 standard; DNA; 4388 BP
                                                                                                                                                             /product= "p95"
                                                                                                                                                                                                                                                                                                                                                                            Christophoridis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gaaatccatgtaaagcagca 20
                                                                                                                                                                                                                                                                  18-SEP-2000; 2000WO-EP09130.
                                                                                                                                                                                                                                                                                                      99EP-0118385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAY-1997 (first entry)
                                                                                                                                              Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 73.0
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-257888/26.
P-PSDB; AAB62180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis
                                                                                                                                                                                                WO200120022-A1
                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                      16-SEP-1999;
                                                                                                                                                                                                                                 22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                          Nielsen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT60073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT60073
   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DX SX E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rab; Rho; GTPase; pharmaceutical; cancer; anti-HIV; tuberculostatic;
protozoacide; atidiabetic; nootropic; neuroprotective; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which are thought to be essential, and to a screening assay for identifying compounds which have a physiological effect on these proteins. Suitable compounds are useful as pesticides and may be used in conjunction with other pesticides and herbicides for crop protection. The gene corresponding to the present sequence is located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                            Drosophila melanogaster; fruit fly; essential gene; screening assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is part of an essential gene from Drosophila melanogaster. Lack of expression of the protein encoded by this gene leads to a lethal or semi-lethal phenotype. The invention relates to 902 nucleic acid sequences from genes encoding proteins
                                                                                                                                                                                                             Drosophila melanogaster essential gene fragment, SEQ ID NO: 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening assays for used for identifying compounds having a physiological effect on proteins identified as being essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 602 BP; 159 A; 131 C; 120 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.0%; Score 16.8; DB 22; 90.0%; Pred. No. 1.2e+02; 1ve 0; Mismatches 2;
                                                                                                                                                                                                                                                                 crop protection; chromosome 3; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 340-341; 695pp; English.
7927 AAATTAATGTAAAGCACCAGGG 7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF57408 standard; DNA; 1752 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang MY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human p95 protein encoding DNA.
                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 AGATCCATGTAAATCAGCAG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000; 2000WO-GB03444.
                                                                                                                                                                                                                                                                                                                                                                                                                                               99GB-0021009
                                                                                                     AAH29132 standard; DNA; 602
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 aaatccatgtaaagcagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davies RW, Kaiser K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-281436/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on chromosome 3.
                                                                                                                                                                                                                                                                                                                                       WO200118547-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-2001
                                                                                                                                                                            17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2001
                                                                                                                                                                                                                                                                  pesticide;
                                                                                                                                        AAH29132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF57408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF57408/c
                                                                                     AAH29132/
                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                g
                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

De Renzis S;

ö

Gaps

ó

Length 1752; Indels

```
WPI; 1993-272882/34
          δλ
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                     This sequence represents the selective marker gene of the invention. This gene encodes an enzyme relating to the biosynthetic system of leucine synthesis. This sequence can be used in a recombinant vector for the transformation of Rhizomucor pusilius. The recombinant vector also includes another DNA sequence encoding a protein. The plasmid and the transformed Rhizomucor pusilius can then be used for the efficient production of useful proteins and peptides, which are encoded by the second DNA sequence in the vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                 Selective marker; enzyme; biosynthetic system; leucine synthesis;
Rhizomucor pusillus; protein production; ss.
                                                                                                                                                                                                                                Novel selective marker gene - used in a transformation system of Rhizomucor pusillus for protein production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             73.0%; Score 16.8; DB 18; Length 4388; 90.0%; Pred. No. 1.6e+02; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4388 BP; 1144 A; 1094 C; 1077 G; 1073 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human brain Expressed Sequence Tag EST00937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                               Claim 1; Page 9-10; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moreno RF, Venter CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ60834 standard; DNA; 281 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gaaatccatgtaaagcagca 20
                                                                                                                                       95JP-0166115
                                                                                                                                                              95JP-0166115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-US01294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0837195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                  (MEIT ) MEITO SANGYO KK.
           Selective marker gene.
                                                                                                                                                                                                         WPI; 1997-126428/12.
                                                                                        JP09009971-A.
                                                                                                                                       30-JUN-1995;
                                                                                                                                                            30-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-1994
                                                                                                               14-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09316178-A
                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ60834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ60834
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
```

```
ö
                                                                                                                                                                   The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in Vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST00937 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also AAQ59041-Q61440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging of most human genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.6; DB 14;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 281 BP; 45 A; 81 C; 91 G; 61 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 25, 2002, 18:17:40 Job time: 16698 sec
                                                                                                                  Example 4; Page 398; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserv
```

	;•1				
is .					
			÷		
		•			
				:	
				•	

```
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Appli
Sequence 9, Appli
Sequence 25, Appl
Sequence 25, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 18, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appl
App
App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38, Appl
Sequence 38, Appl
Sequence 6, Appli
Sequence 6, Appli
                                                             // Search time 301.6 Seconds
(without alignments)
17.271 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appli
Appli
8, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, 1
Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2
Sequence 2
Sequence 1
Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-238-127-1
US-09-338-303-7
US-09-372-399-9
US-08-706-702-25
US-08-706-706-25
US-08-002-114-2
US-08-899-371-2
US-08-899-371-1
US-09-039-5558-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-250-346-21
US-07-885-089B-15
US-07-885-089B-17
US-09-020-956-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-414-335-2
-08-781-891-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-030-607-110
                                                                                                                                                                                                            Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-213-767-1
US-09-128-155-16
                                                                                                                                                                                        351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-171-969-
                                                                                                                                 1 gaaatccatgtaaagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
GenCore version
Copyright (c) 1993 - 2000
                                                                 February 25, 2002, 18:05:49
                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           nucleic search, using sw model
                                                                                                                                                      IDENTITY_NUC Gaport 1.0
                                                                                                                                                                                                                                                                                                                   Issued_Patents_NA:*
                                                                                                         US-09-698-903B-11
                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1351
1608
1613
5183
5243
16442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                       Scoring table:
                                           ı
                                                                                                                                                                                                                                      08
                                           OM nucleic
                                                                                                                                    Seguence:
                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                      Minimum |
Maximum |
                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
```

```
7, Appli
7, Appli
7, Appli
7, Appli
1, Appli
1, Appli
3, Appli
4, Appli
18, Appli
18, Appli
                          Sequence 2
Sequence 7
Sequence 7
Sequence 7
Sequence 7
Sequence 7
Sequence 6
Sequence 6
Sequence 6
Sequence 6
Sequence 6
Sequence 6
Sequence 7
Sequence 6
Sequence 7
Sequence 6
Sequence 6
Sequence 7
Sequence 6
Sequence 7
Sequence 6
Sequence 7
Sequence 7
Sequence 6
Sequence 7
Sequence 7
Sequence 7
Sequence 7
Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KAMSAKI, Hideki
APPLICANT: KAMSAKI, Hideki
APPLICANT: TOKAI, Masaya
APPLICANT: TOKAI, Masaya
APPLICANT: TOKAI, Wasuhiro
APPLICANT: OUCHI, Kozo
TITLE OF INVENTION: DAN EMPERATURE-SENSITIVE FERMENTABILITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
ADDRESSER: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 ROCKefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette – 3.50 inch, 1440 Kb storage.
COMPUTER: IBM PS/V
               PCT - US94 04361-22
US - 08 - 48 + 993B - 7
US - 08 - 48 4 - 158B - 7
US - 08 - 48 4 - 158B - 7
US - 08 - 48 0 - 150A - 7
US - 08 - 458 - 731 - 7
US - 08 - 458 - 731 - 7
US - 08 - 150A - 7
US - 08 - 150A - 7
US - 08 - 150A - 18
US - 08 - 094 - 534 - 18
US - 08 - 1543 - 18
US - 08 - 18 - 18
                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US94-08000-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: J9343700/95
FILING DATE: 28-DECEMBER-1995
APPLICATION NUMBER: PCT/JP96/03862
FILING DATE: 27-DECEMBER-1996
ATTONNEY/AGENT INFORMATION:
NAME: PERTY, LAWRENCE S.
REGISTRATION NUMBER: 31865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Saccharomyces cerevisiae x2180-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08894344C; Patent No. 6172196; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION NUMBER: 31865
TELEPHONE: 212-218-2100
TELEFAX: 212-218-2200
TELEFAX: 712-218-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 8874 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                 1338
1338
1338
1338
1338
2507
2507
18994
18994
18994
35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
.0 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
                               US-08-894-344C-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
STRAIN: X
  155.7
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
155.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
156.2
  0 0 0 0 0 0 0 0
```

FEATURE

```
NESCHIER PLICATION US/09238303B

Sequence 7, Application US/09238303B

Sequence 7, Application US/09238303B

Sequence 7, Application US/09238303B

SEGUENCE 1 NFORMATION:

APPLICANT: Barr, Margaret C.

TITLE OF INVENTION: No. 6284253el Feline Immunodeficiency Virus Nucleotide Sequenc

TITLE OF INVENTION: NOWBER: US/09/238,303B

CURRENT FILING DATE: 1999-01-28

EARLIER APPLICATION NUMBER: US 60/072,927

EARLIER FILING DATE: 1998-01-29

NUMBER OF SEQ ID NOS: 17

LENGTH: 9751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: recombinant viral clone constructed from the genomic DNA of CTHER INFORMATION: a Pallas's cat feline immunodeficiency virus US-09-238-303-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 2460;
         NOVEL GENES ENCODING TRANSPORTER-LIKE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                       MEDIUM TIRE: LIBACOMPATIBLE
COMPUTER: TEM COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: FASESED for Windows 95
SOFTWARE: FASESED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,127
FILING DATE: 06-NOV-1997
PRIOR APPLICATION NUMBER: US/08/964,127
ATORNEY-AGENT INFORMATION:
NAME: CTEWAS, Ph.D. L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/POCKET UNMBER: 07334/038001
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
     TITLE OF INVENTION: NOVEL GENES ENCOD TITLE OF INVENTION: MOLECULES NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CIIY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2242 GAAGTGAATGCAAAGCAGCAGGG 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Coding Sequence
LOCATION: 498...2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                            ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2460 base pair
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : LOCATION:
US-08-964-127-1
                                                                                                            CITY: BOX
STATE: M.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          å
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 8874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 9621;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature

; LOCATION: (9318)

; OTHER INFORMATION: Use of n signifies any of g, a, c

US-09-125-028-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.2; DE
Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Score 17.2;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            % Sequence 1, Application US/08964127 | Sequence 1, Application US/08964127 | Patent No. 6273565 | GENERAL INFORMATION: APPLICANT: Grandearl, Andrew David John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7552 AAATTAATGTAAAGCACCAGGG 7531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7927 AAATTAATGTAAAGCACCAGGG 7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 asatccatgtasagcagcaggg 23
                                                                                                                                    NAME/KEY: cleavage-site
LOCATION: 4388 to 4393
IDENTIFICATION METHOD: S
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                   NAME/KEY: cleavage-site
LOCATION: 1291 to 1296
IDENTIFICATION METHOD: S
                                                                                                                                                                                              NAME/KEY: cleavage-site
LOCATION: 5927 to 5032
IDENTIFICATION METHOD: S
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                          NAME/KEY: Cleavage-site
LOCATION: 7675 to 7680
IDENTIFICATION METHOD: S
US-08-894-344C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 aaatccatgtaaagcagcaggg
                LOCATION: 1 to 8874 IDENTIFICATION METHOD: FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
```

ô

Gaps

ö

Gaps

ò g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08706702
Patent No. 5948614
GENERAL INFORMATION:
APPLICANT: Chatterjee, Deb K.
TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga TITLE OF INVENTION: maritima and Mutants Thereof NUMBER OF SEQUENCES: 26
CORRESPONDENCES: ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                              Length 27;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,702
                                                                                                                                                                                                                                                                                                                DB 4;
AND SPLICE VARIANTS THEROF
             FILE REFERENCE: GH-50020 1
CURRENT APPLICATION NUMBER: US/09/372,498
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: 08/832,399
PRIOR FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SSOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                Score 16.2;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,893
KEFERENCE/DOCKET NUMBER: 0942.2800006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION 0478.

APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-706-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-6CT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
PRIOR APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-6CT-1995
PRIOR APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-6CT-1995
PRIOR APPLICATION NUMBER: US 08/55,057
FILING DATE: 08-SEP-1995
ATTCRNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: US/08/706,702
06-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                      6 gaattccatggaaaccagcag 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              Query Match 70.4%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   1 gaaatccatgtaaagcagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Esmond, Robert W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 202-371-260
TELEFAX: 202-371-2540
                                                                                                                                                                                                                         ; ORGANISM: HOMO SAPIENS
US-09-372-498-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20005-3934
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-706-702-25/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D
COUNTRY:
                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                          ö
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                          ö
                   DB 4; Length 9751;
                                                                                                                                                                                                                                                                                CARLEL INCOMMATION:

GREATLICANT: Bergsma, Derk
APPLICANT: Shabon, Usman
TITLE OF INVENTION: NOVEL HUMAN NEUROTENSIN RECEPTOR TYPE 2
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09372498
Patent No. 6166182
GENERAL INFORMATION:
APPLICANT: Derk J. Bergsma
APPLICANT: USman Shabon
TITLE OF INVENTION: NOVEL HUMAN NEUROTENSIN RECEPTOR TYPE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 27;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                          4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                 Score 16.6;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%; Score 16.2;
85.7%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/832,399
FILING DATE: 02-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GH50020
                                                                                                                     2017 gacatgcagggaaagcagcaggg 2039
                                                                                                                                                                                             KESULT 5
US-08-832-399-9
; Sequence 9, Application US/08832399
; Patent No. 6008050
                                                                                               1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GH5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY.

ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

AUGUNGER: IBM COMPATIBLE
POS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GAATICCAIGGAAACCAGCAG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gaaatccatgtaaagcagcag 21
                 72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
               Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia
STATE: PA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-APR CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-372-498-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-832-399-9
```

q

ò

Gaps

ö

Length 717; Indels

DB 3;

```
AESULT 9
US-09-002-114-2/C
Sequence 2, Application US/09002114
Sequence 2, Application US/09002114
Sequence 2, Application US/09002114
Sequence 3, Application US/09002114
Sequence 2, Application US/09002114
Sequence 2, Application US/09002114
Sequence 2, Application US/09002114
Sequence 3, Application US/09002114
Sequence 4, Application US/0900214
Sequence 4, Application US/0900214
Sequence 4, Application US/0900214
Sequence 4, Application US/0900214
Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FEADMBLE FORM:
MEDIUM TYPE: Diskette
COMFUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ fOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,114
                                                                                                                                                                                                                                                  Score 16.2; Di
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.2; DE
Pred. No. 57;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0450 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                    1 gaaatccatgtaaagcagcaggg 23
                      ; TYPE: nucleic acid
; STRANDEDNESS: both
TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-706-725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 AAAGCCATCTAAAGCAGTAGG 364
                                                                                                                                                                                                                                           Ouery Match 70.4%;
Best Local Similarity 78.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.4%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 aaatccatgtaaagcagcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650-855-05:
TELEFAX: 650-845-4166
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-09-002-114-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-08-899-371-2
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Hughes, A. John
APPLICANT: Hughes, A. John
APPLICANT: Chatterjee, Deb K.

TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                     DB 2; Length 717;
                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,706
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                        Query Match
70.4%; Score 16.2; E
Best Local Similarity 78.3%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32,893
R: 0942.2800005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-SEP-1996
CLASSIETCATION: 435
PRIOR APPLICATION 1047.05
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/689,807
FILING DATE: 14-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/537,400
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/370,190
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
PRIOR APPLICATION NUMBER: US 08/576,759
FILING DATE: 22-DEC-1995
PRIOR APPLICATION NUMBER: US 08/576,759
FILING DATE: 02-OCT-1995
PRIOR APPLICATION NUMBER: US 08/576,759
FILING DATE: 02-OCT-1995
PRIOR APPLICATION NUMBER: US 08/576,759
FILING DATE: 02-OCT-1995
PRIOR APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY-AGENT INFORMATION:
NAME: PAGENCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/08706706
Patent No. 6015668
                                                                                                                                                                                                                                                                                                                                                                                                                                            673 GGNATCCNGGTAAAGCGGCAGGG 651
                                                                                                                                                                                                                                                                                                                                                                                 1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942
RELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2640
TELEFAX: 202-371-2540
                                                              STRANDEDNESS: both TOPOLOGY: both MODECULE TYPE: DNA (genomic) US-08-706-702-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
1: 717 base pairs
nucleic acid
DEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Esmond, Robert W
RATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       717 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-706-706-25/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: V
                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

ó;

Gaps

; 0

Indels

DB 4; Length 1351;

```
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 70.4%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 aaatccatgtaaagcagcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                        San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION:
CTHER INFORMATION:
US-08-899-371-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                 GENERAL INFORMATION:
APPLICANT: Hedrick, Ronald P.
APPLICANT: Antonio, Dolores B.
TITLE OF INVENTION: Detecting Myxobolus, the Cause of Salmonid Whirling TITLE OF INVENTION: Detecting Myxobolus, the Cause of Salmonid Whirling TITLE OF INVENTION: Disease NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsens and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hedrick, Ronald P.
APPLICANT: Andree, Karl B.
APPLICANT: Antonio, Dolores B.
TITLE OF INVENTION: A DNA-Based Diagnostic Test for
TITLE OF INVENTION: Detecting Myxobolus, the Cause of Salmonid Whirling
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . LOCATION: 1..1608
; LOCATION: 1..1608
; OTHER INFORMATION: /note= "18S rRNA gene of Myxobolus
; OTHER INPORMATION: insidiosus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/899,371
FILING DATE: 23-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.2; DB 2;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PULDASTRICATION: 433
PRICAR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,734
FILING DATE: 26-UU-1996
ATTONNEY AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-081310US
TELEFAN: (415) 576-0200
TELEFAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
TYPE: nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 2, Application US/08899371
Patent No. 5962227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08899371
Patent No. 5962227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 ACATCCATGGAAGGCAGCAGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.4%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 aaatccatgtaaagcagg
                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-899-371-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
```

```
ADDRESSE: Towness and Townsend and Crew LLP
STREET: Two Embarcadero Center, Fighth Floor
CITY: San Francisco
STATE: Callifornia
COUNTY: Callifornia
COUNTY: Banhama colus
STATE: Callifornia
COUNTY: Per Floopy disk
STATE: Callifornia
COUNTY: Per Floopy disk
STATE: Callifornia
COUNTY: STATE COUNTY: Callifornia
STATE: Callifornia
COUNTY: STATE CALLING
STATE CALLING
ATTORNEY. CALLING
ATTORNEY. CALLING
STATE CALLING
STATE
S
```

ö

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 16442;
                                                                                                                                                                    DB 2; Length 5243;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
ATTONREY/AGENT INFORMATION:
REGISTRATION NUMBER: 39,317
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 39,317
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPRATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
TENGTH: 16442 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Query Match

To.4%; Score 16.2; DB 3;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3;
                                                                                                                                                       Sequence 208, Application US/08781891
Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/08250346
Patent No. 5932255
GENERAL INFORMATION:
APPLICANT: ANAND, Rakesh
                                                                                                                                                                                                                                                                                                                           Db 4443 AAATCCAGCTATAGCAGCAGG 4463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 12904 GAAATCCATGTAAAGTCACAG 12884
                                                                                                                                                                                                                                                                                   2 aaatccatgtaaagcagcagg 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gaaatccatgtaaagcagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                              ; TOPOLOGY: linear
US-08-414-335-2
                                                                                                                                                                                     Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 CCITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-781-891-208/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-250-346-21/C
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 5183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08414335
| Patent No. 5907078
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: GREENBERT, No. 5907078man M
| APPLICANT: ROSEN, Jeffrey M
| TITLE OF INVENTION: TANSENIC MOUSE MODEL FOR PROSTATE TITLE OF INVENTION: CANCER |
| CORRESPONDENCE ADDRESS: 4 CORRESPONDENCE ADDRESS: 4 CORRESPONDENCE ADDRESS: 4 STREET: 1203 Crystal Plaza Bldg. I, 2001 Jefferson STREET: Davis Highway |
| STREET: Used Grates of America |
| CITY: Arlington |
| STREET: Davis Highway |
| STREET: Davis H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,335
FILING DATE: 31-MAR-1995
CLASSIEGATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: FALLOW, Charles W
REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 1027
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CRRAACTERISTICS:
SEQUENCE CRRAACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.4%; Score 16.2; D
Best Local Similarity 85.7%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                        .
29,768
ER: 016779/0131
                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19710643.9
FILING DATE: 14 "ARK-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016779/0131
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGHH: 5183 base pairs
TYPE: NUCLEIC SIGHE
APPLICATION NUMBER: US/09/039,555B
FILING DATE: 16-MAR-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-039-5558-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 asatccatgtaaagcagcagg 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-414-335-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

ö

```
APPLICANT: MAKINA, ALEAGUAGE
APPLICANT: MAKINA, ALEAGUAGE
APPLICANT: MAMAR, Rashida
APPLICANT: ANNAR, Rashida
APPLICANT: GGILVIE, Donald J
APPLICANT: GGILVIE, DONALD
ITITLE OF INVENTION: DAIL
TITLE OF INVENTION: DAIL
TITLE OF INVENTION: DAIL
STREET: 1100 New York Avenue, N.W.
CITT: Washington
COMPUTER: LO. C.
COUNTRY: U.S.A.
ITITLE OF INVENTION: DAIL
STREET: 1100 New York Avenue, N.W.
CITT: Washington
COMPUTER: DAIL
STREET: 1100 New York Avenue, N.W.
STREET: 1100 New York Avenue, N.W.
COMPUTER: DAIL
STREET: STREET: DAIL
COMPUTER: DAIL
STREET: STREET: DAIL
COMPUTER: DAIL
STREET: DAIL
STREET: DAIL
STREET: STREET: DAIL
COMPUTER: DAIL
STREET: DAIL
STR
```

```
ö
                                            Gaps
                                          ;
0
Query Match 68.7%; Score 15.8; DB 2; Length 199; Best Local Similarity 89.5%; Pred. No. 60; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                ò
```

g

Search completed: February 25, 2002, 18:05:51 Job time: 18599 sec

•		
•		
		•
	•	
	THIS PAGE BLANK (USPTO)	
		•

18.2 79.1 750 13 AZ750976 BZ750976 18.2 79.1 809 11 BF027105 BG118586 18.2 79.1 875 11 BG118586 BG118586 18.2 79.1 95.1 13 CNS0528F AL317832 17.8 77.4 287 10 BE579037 BE579037 17.8 77.4 55.3 10 AV395870 AV395870 17.8 77.4 56.4 10 AV399896 AV390896 17.8 77.4 56.4 10 AV390896 AV387535 17.8 77.4 582 13 AZ107460 AV387535 17.8 77.4 56.2 10 AN361333 17.8 77.4 56.5 10 AN561616 17.8 77.4 56.5 10 AN561616	17.8 77.4 618 13 AZ558735 AZ558735 17.8 77.4 626 10 BE233492 BE333492 17.8 77.4 630 10 BE228191 BE238191 17.8 77.4 657 10 AW054024 AW054024 17.8 77.4 700 11 BG846208 BG846208 17.8 77.4 772 10 AU080746 AU080746	17.4 75.7 221 10 AL507374 17.4 75.7 364 10 BE067433 17.4 75.7 604 13 AQ372694 17.4 75.7 857 13 CNS06GUP 17.4 75.7 975 11 BF348682 17.4 75.7 1011 13 CNS020BG	17.2 74.8 271 10 AA398276 AA398276 17.2 74.8 271 10 AA357388 AW357388 17.2 74.8 271 10 AA357388 AW357388 17.2 74.8 312 10 A1905219 H20500 YN 17.2 74.8 312 10 BB551925 BB251925 17.2 74.8 340 10 AA012198 AA012198 17.2 74.8 357 11 W63225 T9		Actinopterygli; Neopterygli; Teleostel; Acanthomorpha; Acanthopterygli; Percomor Tetraodontidae; Takifugu. CE 1 (bases 1 to 619) RS Elgar, G., Clark, M., Smith, S., Meek, S., W Williams, G. and Brenner, S. Direct Submission AL Submitted (09-JUN-1998) MRC Human Genome Centre, Hinxton, Cambridge, CB10 1SB, UK biohelphdymp.mrc.ac.uk Vector: pBluescript II KS	V_type: phagemid PRIMER: KS DESCR: One pass dye-terminator sequence. Location/Quali 1. 619 /organism="Tak /db_xref="taxc /clone_lib="cc /clone_lib="cc /clone="137116
0 0 0 14111112222222222222222222222222222222	C 25 26 27 27 20 20 30 31	0 23333343354		RESULT 1 FR0032239 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOULC SOULC BASE COUNT ORIGIN
GenCore version 4.5 1t (c) 1993 - 2000 Compugen Ltd. 2h, using sw model 25, 2002, 17:21:13 ; Search time 8261.74 Seconds (without alignments) 29.915 Million cell updates/sec	tgta TC ' G eqs,	chosen para	* *	*** ** umining	20: em_gss_vrt:* 21: em_gss_other:* No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. SUMMARIES Query Ouery The Match Length DB ID Description	3 CNSO50PJ 3 CNSO50NC 3 AZ842531 3 AQ972989 0 AV119745 0 AV119723 0 AV119723 0 AIZ43356 0 BE019857 3 AZ628185
Copyright nucleic search, February 25 US-09-698-9	23 1 gaaatccatg IDENTITY_NUC Gapop 10.0 , 11351937 seq	Total number of hits satis Minimum DB seq length: 0 Maximum DB seq length: 200	Maximum Listing EST:* ES	6: em_estbar 7: em_estro: 8: em_estro: 9: em_htc:* 10: 9D_est1: 11: 9D_est2: 12: 9D_htc:* 13: 9D_gs:* 14: em_gss_f 15: em_gss_f 16: em_gss_l 17: em_gss_l 18: em_gss_l 18: em_gss_l 19: em_gss_l	20: em_gss_vrt 21: em_gss_oth d. No. is the number o re greater than or equ is derived by analysi.	8 8 81.7 8 8 81.7 8 8 81.7 8 80.0 2 79.1 2 79.1 2 79.1 2 79.1 2 79.1 2 79.1

à 8

```
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis
genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musna. I (bases I to 342)

Dunn, D., Aoyadi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Aslan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Welss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases I to 1007)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ842531 342 bp DNA GSS 20-FEB-2001
2M0141J03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0141J03 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Unpublished
Tetraodon nigroviridis genome survey sequence T7 end of clone 001109 of library B from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="B"
/note="Genoscope sequence ID : COTBOOLAEO5C1-end : T7"
239 c 217 g 242 t 26 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="001109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18.8; DB 13;
Pred. No. 2.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 839 GAAATCGATTTAAAGCAGCAGG 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
                                                                         AL345585
AL345585.1 GI:8239355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ842531.1 GI:13012439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gaaatccatgtaaagcagcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                       sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ842531
                                                                                                                                                SOURCE
ORGANISM
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
AZ842531/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                         ACCESSION
                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 916)
Crollius,H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C.,
Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
Bernot,A. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostcmi, Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Tetraodontidae; Tet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                         CNSO50PJ 916 bp DNA GSS 26-JUL-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 001109 of library B from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lb="B"
/note="Genoscope sequence ID : COABOOLAE05C1~end : T7"
/ 223 c 206 g 221 t 13 others
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Characterization and repeat analysis of the compact genome of freshwater pufferfish tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                          Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                          2.7e+02;
                                    Score 18.8; DB 13;
Pred. No. 2.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="001109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.8; DB 13;
Pred. No. 2.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             AL315886.1 GI:9548744
GSS; genome survey sequence.
Tetracdon nigroviridis.
Tetracdon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                           2 adatecatgtaaageageaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             838 GAAATCGATTTAAAGCAGCAGG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gasatccatgtasagcagcagg 22
                               81.7%;
llarity 90.9%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1007 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 916)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
                               Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20296633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20359837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNS05NNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                       RESULT
CNS050PJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
CNS05NNC
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
```

ò

à

```
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhaodfijgr.org
Email: szhaodfijgr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu. Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Female"
//lab_nost="DH10B"
//nab_nost="DH10B"
//nab_nost="DH10B"
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
Brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase.
Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BDH10B electrocompetent cells (BRL Life Technologies).

1 159 c 106 g 164 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One pass dye-terminator sequencing of cosmid cloned genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR0034498 618 bp DNA GSS 27-JUN-199
Fugu rubripes GSS sequence, clone 199F09aF9, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.4; DB 13;
Pred. No. 4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="RPCI-23-317G14"
/clone_l1b="RPCI-23"
  Other_GSSs: RPCI-23-317G14.TJ
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL030865.1 GI:3272979
GSS: genome survey sequence.
Takifugu rubripes.
Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 ACCCATGTAAAGCAGGG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
                          Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 atccatgtaaagcagcaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           .522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL030865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FR0034498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114 gplAR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ972989 522 bp DNA GSS 28-JAN-2000
RPCI-23-317G14.TV RPCI-23 Mus musculus genomic clone RPCI-23-317G14
, DNA sequence.
AQ972989.1 GI:6803442
                                                                                        Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 522)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicallin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 18.4; DB 13;
95.0%; Pred. No. 3.8e+02;
ive 0; Mismatches 1;
                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Resear
84112, USA
7e1: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                       Plate: 0141 row: J column: 03
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                             High quality sequence stop: 342. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC2M0141J03"
                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 ACCCATGTAAAGCAGGG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 atccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ972989/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

Gaps

```
1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                             RESULT 8
AV119723/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI243356/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 205).

Akaninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatan, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Stiuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shipata, Y., Shipata, Y., Shipata, Y., Shipata, Y., Shipata, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Riken Mouse Ests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehatose and its application for the synthesis of full length cDNA
trehatose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                       AV119745 205 bp mRNA EST 30-JUN-1999 AV119745 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2510305L08, mRNA sequence.
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="2610305L08"
/clone_11b="Mus musculus C57BL/6J 10-day embryo"
                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                      Score 18.4; DB 13; Length 618;
Pred. No. 4e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.2; DB 10; Length 205;
Pred. No. 4.5e+02;
0; Mismatches 3; Indels 0;
                                                                                                                            31 others
                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-1-1 Koyadal, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                  1. .618
/organism="Takifugu rubripes"
/db_xref="Laxon:31033"
/clone_lib="cosmid 199F09"
/clone="199F09AP9"
                                                                                                                        141 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="10-day embryo" 36 c 37 g 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .205
/organism="Mus musculus"
                                                                                                                        154 g
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                     362 ACATCCNNGTAAAGCAGCAGGG 383
                                                                                                                                                                                                                                                                                2 aaatccatgtaaagcagcaggg 23
                                                                                                                                                                                               Query Match
Bost Local Similarity 86.4%;
Matches 19; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV119745.1 GI:5301896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex-"mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.0%;
Matches 20; Conservative
                                                                                                                      183 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                        109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN
                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                    AV119745/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                   a
```

```
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 287)
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Fuunayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Sato,K., Shibata,Y., Shiqemco,Y., Shiraki,T., Soqabe,Y., Suqahara
,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Sugahara
,Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9045
Fax: 81-298-36-908
Fax: 81-298-908
Fax: 81-298-9
                                                                                                                                                                                                                                                     AV119723 Mus musculus C57BL/6J 10-day embryo Mus musculus CDNA av119723 Av119723 Av21973 Av119723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="2610305J08"
/clone_lib="Mus musculus C57BL/6J 10-day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALZ43356 444 DP MRNA EST 01-DF
qh30g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1846226 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.1%; Score 18.2; DB 10;
87.0%; Pred. No. 4.6e+02;
live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="10-day embryo"
57 c 52 g 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN Mouse ESTS
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
274 GAAATCCAAGTAAAACAGAAGGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV119723.1 GI:5301874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI243356.1 GI:3838753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.09
Matches 20; Conservative
```

S

```
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
BE019857/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 455)
1 (bases 1 to 455)
2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
A.M., Rosse, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
Mouse whole genome scaffolding with paired end reads from 10kb
10 lasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Urah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ndce="Organ: Dooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_GGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-392087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Scares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1MO480HO8F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                               NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                           Tunor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1011 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.2; DB 10;
Pred. No. 4.8e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:1846226"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soares and M. Fatima Bonaldo.
89 c 97 g 119 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone UUGCIMO480H08 F, DNA sequence. AZ628185
                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 GCAACCAATGTAAAGCAGCAGGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ628185.1 GI:11750375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 79.1%;
1 Similarity 87.0%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84112, USA
Tel: 801 585 5606
                                                                                                                                                                                                                                                                                                                                                      1. .444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 20; Conserve
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ628185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
COMMENT
                                                               REFERENCE
                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
A2628185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase at the polymerase and T4 polymerase at the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114 qib|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 481)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE019857 481 bp mRNA EST 06-JUN-2000 bb60g05.yl NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3029912 5' similar to TR:073698 073698 HYPOTHETICAL 21.5 KD PROTEIN; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0480H08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.1%; Score 18.2; DB 13; Length 455; 87.0%; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0480 row: H column: 08
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 GAAATCCATGTAAGGGAGGAGGG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
BE019857
BE019857.1 GI:8279946
                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                     1. .455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
```

9

```
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
AZ750976/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       á
                                                                                                                                                             /organism="rations saptems
//ob_xref="taxon:9606"
/clone="IMAGE:3029912"
/clone=lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/tab_bost="DHIOB (page-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI: cDNa made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size I.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of california, Berkels) using zAp-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus sutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Marazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 533)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ484979 533 bp DNA GSS 05-OCT-2000 LM0311P16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0311P16 R, DNA sequence. AZ484979 GI:10650348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Diapublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Contact: Robert B. Weiss
University of Utah
Contact: Robert B. Weiss
University of Utah
Contact: Robert B. Weiss
University of Utah
Contact: Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.2; DB 10; Length 481;
Pred. No. 4.8e+02;
0; Mismatches 3; Indels 0.
image.llnl.gov/image/html/iresources.shtml
                                      Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .533
/organism="Mus musculus"
/organism="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0311P16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0311 row: P column: 16
Seq primer: CACACGGAACAGCTATGACC
                                                                                                                                  1. .481
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
High quality sequence stop: 533.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 GAAGTCCATGTAGAGCAACAGGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.1%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ484979/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
```

à g

```
(http://www.nax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 (jbl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 House microta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 750)

Z hao,S., Nlerman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M. Gebregeorgis,E., Mouse BAC End Sequences from Library RPCI-24

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pleter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPen Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.thgr.org/tdb/bac_ends/mouse/bac_end_intro.html Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ750976 750 bp DNA GSS 25-JAN-2001
RPCI-24-128J23.TV RPCI-24 Mus musculus genomic clone RPCI-24-128J23
AZ750976
                                                           /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.2; DB 13; Length 533;
Pred. No. 4.8e+02;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 GAAGTCTATGTAAAGCAGCAGAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ750976.1 GI:12536135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.1%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.1'
Best Local Similarity 87.0'
Matches 20; Conservative
```

```
1 gaaatccatgtaaagcagggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                        RESULT 15
BG118586/c
                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
           á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enklaryota; Metacaa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 809)

NHI-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence start: 32

High quality sequence stop: 801.

Plate: LLCM824 row: o column: 05

High quality sequence stop: 801.

Plate: LCCM824 row: o column: 05

High quality sequence stop: 801.

All coation/Qualifiers

I. 809

//Lone="Mamore Stop: 801.

//Lore="Mamore Stop: 801.

//Lone="Mamore Stop: 801.

//Lone="Mamore Stop: 801.

//Lissue_LYpe="Melanone"

//Lissue_L
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                             /cell_type="Spleen/Brain"
/oote="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
//oote="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
//oote="Vector of the produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF027105 809 bp mRNA EST 10-OCT-2000 601670224F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3953500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.2; DB 11; Length 809;
Pred. No. 5e+02;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                   Length 750;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                   79.1%; Score 18.2; DB 13;
87.0%; Pred. No. 5e+02;
11ve 0; Mismatches 3;
/clone="RPCI-24-128J23"
/clone_lib="RPCI-24"
/sex="Male"
                                                                                                                                                                                                                                            182 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 GGAAGCCATGTAAAGCCGCAGGG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BF027105
BF027105.1 GI:10734817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.1%;
87.0%;
                                                                                                                                                                                                                                               182 c
                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1,
BF027105
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
Linkaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases I to 875)

I (bases I to 875)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Onduct: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Location/Qualifiers

I (875)

About through the Laxon: 9606"

About inches Taxon: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
BUILBS86 875 bp mRNA EST 30-JAN-2001
602348330F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4443391 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.1%; Score 18.2; DB 11; Length 875; 87.0%; Pred. No. 5e+02; tive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 25, 2002, 17:21:17 Job time: 16170 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 GAAGTCCATGTAGAGCAACAGGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                        BG118586.1 GI:12612092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 20; Conserv
```

A10939 Nucleotide A10939 Nucleotide A10943 Nucleotide A18051 DNA used as AR095107 Sequence AX012338 Sequence AX01238 Sequence 149886 Sequence A251013 Transform I44104 Sequence 23 I44104 Sequence 23 I44104 Sequence 23

I44103 TBI251014 TBI251013

3201

I44104

12

AX172441 A60108 A76915 AR098307

AX172440 A71437

A60112 AR098311 AX127748 AX127748

5560 5560 5865

AX127755 Sequence AX127757 Sequence AX127757 Sequence V00090 Agrobacteri X00431 Agrobacteri AX172475 Sequence A10942 Nucleotide AX172463 Sequence AX172463 Sequence AX172463 Nucleotide AX172463 Nucleotide A10943 Nucleotide

AX172463

A10939 A10943 A18051

AR095107

AR098313

1085 1160 1186 1186 1186 1186 1186 2476 3200

149886

X05579 Soybean bet

AX127755 AX127757 AX172478

AX127759 Sequence AX172451 Sequence

Description

ВВ

Length

Match

```
AX127759 21 bp DNA
Sequence 12 from Patent WO0131042.
AX127759
       Score
                         RESULT 1
AX127759
LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
Result
      2
                                                                                                                                                                 0 0 0 0 0 0 0 0 0
                                         February 25, 2002, 18:02:56; search time 2331.3 Seconds (without alignments) 148.604 Million cell updates/sec
                                                                                                                               2944280
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                  1472140 seqs, 8248589755 residues
                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                              - nucleic search, using sw model
                                                                                 1 gcttggactataatacttgac 21
                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                     em_vi:*
em_htgo_hum:*
em_htgo_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                         em_htgo_rod:*
em_htg_hum:*
em_htg_inv:*
em_htg_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                                    em_htg_other:*
                                                                    US-09-698-903B-12
                                                                                                                                           length: 0
length: 2000000000
                                                                                                                                                                                                                                                          gb_ro:*
gb_sts:*
gb_un:*
gb_v1:*
em_ba:*
em_fun:*
                                                                                                                                                                                                                                                                                                             em_in:*
em_om:*
em_or:*
                                                                                                                                                                                                                                                                                                                                         em_pat:*
                                                                                                                                                                                                                                                                                                                                                                 em_sts:*
                                                                                                                                                                                                                                gb_pat: *
gb_ph: *
gb_pl: *
                                                                                                                                                                                                 gb_ba:*
gb_htg:*
                                                                                                                                                                                                                                                                                                                                                            em_ro:*
                                                                                                                                                                                                                                                                                                                                                                                em_un:*
                                                                                                                                                                                                            gb_in:*
gb_om:*
gb_ov:*
                                                                                                                                                                                                                                                                                                                                   em_ov:*
                                                                                                                                                                                                                                                                                                                                               em_ph:*
                                                                                                                                                                                                                                                                                                                                                     em_pl:*
                                                                                                                                                                                                                                                                                                                                                                          em_sy:*
                                                                                                                                                                                          GenEmbl:*
                                                                                                                                                                                                                                                         sed
                                                                    Title:
Perfect score:
                                                                                              Scoring table:
                               OM nucleic
                                                                                                                                           Minimum DB
Maximum DB
                                                                                  Sequence:
                                                                                                                  Searched:
                                                                                                                                                                                         Database
                                          Run on:
```

AJ251014 Transform AX172441 Sequence A60108 Sequence 1 A6098307 Sequence AX72440 Sequence AX77440 Sequence AX7744 Sequence AX127748 Sequence AX127748 Sequence AX127748 Sequence AX127748 Sequence AX127748 Sequence AX127748 Sequence AX16778 Sequence AX16778 Sequence AX16778 Sequence AX16778 Sequence AX16778 Sequence AX1678 ASS Sequence AX1678 ASS Sequence AX16783 Plasmid pPS AR07438 Sequence AX17438 Sequence

Z37515 Binary vect A24782 plasmid pJD AR074387 Sequence AR078675 Sequence

ALIGNMENTS

BINHYGDNA

7811 12095

AR074387

AR074388

15-MAY-2001

PAT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 21)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing same Patent: WO 0131042-A 12 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers 1. .21 /organism="synthetic construct" //db_xref="taxon:32630" /note="primer MDB201" AX127759.1 GI:14134406 source FEATURES

à ద

```
/note="theroretical fusion junction (24) with gene 7 of Ti
plasmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' border flanking region of elite event MS-B2"
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetic construct.
synthetic construct
artificial sequence.
(bases 1 to 415)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing same
Patent: WO 0131042-A 8 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2001
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                     Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 415;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT
                                                                                                                                                                                                                                                                                   12;
             1. .13
/note="beta-1-tubulin sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                          Ouery Match
92.4%; Score 19.4; DB
Best Local Similarity 95.2%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                              /note="polyA site"
220. .225
/note="put.polyA signal"
47 c 38 g 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.4%; Score 19.4; D
Best Local Similarity 95.2%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches
                                 14. .28 /note="puc 13 polylinker" 29. .35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
                                                                                                                                        173. .178
/note="put.polyA signal"
                                                                                                                                                                                                                                                                                                                                                                                                                      AX127755 415 bp DNA
Sequence 8 from Patent WO0131042.
AX127755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX127757 416 bp DNA
Sequence 10 from Patent WO0131042.
AX127757
                                                                   29. .35 'note="Sal I linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .234
/note-"plant DNA"
                                                                                                                                                                                                                                                                                                                                 AX127755.1 GI:14134402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235. .415
/note="T-DNA"
a 55 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX127757.1 GI:14134404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
              misc_feature
                                         misc_feature
                                                                   misc_feature
                                                                                               misc_feature
                                                                                                                                      misc_feature
                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                  polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
AX127755/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
ORGANISM
                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AX127757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                     á
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-tubulin; fusion gene; plasmid.

Synthetic construct.

SM synthetic construct.

artificial sequence.

E 1 (bases 1 to 249)

S Guiltinan, W. J., Velten, J., Bustos, M.M., Cyr, R.J., Schell, J. and

Fosket, D.E.

The expression of a chimeric soybean beta-tubulin gene in tobacco

Location/Qualifiers

1. 249

//organism="synthetic construct"

//db_xref="taxon:32630"

1. 51
                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARGWIUB 249 bp DNA SYN 02-APR-1988 SOybean beta-1-tubulin gene fused to Ti plasmid unit 7 3UTR. X05579 X05579 I GI:58087
                                                                                                                                                                                                                   03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"fusion product (17AA); Protein sequence is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                          synthatic construct.
synthatic construct
synthetic construct
attlificial sequence.
1 (bases 1 to 21)
de Both, G. and de Beuckeleer, M.
Hybrid winter oilsed rape and methods for producing same Patent: WO 0141558 A 12 14-JUN-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 21;
                                                            Length 21;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                 PAT
                                                                                        ;
0
                                                    Query Match 100.0%; Score 21; DB 6; Best Local Similarity 100.0%; Pred. No. 2.1; Matches 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codol_start=1
/transl_table=11
/protein_id="cap084.1"
/db_xref="G:4376141"
/translation="AMAAWASSNWSTDPPMS"
                                                                                                                                                                                                                                                                                                                                                                                                         1. 21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer 201"
       u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DE
Pred. No. 15;
0; Mismatches
     7
                                                                                                                                                                                                          AX172451 21 bp DNA
Sequence 12 from Patent W00141558.
AX172451
AX172451.1 GI:14597563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                         1 gottggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCTTGGACTATAATACCTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ည်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 95.2 Matches 20; Conservative
    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ъ
9
  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                    DEFINITION
ACCESSION
VERSION
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                RESULT
AX172451
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARGMTUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
```

à g ö

 \sim

as

```
148. .528
/note="unknown gene (148 is 1st base in codon) (525 is 3rd
base in codon)"
                            1 (bases 1 to 831)
Dhaese, P., De Greve, H., Gielen, J., Seurinck, J., Van Montagu, M.M. and Schell, J.
Identification of sequences involved in the polyadenylation of higher plant nuclear transcripts using Agrobacterium T-DNA genes
    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                            Direct Submission
Submitted (27-MAY-1983) to the EMBL/GenBank/DDBJ databases
Data kindly reviewed (27-MAY-1983) by Dhaese P.
Location/Qualifiers
                                                                                                                                                                                                                        1. .831
/organism="Agrobacterium tumefaciens"
/strain="(octopine TL-DNA)"
/db_xref="taxon:358"
75. .81
                                                                                                                                                                                                                                                                                                                                                                                                                /note="transcript 7 (alternate)"
                                                                                                                                                                                                                                                                                                                                                        CTA [2]"
                                                                                                                                                                                                                                                                                     /note="CG [1] revised CCAGAGG
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
/protein_id="CAA23429.1"
/db_xref="GI:39181"
/db_xref="SWISS-PROT:P03867"
                                                                                                                                                                                                                                                                                                                  99. .101
/note="CCA [1] revised C1
/citation=[1]
/citation=[2]
132. .67?
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="transcript 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                   EMBO J. 2, 419-426 (1983)
2 (bases 76 to 100)
                   Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nducing) plasmid priA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            664 GCTTGGACTATAATACCTGAC 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.4%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                878 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gcttggactataatacttgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 878)
McPherson, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X00431.1 GI:39150
                                                                                                                                                                                                                                                                                                                                                                                                                                 .672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                               Dhaese, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262
                                                                                                      models
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTDNA
                                                                                                                                                                                                                                                                                old_sequence
                                                                                                                                                                                                                                                                                                                                          old_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                REFERENCE
AUTHORS
                                                                                                                                                                            JOURNAL
COMMENT
                                                                                                                   JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                          FEATURES
                                                                          TITLE
                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
ATTDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTRN7 831 bp DNA BCT 02-SEP-1999
Agrobacterium tumefaciens gene encoding 'transcript 7' mRNA for a protein with unknown function. V00090
V00090.1 GI:39180
V100090.1 GI:39180
Agrobacterium tumefaciens.
                                                                                                                1. 416 //ordanism="synthetic construct" //ordanism="synthetic construct" //ob_xref="laxon:32650" //octe="3' border flanking region of elite event MS-B2"
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                flanking region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2001
         Syluctors artificial sequence.

1 (bases 1 to 416)
Weston,B. and de Beuckeleer,M.
Male-sterile brassica plants and methods for producing same Patent: WO 0131042-A 10 03-MAY-2001;
Aventis CropScience N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         artificial sequence.

1 (bases 1 to 694)
de Both,G. and de Beuckeleer,M.

Hybrid winter oilseed rape and methods for producing same Patent: WO 0141556-A 39 14-JUN-2001;

Aventis CropScience N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 694;
                                                                                                                                                                                                                                                                                              Length 416
                                                                                                                                                                                                                                    others
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .694
/organism="synthetic construct"
/db_xref="texon:32630"
/note="sequence comprising the 5'
RF-BN1 in WOSR"
a 81 c 73 q 242 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DB 6;
Pred. No. 11;
); Mismatches 1;
                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                            Score 19.4;
Pred. No. 12;
                                                                                                                                                                                                                                    152
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX172478 694 bp DNA
Sequence 39 from Patent WOO141558.
AX172478 GI:14597590
                                                                                                                                                                                                   194. .416
/note="plant DNA"
a 72 c 54 g
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                      81 GCTTGGACTATAATACCTGAC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         674
                                                                                                                                                                            1. .193
/note="T-DNA"
                                                                                                                                                                                                                                                                                                                                                     1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                           Query Match 92.4%;
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.4%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct. synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             694 GCTTGGACTATAATACCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gcttggactataatacttgac
synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 92.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                    137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
                                                                                                                                                                            misc_feature
                                                                                                                                                                                                       misc_feature
                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
AX172478/c
LOCUS
   ORGANISM
                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                            AUTHORS
                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                   PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
ATTRN7
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
```

```
/translation="MNFADTPLASLDLDWACEEFIKTYGASPQLETGEVIQTNNGLLY
TYGKGSLSQRTHDTHLKFKERELSFTTIKPAEMKAQQSDLTYYVAIFQSNYFLCVSN
PERGFLECHNRPLYPTA
176 c 138 g 255 t
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence analysis of crown gall tumor T-DNA encoding the 0.7 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agrobacterium tumefaciens.
Agrobacterium tumefaciens
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens crown gall tumor T-DNA from Ti (tumor
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-1996
                                                                                                                                                                                                                     ö
                                                                                                                                                                    Length 831;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcript
Nucleic Acids Res. 12 (5), 2317-2325 (1984)
84169535
                                                                                                                                                                                                                     ä
                                                                                                                                                                    Score 19.4; DB 1;
Pred. No. 11;
0; Mismatches 1;
```

```
A10942.1 GI:492369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1085 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A10939.1 GI:492367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                   ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A10939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
AX172463/c
LOCUS
                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                             AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                     VERSION
KEYWORDS
                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
A10939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                   /transl_table=11
/protein_id="CAA25129.1"
/protein_id="Gra25129.1"
/db_xref="Gr:33151"
/db_xref="SHISP_PROT:P03867"
/translation="MNPADTPLASLDLDWACEFIKTYGASPQLETGEVIOTNNGLLY
LYGKGSLSQR.HDTHLKFKERERELSFTTIKPAEMKAQQSDLTYYVAIFQSNYFLCVSN
PENGFLECHNRPLYPIVAHGSMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/db_xref="taxon:32630"
/note="sequence comprising the 5' flanking region of MS-BM1 in WOSF |
134 c 173 g 293 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct.

**Synthetic construct

**Synthetic construct

**Synthetic construct

**Synthetic synthetical

**I (bases 1 to 909)

**I (bases 1 to 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19.4; DB 1; Length 878;
Pred. No. 11;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.4%; Score 19.4; DB 6; Length 909; Best Local Similarity 95.2%; Pred. No. 11; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A10942 1037 bp DNA PAT 2
Nucleotide sequence 4 from patent number DE3920034.
A10942
                                             /organism="Agrobacterium tumefaciens"
/strain="plasmid priA6"
/db_xref="taxon:358"
                                                                                                                                                                                                     /note="polyadenylation signal"
109. 489
/note="unidentified reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="polyadenylation signal"
189 c 139 g 262 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX172475 909 bp DNA
Sequence 36 from Patent W00141558.
AX172475
AX172475.1 GI:14597587
     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 g
                                                                                                                                                        /note="TATA-box"
68. .613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625 GCTTGGACTATAATACCTGAC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.4%;
Best Local Similarity 95.2%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gottggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309
                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                             promoter
                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
AX172475/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
A10942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="sequence comprising the 5' flanking region of RF-BN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 10.77,
de Both, G. and de Beuckeleer, M.
Hybrid winter oilseed rape and methods for producing same
Patent: WO 0141558-A 24 14-JUN-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                             Query Match 92.4%; Score 19.4; DB 6; Length 1037; Best Local Similarity 95.2%; Pred. No. 11; Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 1077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence 1 from patent number DE3920034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                                 Location/Qualifiers
1. 1037
/organism="unidentified"
/db_xref="taxon:32644"
a 174 c 166 g 359
                                                                                        Patent: DE 3920034-A 4 31-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.4%; Score 19.4; F
95.2%; Pred. No. 11;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347
                                                                                                                                                                                                                                                                                                                                                                                                                                      AX172463 1077 bp DNA
Sequence 24 from Patent WO0141558.
AX172463
AX172463.1 GI:14597575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="pGEM -T vector"
1061. 1077
/note="pGEM -T vector"
a 148 c 151 g 34
                                                                                                                                                                                                                                                                                                              980 GCTTGGACTATAATACCTGAC 960
unidentified.
unidentified
unclassified.
1 (bases 1 to 1037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gcttggactataatacttgac 21
```

```
317 c
                                                                                                                                                                                                                                                Query Match 92.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                               ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown
                                                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
                                                                                                                                            polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                RESULT 15
AR095107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="sequence derived from tapetum specific promoter of Nicotiana tabacum"
167. .790
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                       27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1994
                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                       Score 19.4; DB 6; Length 1085; Pred. No. 11; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Length 1160;
                                                                                                                                                                                                                                                                                   A10943 1160 bp DNA PAT 2'
Nucleotide sequence 5 from patent number DE3920034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="neomycine phosphotransferase gene"
167. .790
                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA PAT neo gene seq ID No:2.

    .1186
    /organism="synthetic construct"
/db_xref="taxon:32630"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.4%; Score 19.4; DB
95.2%; Pred. No. 11;
11ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Patent: DE 3920034-A 5 31-MAY-1990;
Location/Qualifiers
1. .1160
                      Patent: DE 3920034-A 1 31-MAY-1990;
Location/Qualifiers
1. .1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 9209696-A 2 11-JUN-1992;
Location/Qualifiers
                                                          /organism="unidentified"
/db_xref="taxon:32644"
218 c 155 g 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
/db_xref="taxon:32644"
194 c 188 g 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 1044 GCTTGGACTATAATACCTGAC 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A18051 1186 bp
DNA used as a probe for
A18051
A18051.1 GI:583120
                                                                                                                                                                                                        969 GCTTGGACTATAATACCTGAC 989
                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gcttggactataatacttgac 21
                                                                                                                                        92.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 1186)
(bases 1 to 1085)
                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 1160)
                                                                                                                                                                                           1 gcttggactataatacttgac
                                                                                                                                                                                                                                                                                                                          A10943.1 GI:492370
                                                                                                                                       Query Match
Best Local Similarity 95.29
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Conservative
                                                                                                                                                                                                                                                                                                                                                  unidentified
unidentified
                                                                                                                                                                                                                                                                                                                                                                              unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 20; Conserv
                                                                                      369 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ø
                                                                                                                                                                                                                                                                                                            A10943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                           RESULT 13
A10943
                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
JOURNAL
                          JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                            ò
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
```

```
/transl_table=11
/protein_id="CAA01373.1"
/protein_id="CAA01373.1"
/db_xref="Col:4529900"
/translation="NBLQDEABLENLATTGVPCAAVLDVVTEAGRDWLLLGEVPGQD
LLSSHLAPAEKVS.HADAMRRLHTLDPATCPPDHQAKHRIERRRTRWEAGLVDQDDLD
EEHQGLAPAELKRARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADR
                                                                                                                                                                       YODIALATRDIAEELGGEWADRFLVLYGIAAPDSORIAFYRLLDEFF"
1055. .1186
/note="3" regulatory sequence containing the polyadenylation site derived from agrobacterium T-DNA gene 7"
/gene="neomycine phosphotransferase gene"
/note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                              DB 6; Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1186;
                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Universitied.
1 (bases 1 to 1186)
D'Halluin,K. and Gobel,E.
Process for transforming monocotyledonous plants
Patent: US 6002070-A 2 14-DEC-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.4%; Score 19.4; DB
95.2%; Pred. No. 11;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                           Score 19.4; DB
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                        300 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AR095107 1186 bp DNA
Sequence 2 from patent US 6002070.
AR095107 GI:10022665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 25, 2002, 18:02:56 Job time: 18584 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
317 c 325 g
                                                                                                                                                                                                                                                                      325 g
                                                                                                                                                                                                                                                                                                                                                                                                                 92.4%;
                                   translation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gcttggactataatacttgac
```

us-09-698-903b-12.rge

```
February 25, 2002, 18:17:40 ; Search time 716.55 Seconds (without alignments) 25.126 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                        1861242
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                  US-09-698-903B-12
21
1 gcttggactataatacttgac 21
                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                     Run on:
```

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	PCR primer B02, to	PCR primer for vec	Right (5') border	Left (3') border f	Nucleotide fragmen	Nucleotide fragmen	USP-Promoter-casse	Right flanking reg	Lequmin-signalpept	USP-signalpeptide	Chimeric neo gene
SUMMARIES	AAD07001	AAH25431	AAD06997	AAD06999	AAH25454	AAH25451	AAQ04705	AAH25439	AAQ04703	AAQ04706	AAQ25707
% Query Match Length DB	22	22	22	22	22	22	11	22	11	11	13
	21	21	415	416	694	606	1037	1077	1085	1160	1186
% Query Match	100.0	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4
Score	21	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4
Result No.	-	7	с С	4	ပ	و د	7	ထ ပ	6	10	11

Gaps

ö

21;

Length Indels

22; 1;

DB

Score 19.4; Di Pred. No. 1.1; Mismatches

92.4%;

;

Conservative

Query Match Best Local Similarity Matches 20; Conserv

21 21

1 gcttggactataatacttgac 1 gcttggactataatacctgac

ò g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybrid seed; male-sterility gene;
barstar gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene (e.g. barnase gene), and the other plant has an expression cassette comprising a fertility restorer gene (e.g. barstar gene), integrated into the genome. The fartility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. PCR primers AAH2429-31 were used to amplify fragments of a vector in a transgenic plant which carries the TA29-barnase transgene.
                            seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is PCR primer which is used to recognise foreign DNA and a flanking sequence of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                 Gaps
                       to a transgenic Brassica plant or its
                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                            Score 21; DB 22; Length 21;
Pred. No. 0.17;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer for vector fragments in transgenic plant MS-BN1.
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                  Sequence 21 BP; 6 A; 4 C; 4 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic plant; winter oilseed rape;
fertility restorer gene; barnase gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 43; 98pp; English.
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                          100.0%;
                     relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                De Beuckeleer M;
                                                                                                                                                                                                                                                                                                          gcttggactataatacttgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2000; 2000WO-EP12872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0457037
                                                                                                                                                                                                                                                                                                                                                                                                                             AAH25431 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-381419/40.
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200141558-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Both G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH25431;
                                                                                                                                                                                                                                                                                                                                                                                             RESULT
AAH25431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                           *8888888888888
                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                           g
```

```
ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                 transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DB 22; Length 415; Pred. No. 1.3; 0; M1smatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                    Right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                                         Location/Qualifiers
1.234
/*tag= a
/rote= "Corresponds to plant DNA"
235.415
/*tag= b
/note= "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; 53pp; English.
                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                      (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
         AAD06997/c
ID AAD06997 standard; DNA; 415
                                                                                                                                                                  Chimeric - Agrobacterium sp.
Chimeric - Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                   26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                              99US-0430497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Beuckeleer M;
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcttggactataatacttgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                           male-sterility gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-300517/31.
                                                                                                                              MS-B2 elite event;
                                                                                                                                                                                                                                                                                                                  WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page
                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                               misc_feature
                                                                           06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                          03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               Weston B,
                                                   AAD06997:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335
RESULT
                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
(first entry)
                                                                                 WO200141558-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200141558-A1.
       22-AUG-2001
                                                                                                                                    38-DEC-1999;
                                                                                                    14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2001.
                                                                                                                                                                        De Both G,
                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH25451;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
                                                                                                                                                                                                                                                                                                                                                  by
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                  event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                              Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                Left (3') border flanking region of elite event MS-B2
                                                                                                                                                   Location/Qualifiers
1..193
/*tag- a
/94..416
/*tag- b
/note- "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19.4; DB 22;
Pred. No. 1.3;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 52; 53pp; English.
                              AAD06999 standard; DNA; 416 BP.
                                                                                                                                                                                                                                                                                             (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.48;
                                                                                                                           Chimeric - Agrobacterium sp.
Chimeric - Brassica sp.
                                                                                                                                                                                                                                                            26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
AAH2454/C
ID AAH25454 standard; DNA; 694
XX
AC AAH25454;
                                                                                                                                                                                                                                                                             990S-0430497
                                                                                                                                                                                                                                                                                                              De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcttggactataatacttgac
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 92.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                 MS-B2 elite event; trans
male-sterility gene; ds
                                                                                                                                                                                                                                                                                                                               WPI; 2001-300517/31.
                                                                                                                                                                                                                          WO200131042-A2
                                                                                                                                                     Key
misc_feature
                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                             29-OCT-1999;
                                                                06-AUG-2001
                                                                                                                                                                                                                                          03-MAY-2001
                                                                                                                                                                                                                                                                                                              Weston B,
                                                AAD06999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Н
                      AAD06999
```

셤 ò

```
The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene (e.g. barnase gene), and the other plant has an expression cassette comprising a fertility restorer gene (e.g. barstar gene), integrated into the genome. The fertility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. The present sequence represents a fragment from a vector comprising the
                                                           hybrid seed; male-sterility gene; barstar gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene; fertility restorer gene; barnase gene; barstar gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Nucleotide fragment of a vector comprising TA29-barstar transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide fragment of a vector comprising TA29-barnase transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 694 BP; 298 A; 81 C; 73 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TA29-barstar transgene from transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.4%; Score 19.4; DB 95.2%; Pred. No. 1.3; ive 0; Mismatches
                                                               Transgenic plant; winter oilseed rape; fertility restorer gene; barnase gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 94; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH25451/c
ID AAH25451 standard; DNA; 909 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     694 GCTTGGACTATAATACCTGAC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                   36-DEC-2000; 2000WO-EP12872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gcttggactataatacttgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
```

Gaps

```
Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene;
fertility restorer gene; barnase gene; barstar gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene (e.g. barnase fertility restorer gene (e.g. barnatar gene), integrated into the genome. The fertility restorer gene (e.g. barstar gene), integrated into the genome. male-sterility gene. The plant pair is useful for producing hybrid seed. Flants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. The present sequence represents the the right flanking region of a vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                        HindIII-Ort in the 3' polylinker (1032-1037) for cloning the cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is transfected.
                                                                                                                                                                         ő
                                                                                                                                               Length 1037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1077;
                                                                                                                                                                         Indels
                                                                                          Sequence 1037 BP; 338 A; 174 C; 166 G; 359 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1077 BP; 430 A; 148 C; 151 G; 347 T; 1 other;
                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                               Right flanking region in transgenic plant BN-RFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.4%; Score 19.4; DB 22;
95.2%; Pred. No. 1.4;
1ve 0; Mismatches 1;
                                                                                                                                              DB
                                                                                                                                       92.4%; Score 19.4; Di
95.2%; Pred. No. 1.4;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 58; Page 88-89; 98pp; English.
                                                                                                                                                                                                                                                                         439/c
AAH25439 standard; DNA; 1077 BP.
                                                                                                                                                                                                                      941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ž
                                                                                                                                                                                              21
                                                                                                                                                                                     1 gcttggactataatacttgac
                                                                                                                                                                                                      921 gcttggactataatacctgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2000; 2000WO-EP12872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Both G, De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0457037
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                               20; Conservative
                                                                 See also AAQ04703-Q04706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gcttggactataatacttgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                 Best Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200141558-A1.
                                                                                                                                                                                                                                                                                                                                        22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                             AAH25439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                2222XX
                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                               The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene (e.g. barnase fertility restorer gene (e.g. barstar gene), integrated into the genome. The fertility restorer gene (e.g. barstar gene), integrated into the genome. male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the plant pair is useful for producing hybrid seed. The present sequence represents a fragment from a vector comprising the present sequence represents a fragment from a vector comprising the plants.
                                                                                                                                     Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The unique BglII-Ort (720-725) site is for ligating foreign DNA and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Length 909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Incorporation of DNA into higher plant genome - by specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foreign DNA incorporation, recombinant DNA techniques; higher plant genome; legumin; USP-Pr.17-1; ss.
                                                                                                                                                                                                                                                                                                                                                                               Sequence 909 BP; 309 A; 134 C; 173 G; 293 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                          92.4%; Score 19.4; DB llarity 95.2%; Pred. No. 1.3; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hai NV,
                                                                                                                                                                                        Example 4; Page 93; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baumlein H, Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USP-Promoter-cassette USP-Pr.T7.1
                                                     (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ04705 standard; DNA; 1037 BP
                               99US-0457037.
                                                                                  De Beuckeleer M;
 06-DEC-2000; 2000WO-EP12872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gcttggactataatacttgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               909 GCTTGGACTATAATACCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89DE-3920034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; ; pp; German.
                                                                                                            WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Wes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1990-172459/23.
                                                                                 Both G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE3920034-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ04705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ04705
ID AAQ0
ð
```

ó

S

g

```
/*tag= a
/product=signalpeptide
747..817
          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ25707 standard; DNA; 1186
                                                                                                                                                                                                                                                                                                                                                                                                                               92.4%;
ilarity 95.2%;
Conservative (
                                                                                                                           89DE-3920034
                                                                                                                                                  88DD-0319887
                                                                                                                                                                        (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                                                                                   recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                          Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                        See also AAQ04703-Q04706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric neo gene probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9..790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                   WPI; 1990-172459/23.
P-PSDB; AAR05199.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                           20-JUN-1989;
                                                                                                                                                  19-SEP-1988;
                                                                              DE3920034-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-1992
                                                                                                    31-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ25707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
promoter
                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ25707
  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Legumin gene B4 is used. The unique BgIII-Ort (815-820) site is for ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1080-1085) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected.
                                                                                                                                                           Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; legumin; B4 gene; signalpeptide; Le-Sig.T7.; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19.4; DB 11; Length 1085; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                               Incorporation of DNA into higher plant genome - by specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; signalpeptide; USP-Sig.T7.; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1085 BP; 368 A; 219 C; 155 G; 343 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         'n,
                                                                                                                                                                                                                                                                                                                                                                        Mobus
                                                                                                                                                                                            Location/Qualifiers
747..814
/*tsg= a
/product=Legumin-signalpeptide
                                                                                                                                                                                                                                                                                                                                                                        Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                     Legumin-signalpeptide cassette Le-Sig.T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USP-signalpeptide cassette USP-Sig.T7.
                                                                                                                                                                                                                                                                                                                                                                        Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA004706 standard; DNA; 1160 BP
                                                                AAQ04703 standard; DNA; 1085 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    980 GCTTGGACTATAATACCTGAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.4%;
95.2%;
                                                                                                                                                                                                                                                                                                    89DE-3920034
                                                                                                                                                                                                                                                                                                                                                 (PFLA-) VE KOMB PFLANZENZUC.
                                                                                                                                                                                                                                                                                                                         88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant DNA techniques.
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.4 Best Local Similarity 95.2 Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Baumlein H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also AAQ04703-Q04706
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-172459/23.
                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR05198
                                                                                                              12-OCT-1990
                                                                                                                                                                                                                                                                                                    20-JUN-1989;
                                                                                                                                                                                                                                                                                                                         19-SEP-1988;
                                                                                                                                                                                                                                                     DE3920034-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1990
                                                                                                                                                                                                                                                                             31-MAY-1990,
                                                                                                                                                                                                                                                                                                                                                                        Bassuner R,
                                                                                        AAQ04703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ04706;
                                            6
                                            RESULT
AAQ04703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ04706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
```

윱

ò

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum; neomycine phosphotransferase; Agrobacterium; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
"sequence derived from tapetum specific
promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1160;
                                                                                                                                                                                                                          The unique BglII-Ort (890-895) site is for ligating foreign DNA and the HindIII-Ort in the 3' polylluker (1155-1160) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected.
                                                                                                              Incorporation of DNA into higher plant genome - by specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
/note= "3' regulatory sequence contg. the
polyadenylation site derived from
Agrobacterium T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= neomycine_phosphotransferase 791..1186
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1160 BP; 369 A; 192 C; 188 G; 411 T; 0 other;
  Wobus U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.4; DB 11;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
    Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
Bassuner R, Baumlein H, Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
```

```
Transgenic seed; marker; aleurone-specific promoter; Plasmid DV131; GFP:NPTII fusion protein construct; L3/BGFP:NPTIL/Tr7; maize R gene; expressation cassette; maize L3 oleosin gene; chimeric gene; transgene; MGFP:NPTII translational fusion; Tr7 terminator; Luciferase gene; assay; Green fluorescent protein; Gree fusion; selection; screening; expression; automated seed screening technique; screening; marker; embryogenic tissue; implementation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The HindIII-ECORI fragment (AAT39337) of plasmid pTS88 contains barstar DNA under control of a 35S promoter. The plasmid was used with prS174 (see also AAT39336) contg. barnase DNA under control of the stamen-specific promoter EI to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pVB136 (see also AAT39338) contg. barnase DNA under control of the stamen-specific PCA55 promoter to produce male sterile malize plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible low level expression of barnase DNA in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid DV131 comprising L3/EGFP:NPTII/Tr7 expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.4%; Score 19.4; DB 17; Length 1303; 95.2%; Pred. No. 1.4;
            of gene 7 og Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                          /note= "polylinker of pgEM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.4;
); Mismatches
                                                                                                                                                                                                                                                                            Cornelissen M, Michiels F;
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 38; 56pp; English.
                                                                                                                                                                                                                                      (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1178 gcttggactataatacctgac 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ29122 standard; DNA; 3153 BP.
                                                            pGEM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gcttggactataatacttgac 21
                                                                                                                                                                          96WO-EP00722.
                                                                                                                                                                                                          95EP-0400364.
                        1288..1303
                                            /*tag= (/label- |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                        WPI; 1996-402373/40.
                        misc_feature
                                                                                                     WO9626283-A1
                                                                                                                                                                      21-FEB-1996;
                                                                                                                                                                                                        21-FEB-1995;
                                                                                                                                                                                                                                                                          Botterman J,
                                                                                                                                      29-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9960129-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ29122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ29122
     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                             Two transformed corn plants were analysed by means of Southern hybridisation. As a probe, a 1184 bp EcoRI-HindIII fragment derived from another plasmid was used. The sequence of that plasmid is given below. Results showed that at least a chimeric neo gene was integrated into the plant genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function= region containing polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function= 35S promoter of cauliflower mosaic virus strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                               Transforming monocotyledonous plants e.g. cereals · comprises wounding and/or degrading cells of intact plant tissue or embryogenic callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.4%; Score 19.4; DB 13; Length 1186; 95.2%; Pred. No. 1.4; 1.4; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
transgenic plant; rice; Oryza sativa; maize; corn; Zea mays;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= Bacillus amyloliquefaciens barstar
968..1287
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1186 BP; 244 A; 317 C; 325 G; 300 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "polylinker of pGEM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                               Disclosure; Page 60; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
                                                                                                                                                        ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT39337 standard; DNA; 1303 BP
                                                                                                                                               (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/label= barstar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gottggactataatacttgac 21
                                                                   91WO-EP02198.
                                                                                                   90EP-0403332.
91EP-0401888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/label= pGEM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- P35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= d
/label= 3'97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695..967
                                                                                                                                                                               Dhalluin K, Goebel E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 694
                                                                                                                                                                                                                 WPI; 1992-217075/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 20; Conserv
                                                              21-NOV-1991;
WO9209696-A
                               11-JUN-1992.
                                                                                               23-NOV-1990;
                                                                                                                   08-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT39337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT39337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
```

à 셤 ó

7

ö

Gaps

ö

Indels

```
"n" in the sequence refers to not known nucleotides. pPS029 is identical to pVE36 (AAQ15144), but carries both the aminoterminal modification and the internal modification of the Bt ICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "n" in the sequence refers to not known nucleotides. pPS029 (AAQ14529) is identical to pVE36, but carries both the aminoterminal modification and the internal modification of the Bt ICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3201;
                                                                                                                                                                                                                                                                                     Length 3201;
Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis; insecticidal crystal protein; ICP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                          Sequence 3201 BP; 880 A; 710 C; 720 G; 886 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3201 BP; 915 A; 651 C; 700 G; 930 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.4; DB 12;
Pred. No. 1.5;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                 Score 19.4; DB Pred. No. 1.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dockx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 6(c); 78pp; English.
                                                                          Disclosure; Fig 6(c); 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                   See also AAQ14529, AAQ15142-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequence.
See also AAQ14529, AAQ15142-44.
                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ15144 standard; DNA; 3201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pVE36 Bt ICP coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.4%;
95.2%;
                                                                                                                                                                                                                                                                                   92.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-EP00733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cornelissen M, Soetaert P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90EP-0401055
                                                                                                                                                                                                                                                                                                                                                               1 gcttggactataatacttgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PLAN-) PLANT GENETIC SYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-339820/46.
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                         sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deletion; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9116432-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ15144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                      coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ15144
   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                             The present DNA sequence is the plasmid DV131, that is used in the generation of GFP:NPTII fusion protein constructs. It contains an expression cassette comprising, a promoter from the maize 13 oleosin gene, the coding sequence of EGFP:NPTII translational fusion, excised from DV126 and the Tr7 terminator. This plasmid is used to carry a chimeric gene, comprising an aleurone-specific promoter like 13, that is operably linked to the gene encoding a screenable marker, like Green fluorescent protein (GFP), luciferase or maize R gene. The gene fusions allow both selection and screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in embryogenic tissues, allowing selection and screening of viable creaming of transgenic seads. Screening of transgenic seads avoids the need for growing and assaying of seeds for transgenes and allows implementation of automated seed screening techniques for the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                           Screenable marker genes useful for identification of transgenic seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.4%; Score 19.4; DB 21; Length 3153; 95.2%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus thuringiensis; insecticidal crystal protein; ICP; deletion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3153 BP; 801 A; 857 C; 756 G; 739 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dockx J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                             Example 1; Page 164-166; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΣÌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ14529 standard; DNA; 3201 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pPS029 Bt ICP coding sequence.
                                                                                         (DEKA-) DEKALB GENETICS CORP
                 99WO-US11023
                                                    98US-0080625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91WO-EP00733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soetaert P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90EP-0401055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2759 gcttggactataatacctgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PLAN-) PLANT GENETIC SYST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                              Spencer TM;
                                                                                                                                                                    WPI; 2000-072441/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-339820/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                          for plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cornelissen M,
                 18-MAY-1999;
                                                    18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9116432-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-1991,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ14529;
                                                                                                                              Kriz AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

14 AAQ14529

ð g ö

Gaps

;;

Tue Feb 26 09:11:31 2002

Db 3105 gcttggactataatacctgac 3125

Search completed: February 25, 2002, 18:17:41 Job time: 16699 sec

us-09-698-903b-12.rng

Appli Appli Appli Appli Appli Appli Appli Appli

Searched:

Run on:

```
Sequence 1, Appil
Sequence 19, Appl
Sequence 3, Appli
Sequence 99, Appli
                            Sequence
Sequence
Sequence
                                                                                                                                               Sequence
                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ALEXANDLIA
STATE: VICTORIA
COUNTRY: United States
ZIP: 22313-1404
COUNTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS STEME: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING DATE: 24-MAY-1993
CLASSIFICATION NUMBER: B0040332.1
FILING APPLICATION APA:
APPLICATION NUMBER: EP 91401888.2
FILING APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: CTANG-PEULY, SHATON:
NAME: CTANG-PEULY, SHATON:
NAME: CTANG-PEULY, SHATON:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFRAX: (703) 836-6201
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE: INFORMATICES:
TENNYMEY. 1186 hase pairs
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08064121
Patent No. 5641664
GENERAL INFORMATION:
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: PROCESS FOR PRANSFORMING
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
MUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
          US-08 424-406-2
US-08 464-523B-8
US-08 464-523B-8
US-09 437-457-13
US-08 6410-540-1
US-08 642-073-3
US-08 642-073-4
US-08 410-540-3
US-08 6410-540-3
US-08 6410-540-3
US-08 6410-540-3
US-08 6446-923-1
US-08 646-923-1
US-08 646-923-1
US-08 646-923-1
US-09 65-668A-1
US-09 550-433-1
US-09 550-433-1
                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                     US-08-064-121-2
 115.
115.
115.
115.
114.
 0000 00
                                                                                                                                                              00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5, Appli
4, Appli
5, Appli
4, Appli
4, Appli
1, Appli
2, Appli
23, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Appl
Sequence 5, Appli
Patent No. 5428147
Sequence 88, Appl
                                                                                                                  (without alignments)
15.769 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                 ; Search time 301.6 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-238-863-88
US-08-443-407-88
PCT-US95-05600-232
US-07-968-971A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-817-188-2
US-08-232-016-23
US-08-232-016-22
US-08-549-680A-5
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-084-889-2
US-08-884-440-2
US-08-080-625-3
US-08-453-104-23
US-08-453-404-23
US-08-694-824-23
US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-080-625-2
US-09-080-625-5
US-09-080-625-4
US-08-817-188-1
US-08-817-188-1
US-08-817-188-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-894-440-4
-08-894-440-4
                                                                                                                                                                                                                                                             351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-894-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                 February 25, 2002, 18:05:51
                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                       1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5428147-1
                                                                                                                                                                                                                IDENTITY_NUC Gapox 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_NA:*
                                                                                                                                                   US-09-698-903B-12
                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11186
11186
11186
11180
33200
33200
33200
33201
33336
5560
5560
5564
5564
5564
7568
7568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
```

Result õ υu

```
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
FILING DATE: 24-MAY-1993
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOY-1990
PRIOR APPLICATION UNDER: EP 91401888.2
APPLICATION UNDER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= NPTII
                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTT-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 1113 GCTTGGACTATAATACCTGAC 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gettggaetataataettgae 21
                       LENGTH: 1186 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.29
Matches 20; Conservative
SEQUENCE CHARACTERISTICS:
                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                     NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: 9..790
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                           NAME/KEY: -
LOCATION: 791..1186
LOCATION: /label= 3/g7
OTHER INFORMATION: /note= "3' requiatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium OTHER INFORMATION: T-DNA gene 7"
  NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION: /note= "sequence derived from
OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.4%; Score 19.4; DB 1; Length 1186; 95.2%; Pred. No. 0.3; Live 0; Mismatches 1; Indels 0
                                                                                                                                                                                                    /label- NPTII
/note- "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WESULT 2

US-08-478-015-2

Sequence 2, Application US/08478015

Febent No. 5712135

GENERAL INFORMATION:
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STREET: P.O. Box 1404
CITY: Alexandria
STREET: P.O. Box 1404
CONTRY: United States
IP: 22313-1404
COMPUTER: IPP PC COMPATIBLE
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PREABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Datentin Release #1.0, Version #1.30
CURRENTING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENTING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 23-JUN-1991
PRIOR APPLICATION NUMBER: US 08-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 010830-088
TELECOMMUNICATION INFORMATION:
TELEBENOME: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D 1113 GCTTGGACTATAATACCTGAC 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.28
Matches 20; Conservative
                                                                                                                                         NAME/KEY:
LOCATION: 9..790
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-064-121-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
/note= "coding sequence of neomycine phosphotransferase ge
                                                                                                                                                                                                                                                                                   COCATION: 791..1186
CHER INFORMATION: /label= 3/g7
CHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylat
CHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"
US-08-478-015-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
/note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.4%; Score 19.4; DB 1; Length 1186; 95.2%; Pred. No. 0.3; tive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-475-975-2
US-08-475-975-2
Sequence 2, Application US/08475975
Patent No. 6002070
CENERAL INFORMATION:
PAPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTVLEDONOUS PLANTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STRRET: George Mason Bldg., Washington & Prince Sts.
STREET: George Mason Bldg., Washington & Prince Sts.
STREET: Virginia
STATE: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
PULSSIFICATION DATA:
CURSUR DATE: US/08/475,975
FILING DATE: US/08/475,975
CURSUR DATE: OUT-UND-1995
CURSUR DATE: DATE: US/08/475,975
```

```
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 1113 GCTTGGACTATAATACCTGAC 1133
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: - 791..1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: - . . . 790
LOCATION: 9.. 790
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-084-889-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /label= 3'97

OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium US-08-475-975-2
                                                                                                                                                                                                                                                                                                                                                                                              /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.4%; Score 19.4; DB 3; Length 1186; 95.2%; Pred. No. 0.3; 1; Indels 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: OBEL. Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
STATE: Virginia
COUNTRY: United States
STATE: PLANTINA MADERIAL STATES
COMPUTER PRADABLE FORM:
UNDITED PLANTING ALEXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMUNICATION INFORMATION:
TELECAX: (703) 836-5021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09/084,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09084889 Patent No. 6074877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D 1113 GCTTGGACTATAATACCTGAC 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gettggactataataettgae 21
                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.2'
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         791..1186
                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 9.790
COCATION: 9.790
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                 ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-084-889-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
LOCATION: 791.1186
OTHER INFORMATION: /Label= 3'97
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium OTHER INFORMATION: T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI
OTHER INFORMATION: fragment of pTS88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08894440
; Sequence 2, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.4%; Score 19.4; DB 3; 95.2%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: CTRING-FULY, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
```

Gaps

ö

```
Sequence 23, Application US/08453104

Patent No. 563346

GENERAL INFORMATION

APPLICANT: CORNELISSEN, Marc

APPLICANT: STAM, Maike

APPLICANT: STAM, Maike

APPLICANT: DOCKX, Jan

TITLE OF INVENTION: INDECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

TITLE OF INVENTION: IN PLANT CELLS

NUMBER OF SEQUENCES: 23
                                                                           92.4%; Score 19.4; DB 4; Length 3153; 95.2%; Pred. No. 0.32; 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19.4; DB 1; Length 3200;
Pred. No. 0.32;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
COCATION: 2078..2082
CTHER INFORMATION: /note= "Nucleotides 2078-2082
CTHER INFORMATION: wherein N is not known."
US-08-453-104-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMUNICATION INFORMATION:
TELEPRIONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.4%;
Best Local Similarity 95.2%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                  Conservative
; TOPOLOGY: linear
US-09-080-625-3
                                                                                                Best_Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                          US-08-453-104-23
                                                                             Query Match
                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                             PEATURE:
MAME/KEY: misc_feature
LOCATION: (36). (694)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-080-625-3
| Sequence 3. Application US/09080625
| Sequence 3. Application US/09080625
| Patent NO. 6307123
| GENERAL INFORMATION:
| APPLICANT: Kriz, Alan L. APPLICANT: Spencer T. Michael
| TITLE OF INVENTION: IDENTIFICATION
| TITLE OF INVENTION: IDENTIFICATION
| UNMBER OF SEQUENCES: 19
| CORRESPONDENCE ADDRESS: 19
| CORRESPONDENCE ADDRESS: Arnold White & Durkee STERET: PO. Box 4433
| CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19.4; DB 3; Length 1303;
Pred. No. 0.3;
0; Mismatches 1; Indels 0
                                                                                                                                                           FEATURE:
NAME/KEX: misc_feature
LOCATION: (695). (967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/080,625
                      LOCATION: (1)...(35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Robert E.
REGISTRATION NUMBER: P-42,628
REFERENCE/DOCKET NUMBER: DEKM:161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3153 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
... LOCATION: (1288)..(1303)
; OTHER INFORMATION: POLYlinker of pGEM2
US-08-894-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
```

ö

Gaps

ó

S

```
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROFEIN GENES AND THEIR EXPRESSION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOCTABER, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                 ANDERSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature;
LOCATION: 2151.2155
CTHER INFORMATION: /note= "Nucleotides 2151-2155;
CTHER INFORMATION: wherein N is not known."
US-08-453-104-22
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.4%; Score 19.4; DB 1; 95.2%; Pred. No. 0.32; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Rea, Teresa s

REGISTRATION NUMBER: 30,427

REFERENCE/DOCKET NUMBER: 010830-032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTOWNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/08694824
Patent No. 5877306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3105 GCTTGGACTATAATACCTGAC 3125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-694-824-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: CORNELISSEN, MATC
APPLICANT: CORNELISSEN, MAIC
APPLICANT: STAM, MAIKE
APPLICANT: STAM, MAIKE
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: IN SECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.4; DB 2; Length 3200;
Pred. No. 0.32;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STATE: Virginia COUNTRY: United States ZIP: 22313-1404
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; LOCATION: 2078..2082; OTHER INFORMATION: /note= "Nucleotides 2078-2082; OTHER INFORMATION: wherein N is not known."
US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 09-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/694,824 FILING DATE: 09-AUG-1996
                                                                                                                                                           Sequence 23, Application US/08694824
Patent No. 5877306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 22, Application US/08453104
Db 3032 GCTTGGACTATAATACCTGAC 3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.4%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.4°
Best Local Similarity 95.2°
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-453-104-22
                                                                                                                                      US-08-694-824-23
                                           g
  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.4; DB 4; Length 3336;
Pred. No. 0.33;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box 4433
CITY: Houston
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
FILING DATE:
                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Hanson, Robert E.
REGISTATION NUMBER: P 42,628
REFERENCE/DOCKET NUMBER: DEKM:161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3336 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DALL.

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HADSON, ROBERT E.
REGISTRATION NUMBER: P-42,628
REBERRENCE/DOCKET NUMBER: DEKM:16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3694 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnold White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09080625
Patent No. 6307123
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2942 GCTTGGACTATAATACCTGAC 2962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gettggactataataettgae 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.29
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-09-080-625-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-080-625-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-080-625-2
Sequence 2, Application US/09080625
Sequence 2, Application US/09080625
Sequence 2, Application US/09080625
Sequence 2, Application US/09080625
Sequence 2, Alan L.
APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: IDENTIFICATION
UNDARROY OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALOID White & Durkee
STREET: P.O. Box 4433
CITY: Houston

CITY:
The Correspondence of the Corresponde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.4%; Score 19.4; DB 2; Length 3201; 95.2%; Pred. No. 0.32; tive 0; Mismatches 1; Indels 0
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
21P: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWMATE: PETENTEN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 16-DEC-1995
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: REA, TAFESS S
REPERENCE/DOCKET NUMBER: 010830-032
FILENCAMUNICATION NUMBER: 010830-032
TELECOMMUTICATION NUMBER: 010830-032
TELECOMMUTICATION NUMBER: 010830-032
TELEDAMINICATION NUMBER: 010830-032
TELEDAMINICATION NUMBER: 010830-032
TELEBRAX: (703) 836-6620
INFORMATION POR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
TELEMETAX: 1703 B36-2021
TELEMETAX: 1703 B36-6620
TELEMETAX: 1703 B36-6620
TELEMETAX: 1703 B36-6620
TELEMETAX: 1703 B36-6620
TELEMETAX: 1703 B36-8016
TELEMETAX: 1704 B36-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: 2151.2155

OTHER INFORMATION: /note= "Nucleotides 2151-2155

OTHER INFORMATION: wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3105 GCTTGGACTATAATACCTGAC 3125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gottggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

g

ô

```
NAME/KEY: misc_feature
LOCATION: Complement((97)...(330))
OTHER INFORMATION: 3'97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCHER INFORMATION: Tonollement((883)..(2608))
OTHER INFORMATION: Promoter region of Rubisco small subunit gene of OTHER INFORMATION: Arabidopsis thaliana (PSSU)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2658)..(3031))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the OTHER INFORMATION: 9' nos: 3' untranslated region containing the OTHER INFORMATION: gene of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: Complement((3368)...(4876))
OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotiana OTHER INFORMATION: tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/08817188
; Patent No. 6074876
; GENERAL INFORMATION.
; APPLICANT: DE BLOCK, MARC
; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: Complement((331)..(882))
OTHER INFORMATION: bar: region coding for phosphinotricin acetyl
OTHER INFORMATION: transferase
                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.4%; Score 19.4; DB 3; 95.2%; Pred. No. 0.34; Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: Complement((4922)..(4946))
; OTHER INFORMATION: LB: T-DNA left border
US-08-817-188-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
Complement((883)..(2608))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GCTTGGACTATAATACCTGAC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gcttggactataatacttgac 21
                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 20; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-817-188-5/c
                                                                                                                  LENGTH: 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08817188
Patent No. 6074876
GENERAL INFORMATION
GENETIC DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
GURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                          DB 4; Length 3694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.4; DB 4; Length 3877; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
TITLE OF INVENTION: IDENTIFICATION
WUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                       Score 19.4; DB Pred. No. 0.33;
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Robert E.
REGISTRATION NUMBER: P-42,628
REFERENCE/DGCKET NUMBER: DEKM:161
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arnold White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        Sequence 4, Application US/09080625
Patent No. 6307123
                                                                                                                                       3300 GCTTGGACTATAATACCTGAC 3320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3483 GCTTGGACTATAATACCTGAC 3503
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (512) 418-3000
TELEFAX: (512) 44-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3877 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                             1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gcttggactataatacttgac 21
                     Query Match 92.4%;
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-817-188-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
US-09-080-625-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hou
STATE: TX
COUNTRY:
                                                                                                                                                                                                                             RESULT 13
US-09-080-625-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                             à
                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

Gaps

ö

Length 4946; Indels

```
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW142
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(25)
OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from OTHER INFORMATION: prib653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (84)..(296)
UCCATION: (84)..(296)
UCCATION: (94)..(296)
UCCATION: (94)..(296)
UCTHER INFORMATION: 3' 97: 3' untranslated region containing the OTHER INFORMATION: 901yadenylation signal of gene 7 of Agrobacterium OTHER INFORMATION: T-DNA
NAME/KEY: misc_feature
LOCATION: (318)..(869)
UCCATION: (318)..(869)
UTHER INFORMATION: bar: region coding for phosphinotricin
UTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (5476)..(5479)
OTHER INFORMATION: region with unknown sequence (may contain up to 20
OTHER INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (4483)..(4671)
OTHER INFORMATION: IV2: region corresponding to the second intron of
OTHER INFORMATION: the ST-LSI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (5533)...(5560)
OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
OTHER INFORMATION: pTIB6S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: misc_feature
LOCATION: (5058). (5059)
OTHER INFORMATION: region with unknown sequence (may contain up to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU: promoter region of Rubisco small subunit
OTHER INFORMATION: gene of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (5077)..(5078)
OTHER INFORMATION: region with unknown sequence (may contain up
OTHER INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (3059)..(5056)
OTHER INFORMATION: uidA: region coding for beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (5067)..(5502)
OTHER INFORMATION: P35S: 35S promoter region of CaMV
EARLIER FILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 5
LENGTH: 5560
                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-817-188-5
```

```
      Query Match
      92.4%; Score 19.4; DB 3; Length 5560;

      Best Local Similarity
      95.2%; Pred. No. 0.34;

      Matches
      20; Conservative
      0; Mismatches
      1; Indels
      0; Gaps
      0;

      Qy
      1 gcttggactataatacttgac
      21

      Db
      150 GCTTGGACTATAATACCTGAC
      130
```

Search completed: February 25, 2002, 18:05:52 Job time: 18600 sec

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

```
AU042554 AU042554
AI115372 uj33912.x
BE325283 WT91200065
AZ411070 1M0184B01
AQ418178 RPC111-60
BF978014 602147907
BB337839 BB337839
AA013302 ze28d06.r
AA554565 nx30802.s
BF641371 RC2-HT107
AZ273622 RPC1-23-8
H04932 y1744h05.r1
AQ710257 HS_5220_A
AQ493489 HS_565_B
BE54649 TCBAP1E46
AG023449 Oryza sat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 344)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                               vp37b11.r
vm87a06.r
AU021898
                                                                                                                                                                                                 vv89d09.r
HS_2052_A
AU017121
                                                                                                                                                                                                                                                          vt32f04.r
AU042554
                                    BB103479
EST02498
BB117588
BB235252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ117151 344 bp DNA GSS 22-SEP-1998 HS_2188_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=7 Row=G, DNA sequence. AQ117151.1 GI:3494942 GSS.
                                                                                                         AU021901
AU021997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                     AA407887 BB117588 BB235252 BB0021901 AU021997 AU
                                                                                                                                             AA823300
AA606880
AU021898
AA763279
AQ236085
AU017121
AA690887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
721: (206) 616-3887
Frax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .344
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 344 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ493489
BE246449
AG023449
                                                     AA407887
BBB17588
BBB21583
AU021907
AA021997
AA606880
AA763279
AA763279
AA763279
AA7632698
AU017121
AA690887
AA690887
AA690887
AA690887
                                                                                                                                                                                                                                                                                                                                                                    AQ198178
AQ201499
                                                                                                                                                                                                                                                                                                                                                                                                                                            AA013302
AA554565
BF841371
                                                                                                                                                                                                                                                                                                              BE325283
AW109828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             row: G column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                           BB337839
                                                                                                                                                                                                                                                                                                                                                      AZ411070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ710257
                                                                                                                                                                                                                                                                                                                                                                                                          BF978014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Tagged Connector
 Plate: 2188 rov
Class: BAC ends
0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

0.00

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
AQ117151/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
 υU
                                                                          U
                                                                                                                                                   00
                                                                                                                                                                                                                                                            O
                                                                                                                                                                                                                                                                                                                  ပ
                                                                                                                                                                                                                                                                                                                                             000
                                                                                                                                                                                                                                                                                                                                                                                                                                                υυ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ117151 HS_2188_A
AQ464390 1M0273D15
AV035892 AV035892
AQ172470 HS_3190_B
AI675738 wc40h04.x
BE80728 ST44904.y
AZ133172 OSJNBD010
AA310103 EST180941
B74437 CIT-HSP-202
AQ666336 HS_53_A
BE846195 232148 BA
                                                                                                                                             (without alignments)
27.314 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            ; Search time 8261.74 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                     22703874
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                 11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                          February 25, 2002, 17:21:17
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ117151
AZ464390
AV035892
AQ172470
A1675738
BE802728
AZ133172
AA310103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ666336
AQ836967
BE846195
                                                                                                                                                                                                                                         21
                                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                       1 gcttggactataatacttgac
                                                                                                                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΩI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_gss_vrt:*
em_gss_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est2:*
gb_htc:*
gb_gss:*
em_gss_fun:*
em_gss_hum:*
                                                                                                                                                                                                   US-09-698-903B-12
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_gss_inv:*
em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_gss_pro:*
em_gss_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
113
113
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_estfun:*
em_esthum:*
em_estin:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_estom:*
em_estpl:*
em_estba:*
em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_htc:*
gb_est1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_estov:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633
2291
415
4449
470
483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               888880.0
880.0
800.0
800.0
800.0
800.0
800.0
```

Score

2 υ

Result

17.4 116.8 116.8 116.8 116.8 116.8 116.8 116.8 116.8

υv

υ

õ

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
AV035892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                    δŏ
                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="texon:1000"
/db_xref="texon:1000"
/clone="UGCIM0273D15"
/clone="UGCIM0273D15"
/clone="UGCIM0273D15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42D1; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared hydrocitides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 633)
Dunn,D., Aoyal,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plannid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ464390 633 bp DNA GSS 04-OCT-2000
1M0273D15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0273D15 R, DNA sequence.
/clone="Plate=2188 Col=7 Row=G"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" 53 c 85 g 101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIC,
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
The Salary Of Utah
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                               82.9%; Score 17.4; DB 13; Length 344; 94.7%; Pred. No. 2.4e+02; 1.ve 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: D column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                        ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 633.
Location/Qualifiers
                                                                                                                     85 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A2464390.1 GI:10622515
                                                                                                                                                                                                                                                                                                                                       2 cttggactataatacttga 20
                                                                                                                                                                                                             Query Match 82.9
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ464390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
```

```
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 291)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukudishi, Y., Fukushi, Y., Kunayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Stuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Saco, K., Shibata, Y., Shigemico, Y., Sizuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muramatsu, M., Okazaki, Y. and Hayashizaki, Y., Yoshino, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-9145
Fax: 81-298-36-9095
Fax: 81-298-36-9095
Fax: 81-298-36-9096
inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV035892 291 bp mRNA EST 22-NOV-1999
AV035892 Mus musculus adult C57BL/6J placenta Mus musculus cDNA
clone 1600016H12, mRNA sequence.
AV035892 GI:4855557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adult C57BL/6J placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.9%; Score 17.4; DB 13;
llarity 94.7%; Pred. No. 2.6e+02;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

80.0%; Score 16.8; DB 10;
Best Local Similarity 90.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="placenta"
/dev_stage="adult"
56 c 66 q 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="1600016H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex-"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 CTTGGACTAAAATACTTGA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 cttggactataatacttga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN Mouse ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
```

```
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE802728
BE802728.1 GI:10233840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 GCTTGGACTATAATAATTA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gcttggactataatacttga 20
                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                              1. .449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
BE802728/c
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                              Holzman,T.,
Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                  AQ172470 415 bp DNA GSS 17-OCT-1998 HS_3190_B2_H07_MR CIT Approved Human Genomic Sperm Library D Homo saplens genomic clone Plate=3190 Col=14 Row=P, DNA sequence. AQ172470 GI:3569837
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wc40h04.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321143 3' similar to gb:M73255_rnal VASCULAR CELL ADHESION PROTEIN 1 PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3190 Col=14 Row=p"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108" 151 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 16.8; DB 13; Length 415; 90.0%; Pred. No. 4.8e+02; ive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TEI: (206) 616-3818
Exx: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 415.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Tagged Connector
Plate: 3190 row: P column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI675738.1 GI:4876218
                cttggactataatacttgac 21
                                13 CTTGGACTATTATACTGGAC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 CTTGGAATATAATGCTTGAC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 cttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: BAC ends
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI675738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                 Hood, L
                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                               RESULT 4
AQ172470
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
AI675738/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
              ~
                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
              ð
                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
Inductional contents of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: prostate; Vector: pT713D-Pac (Pharmacia)
with a modified polylinker; plasmid DNA from the
normalized library NCI CGAP_PT22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The diver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Scares and M. Fatima Bonaldo. "
a
77 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choses 1 to 449)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Waylie, T., Underwood, K., Steptco, M., Thaising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ker, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, P., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ST 20-SEP-2000 ST44904.Yl Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: 6m-c1051-943 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 16.8; DB 10; Length 449; 90.0%; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2321143"
/clone_lib="NCI_CGAP_Pr28"
```

```
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA310103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote—"Vector: pBluescript II SK+; Site_I: ECORI; Site_2:
XhoI: The CDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. ECORI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
CDNA fragments were directionally cloned into the
ECORI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DHIOB host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                   This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information edil: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones/genomesystems.com or info@genomesystems.com web site: www.genomesystems.com High quality sequence stop: 402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

I Chases I to 470;

Wing, R. A. and Dean, R. A.

MAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ133172 470 bp DNA GSS 02-JUN-2000 OSJNBbOLO8PO5r CUGI Rice BAC Library (ECORI) Oryza sativa genomic AZ133172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                            1. .449.
/organism="Glycine max"
/organism="Glycine max"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1051-943"
/clone="Ib="Gm-c1051"
/clone=Lib="Gm-c1051"
/lasue_Lype="floral meristematic mRNA"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 16.8; DB 11; Length 449; 90.0%; Pred. No. 4.8e+02; 1.1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 101
High quality sequence stop: 368.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 CTTGGACTATAAAAGTTGAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ133172.1 GI:8212071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 cttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
AZ133172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
/gittain-"Japonica |
/gittain-
```

S

```
ø
                                                                                                                                                     160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                      AQ666336/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                     á
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Durithing (1997)
Other_GSSs: CIT-HSP-2028F18.TR
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Fararyotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
The: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B74437 487 bp DNA GSS 24-OCT-1998 CIT-HSP-2028F18.TF CIT-HSP Homo sapiens genomic clone 2028F18, DNA
                                                                                                                                                                                                    Email: arkerlavetigr.org
For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
for clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 487)
Adms, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Jurkat T-cells v"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 483;
                                                                                                                                  772 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.8; DB 10;
Pred. No. 4.9e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="ATCC (inhost):156165"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 t
                                                                    Other ESTs: THC122434
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .487
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 GCTTGGACGAAAATNCTTGAC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B74437.1 GI:2770124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: Lass. BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B74437
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                    JOURNAL
                                                      MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3618
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 505) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoR1 and EcoR1 Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoR1 sites" 4 others
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ666336 505 bp DNA GSS 23-JUN-1999 HS_5374_Al_H01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=950 Col=1 Row=O, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
/db_xref="GDB:7048076"
/db_xref="texon:9606"
/db_xref="texon:9606"
/clone_1ib="CIT-HSP"
/clone_lib="CIT-HSP"
/cell_type="Sperm"
/cell_type="Sperm"
/note="Vector: pBelobACI1; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="Plate=950 Col=1 Row=0"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                          Score 16.8; DB 13;
Pred. No. 4.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                       126 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 505.
Location/Qualifiers
                                                                                                                                                                                                                    100 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ666336
AQ666336.1 GI:5174104
                                                                                                                                                                                                                                                                                                                             80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 CTTGGACTGTAATACTTGTC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                          101 c
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 cttggactataatacttgac
                                                                                                                                                                                                                                                                                                                                Query Match 80.03
Best Local Similarity 90.03
Matches 18; Conservative
                                                                                                                                                                                          HindlII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
```

```
genomic, DNA sequence.
BH132866
BH132866.1 GI:15091927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 CTTGGACTCTAATCCTTGAC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Entamoeba histolytica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 cttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.0
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150
                                                                                                                                                                                                                                                                                                                                                                                                      source
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                        JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
BH132866/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                            REFERENCE
                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 537)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                        Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center

10 Indersity of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3887

Email: (306) 616-3887

Clones may be purchased from Research Genetics (info@resgen.com).

Plate: 4553 row: G column: 17

Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108" 3 others
                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                              AQ836967 537 bp DNA GSS 30-AUG-1999 HS_4553_A1_D09_T7A CIT Approved Human Genomic Sperm Library D saplens genomic clone Plate=4553 Col=17 Row=G, DNA sequence. AQ836967.1 GI:5806929
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2000
                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
          Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE846195 600 bp mRNA EST 2
32148 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.
BE846195.1 GI:10283019
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
   80.0%; Score 16.8; DB 13;
90.0%; Pred. No. 4.9e+02;
11ve 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d;
. 5e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%; Score 16.8; DB 13; 90.0%; Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 537

Organism-"Homo sapiens"

/db_xref-"taxon:9606"

/clone="Plate=4553 Col=17 Row-G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                    500 CTTGGAGTATTATACTTGAC 481
                                                               2 cttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 CTTGGACTAGAATACTTTAC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 cttggactataatacttgac 21
                Best Local Similarity 90.0 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
     Query Match
                                                                                                                                              RESULT 11
AQ836967
                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
BE846195
                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                            g
```

```
PREPRENCE

ANTHORN
BOST FAILTREAM
CONNERN
CONN
```

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB103479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                  /db.xrefarne="HM1:IMSS"
/db.xrefarne="HM1:IMSS"
/db.xrefarne="HM1:IMSS"
/db.xrefarne="Laxon:5759"
/clone_lib="Entamoba histolytica Sheared DNA"
/note="Vector: pH0S1; Site_1: Bst I; Constructed at The
/note="Vector: pH0S1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ670679 968 bp DNA GSS 14-DEC-2000
ENTHD34TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 968)
Loftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.0%; Score 16.8; DB 13;
90.0%; Pred. No. 5.3e+02;
11ve 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Entamoeba histolytica"
                                                                                                                    /organism-"Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
Class: shotgun
High quality sequence start: 18
High quality sequence stop: 742.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 94
High quality sequence stop: 406.
Location/Qualifiers
1. 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="HM1:IMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13-Forward
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ670679.1 GI:11807825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic, DNA sequence.
AZ670679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 GCTTGGACTAAAATATTTGA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Entamoeba histolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gcttggactataatacttga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dq 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
AZ670679/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 301)

S. (hases 1 to 301)

Ronno, H., Alaawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci

P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,

Ilawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Isawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Kiyosawa, H., Kojima, Y., Kodowa, S., Karihara, C., Kusakabe, M.,

Matsuyama, T., Miki, K., Mizuno, Y., Nakamura, C., Kusakabe, M.,

Non, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Wotca, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Fax: 81-45-503-9216

Fax: 81-45-503-9216

Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,
'N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
'Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB103479 301 bp mRNA EST 27-JUN-2000 BB103479 RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck Mus musculus cDNA clone 9430087K10 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8; DB 13; Length 968;
Pred. No. 5.4e+02;
0: Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB103479.1 GI:8756047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 GCTTGGACTAAAATATTTGA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gcttggactataatacttga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
```

```
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9430087K10"
/clone="1b="RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck"
/tissue_type="embryonic body between diaphragm region and neck"
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                           Query Match

Query Match

Best Local Similarity 94.4%; Pred. No. 7.1e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ttggactataatacttga 20
                                                                                                                                                                                                                                                                                                                                               75
                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

Search completed: February 25, 2002, 17:21:20 Job time: 16173 sec

ö

Description

DB

Length

Match Query

Result

AX127760 AX172481 BNACRUC 124540 183673 BNCRUA BNCIG AL139402

ATHCRA1AA AB005239

84544 167645 639

ATCRA1

1624 3113 3113 3113 3198 10959 2346 2346

AX127760 Sequence
AX172481 Sequence
M16860 Rapeseed cr
124540 Sequence 20
183673 Sequence 20
X14555 Brassica na
X59294 B.napus BnC
AL139402 Human DNA
X14312 Arabidopsis
M37247 A.thaliana
X59295 B.napus BnC
AR007884 Trypanoso
AC077680 Glardia 1
AC039215 Homo sapi
AC039215 Drosophil
AL035680 Arabidops
AC016794 Drosophil
AC050545 Drosophil

AC007864 AC070680 AC039716 AC039716 AC08049 AC08738 AC084135 AC084135 APO02744 BNCRU4SU8 APO02744 AC016375 AC016794 AC016794 AC016794 AC016719 AC016719 AC016719 AC016719 AC016870 AC016870 AC016870 AC016870 AC016870 AC016870

1083 3394 160457 161416 170871 153865

2876 18177 45980 63855 77862

176732 178257 198372

184055 249001

```
Score
                                               19.4
118.8
118.8
118.8
118.8
118.8
                                                                                   116.8
116.8
116.8
116.8
116.8
116.8
                           g
                                                                              υ
                                                                                        000
                                                                                                                                       O
                                                                                                                                                       0 0 0
                                                                                                                                                                                      0000
                                                                                                                                                                                                                     0 00
                             February 25, 2002, 18:02:56 ; Search time 2331.3 Seconds
(without alignments)
155.680 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                       1472140 seqs, 8248589755 residues
                                                                                                Total number of hits satisfying chosen parameters:
                                                              1 aacgagtgtcagctagaccagc 22
                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                    - nucleic search, using sw model
                                                                        IDENTITY_NUC Gapor 10.0 Gapor 1.0
                                                                                                                                                                                                                                                                                                                em_htgo_inv: *
em_htgo_rod: *
em_htg_hum: *
em_htg_inv: *
em_htg_rod: *
                                                                                                                                                                                                                                                                                                                                           em_htg_other:*
                                                   US-09-698-903B-13
22
                                                                                                                                                                                                                                                                                                       em_vi:*
em_htgo_hum:*
                                                                                                            seq length: 0 seq length: 2000000000
                                                                                                                                                                              9b_ph:*
9b_ph:*
9b_pr:*
9b_pr:*
9b_ro:*
9b_sr:*
9b_sr:*
em_ba:*
                                                                                                                                                                                                                                        em_hum:*
em_in:*
em_om:*
em_or:*
                                                                                                                                                                                                                                                                   em_pat:*
em_ph:*
                                                                                                                                                                                                                                                                                  em_ro:*
em_sts:*
                                                                                                                                                      gb_ba:*
gb_htg:*
                                                                                                                                                                                                                                                              em_ov:*
                                                                                                                                                                                                                                                                                                  *: un _ ша
                                                                                                                                                                gb_in:*
gb_om:*
gb_ov:*
                                                                                                                                                                                                                                                                             em_pl:*
                                                                                                                                                                                                                                                                                             em_sy:*
                                                                                                                                                 GenEmbl:*
                                                                                                                                                                                               Perfect score:
Sequence:
                                                                        Scoring table:
                                                                                                            Minimum DB 8
Maximum DB 8
                     OM nucleic
                                                                                        Searched:
                                                                                                                                                Database
                               Run on:
```

AC016870 Homo sapi AC011781 Homo sapi AL161566 Arabidops AL03824 Drosophil AC01700 Homo sapi AX330716 Sequence AC025522 Homo sapi AC079234 Homo sapi AC079234 Homo sapi AC079234 Homo sapi AC051132 Homo sapi AC050572 Homo sapi AC050578 Homo sapi AC050578 Homo sapi AC050578 Homo sapi AC026358 Homo sapi

Homo sapi Homo sapi Homo sapi Arabidops Drosophil

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	15-MAY-2001					producing same											
S	E- 4 0									methods fo	01;				struct"		
ALIGNMENTS	ax127760 22 hp nNa	13 from Patent	AX12//60 AX127760.1 GI:14134407	•	synthetic construct.	synthetic construct	artificial sequence.	1 (bases 1 to 22)	Weston, B. and de Beuckeleer, M.	Male-sterile brassica plants and r	Patent: WO 0131042-A 13 03-MAY-2001;	Aventis CropScience N.V. (BE)	Location/Qualifiers		/organism="synthetic construct"	/db_xref="taxon:32630"	/note="primer CVZ7"
	RESULT 1 AX127760	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	JOURNAL		FEATURES	sonrce			

```
LAGNNPOGGVWIEGREGOPORNILMGFFPEULAKAFKIDVRPAGOLONGODNRONIEN
VOGPFSVIRPLESGRPOEFVNGLEFTICSARCTDNLDDPSNADVYRPQGOTSTLNS
YDLPILKFERLSALRGSIRONANVENDOMNANNAVENTDGEBHVQVVNDNGDRYFDG
QVSGCQLLSIPOGFSVVRRATSEGPFNIEFKENNAVLYTDGEBHVQVVNDNGDRVFDG
GYOISLEEARRVKFNTIETTLTHSSGPRSYGGPRKADA
                                                                                    Unclassified.

1 (bases 1 to 3113)
van Ooijen,A.J.J., Rietveld,K., Hoekema,A., Pen,J., Sijmons,P.C., Verwoerd,T.C. and Quax,M.J.
Production of enzymes in seeds and their use
Patent: US 5543576-A 20 06-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 22; DB 8; Length 1624; 100.0%; Pred. No. 0.098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                               /note="cruciferin alpha subunit"
                                                                                                                                                                                                                                                                           /note="cruciferin beta subunit"
57 a 425 c 387 g 355 t
upstream of Ncol site.
         17. .1483
/note="cruciferin precursor"
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124540 3113 bp DNA
Sequence 20 from patent US 5543576.
124540 GI:1604410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/protein_id="AAA32988.1"
/db_xref="GI:167134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
685 c 586 g
                                                                                                                                                                                                                                                                                                                                                                                                                                          98 AACGAGTGTCAGCTAGACCAGC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
Unclassified.
1 (bases 1 to 3113)
                                                                                                                                                                                                                                                            911. .1480
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                             457 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         961 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
                                                                                                                                                                                                                                                                                                          70 bp
                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
I24540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
183673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota 'Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta; eudicotyledons, core eudicots; Sosidae, eurosida II; Brassicales; Brassicaceae, Brassica.

1 (bases 1 to 1624)
Simon,A.E., Tenbarge,K.M., Scofield,S.R., Finkelstein,R.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crouch,M.L.

Nucleotide sequence of a cDNA clone of Brassica napus 12S storage protein shows homology with legumin from Pisum sativum Plant Mol. Bill. 5, 191-201 (1985)
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 storage protein; cruciferin.
Rapeseed (cultivar Tower) embryo (26-day post anthesis), cDNA
                                                                                                                                                                                                                                            03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-1993
                                                                                                                                                                                                                                                                                                              synthetic construct.
synthetic construct
synthetic construct
artificial sequence.
1 (bases 1 to 22)
de Both, 6. and de Beuckeleer, M.
Hybrid winter oilseed rape and methods for producing same Patent: WO 041558-A 42 14-70N-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                  Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Query Match

Bost Local Similarity 100.0%; Pred. No. 0.081;

Matches 22; Conservative 0; Mismatches 0; Indels
                                                             Score 22; DB 6; Length 22
Pred. No. 0.081;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                            PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1. .1624
7. product="CRUC mRNA"
17. of
/note="cruciferin signal peptide"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer BNA05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BNACRUC 1624 bp mRNA
Rapeseed cruciferin mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٣
                                                                                                                                                                                                                                     AX172481 22 bp DNA Sequence 42 from Patent WO0141558.
    Б
    ø
                                                                                                                        AXÎ72481
AX172481.1 GI:14597593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AACGAGTGTCAGCTAGACCAGC 22
                                                             Query Match

Best Local Similarity 100.0%;
Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 aacgagtgtcagctagaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M16860
M16860.1 GI:167133
    O
 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA, clone pcl.
Brassica napus
    ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                  DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
```

JOURNAL

FEATURES

REFERENCE AUTHORS

RESULT AX172481 LOCUS

ð a ö

Gaps

;

ACCESSION VERSION KEYWORDS SOURCE

RESULT BNACRUC

à 8 ORGANISM

REFERENCE AUTHORS JOURNAL FEATURES

TITLE

mRNA

10-AUG-1998

ö

Gaps

ő

07-0CT-1996

m

us-09-698-903b-13.rge

```
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                              RESULT
                                                                                       ORIGIN
                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAGUNPOGOVWIEGEROOPOKNILNGFTPEVLAKAFKIDVRFAQULONGONTIL
VOGPFSVIRPLRSORPOEEVNGLEETICSARCIDNILDDFSNADVYKPQLGYISTLNS
VDCPLILRFLRLSALRGSIRONAVLPOWNANDNAVLYVTDGEAHVQVVNDNGDRVFDG
QVSGGQLLSIPQGFSVVRRATSEOPFWIEFRTNANAVINTLAGRTSVLRGLFEVISN
GYQISLEBARRVKFNTIETTLTHSSGPASYGGPRKADA
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MARLSSLLSFSLALLTFLHGSTAQQFPNECQLDQLNALEPSHVL
KAEAGRIEVWDHHAPQLRCSGVSFVRYIIESKGLYLPSFFSTARLSFVAKGEGLMGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 3113)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ryan, A.J., Royal, C.Í., Hutchinson, J. and Shaw, C.H.
Genomic sequence of a 12S seed storage protein from oilseed rape
(Brassica napus c.v. jet neuf)
Nucleic Acids Res. 17 (9), 3584 (1989)
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                10-FEB-1999
Van Ooijen, A.J.J., Rietveld, K., Hoekema, A., Pen, J., Sijmons, P.Christian, Verwoerd, T.Cornelis and Quax, W.Johannes. Production of enzymes in seeds and their use Patent: US 5714474 A 2 03-FEB-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-MAR-1989) Ryan A.J., Department of Biological Sciences, University of Durham, South Road, Durham, DH1 3LE,
                                                                                                                                                                                                                          ó
                                                                                                                                                                                          6; Length 3113;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="leaf"
644. .650
/note="pot. TATA-box"
680. .3010
/note="primary transcript"
join(709. .991,1220. .1581,2049. .2870)
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                  PLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cruA gene; cruciferin; seed storage protein.
                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                BNCRUA 3113 bp DNA
Brassica napus cruA gene for cruciferin.
X14555
                                                                                                                                                                                      Score 22; DB 6;
Pred. No. 0.1;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SWISS-PROT:P11090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brassica napus"
/strain="Jet Neuf"
/db_xref="taxon:3708"
                                                                                                                      882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA32692.1"
/db_xref="G1:17811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="cruciferin"
                                                                                  1. .3113
/organism="unknown"
1 684 c 586 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                      586 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         992. 1219
/note="intron I"
1582. 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1582. .2048
/note="intron II"
                                                                                                                                                                                      Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                          790 AACGAGTGTCAGCTAGACCAGC 811
                                                                                                                                                                                                                                                        1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 3113)
                                                                                                                                                                                                                                                                                                                                                                                                                               X14555.1 GI:17810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica napus
                                                                                                                    961 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Ac
89263796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ryan, A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                    BASE COUNT
                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                  TITLE
                                                                                                                                                                                                                                                                                                                                                              BNCRUA
                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                        g
```

```
RVQGPFSVIRPPLRSQRPQETEVNGLEETICSARCTDNLDDPSNADVYKPQLGYISTL
NSTDLELREFLALLASIRGSIRQNAMULLVQWNANANALYTYTGGEAHVQVVNDNGDRVF
DGOVSQGOLLSIPQGESVVKRATSEDFRMIEEKTNANAOLNTLAGRTSVLRGLPLEVI
SNGYQISLEERARRVKFNTIETTLTHSSGPASYGGPRKADA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"cruciferin storage protein"
/protein_id="CAA41984.1"
/brotein_id="C13-7629194.1"
/db_xxef="SWISS-PROY:P33523"
/tb_xref="SWISS-PROY:P35513"
/translation="MARLSSLLSFSLALLIFLHGSTAQQFPNECQLDQLNALEPSHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAEAGRIEVWDHHAPQLRCSGVSFVRYIIESKGLYLPSFFSTAKLSFVAKGEGLMGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Brassica. 1 (Jases 1 to 3198)
Breen, J. P. and Crouch, M. L.
Molecular analysis of a cruciferin storage protein gene family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1584,2069. .2488,2653. .>3057)
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(709. .991,1220. .1584,2069. .2488,2653. .3057)
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (24 APR-1991) Breen J.P., Jordan Hall, Indiana
Submitted; Diomington, IN 47401, USA
See also M16860 & X59295 (for BnC2 gene).
Location/Qualiflers
                                                                                                                                                                                                                      ö
                                                                                                                                                                        100.0%; Score 22; DB 8; Length 3113;
nilarity 100.0%; Pred. No. 0.1;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             B.napus BnCl gene for cruciferin storage protein. X59294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 19 (6), 1049-1055 (1992) 92379259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cruciferin; cruciferin storage protein
                                                                                      ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .3198
/organism="Brassica napus"
                                                                                      881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="c.v. Tower"
/db_xref="taxon:3708"
/cell_ilne="EB8767"
/clone_ilne="Ch4a"
/clone="lambda BnC1"
/gone="Bn01"
/gone="Bn01"
2915. .2920
/note="polyA signal"
2989. .2994
/note="polyA signal"
a 685 c 586 g
                                                                                                                                                                                                                                                                                      190 AACGAGTGTCAGCTAGACCAGC 811
                                                                                                                                                                                                                                                               1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               709. .3057
/gene="BnC1"
join(709. .993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <709. .991
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 3198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=1
992. .1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica napus
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breen, J.P.
                                                                                      961
                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rape
```

```
IMPORTANT: This sequence is not the entire insert of clone RP4-808F24 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-774610 is at 10860 in this sequence. The true right end of clone RP6-227L5 is at 100 in this sequence.
Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2797. .3221)
/note="match: GSS: Em:B83505"
5384. .5631
/note="LIMB8 repeat: matches 5924. ,6175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5682. .5791
/note="LIMB8 repeat: matches 5654. .5773 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9300. 9420
/note="MERSB repeat: matches 1. .128 of consensus"
complement (916 ..10040)
/note="match: 6SS: Em:AQ369714"
10048. .10487
/note="LIME3 repeat: matches 5455. .5901 of consensus"
10509. .10820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6792. 6940
/hote="LTR37A repeat: matches 268. 420 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6941. 6978

Anote-"19 copies 2 mer ta 92% conserved"
6980. 7218

Anote-"LTR37A repeat: matches 47. 282 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 291. .600 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .320 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7440. .7486
/note="LTR37A repeat: matches 1. .47 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8540. .8922

/note="MSTA repeat: matches 1, .426 of consensus"

complement(8828. .9278)

/note="match: GSS: Em:AQ223257"

complement(8948. .9266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19.4; DB 9; Length 10959;
Pred. No. 3.7;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis CRAI gene for 12S seed storage protein. X14312 X14312.1 GI:16231
                                                                                                                                                                                                                                                                                                                                                                                                        2314. .2355
/note="21 copies 2 mer gg 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRA1 gene; seed storage protein; storage protein.
thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i repeat: matches 201.
2220 g 3301 t
                                                                                                                                                                                                                                                                                                                                                              complement(1. .87)
/note="match: STS: Em:HS227L5T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8948. .9266)
/note="match: GSS: Em:B53441"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2339. .2342 /note="unidirectional dGTP"
                                                                                                                                                                                                                           /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                     /chromosome="X"
/map="p11.23-11.4"
/clone="RP4-808F24"
/clone_lib="RPCI-4"
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7197 AAGGAGTGTCAGCTAGACCAG 7217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="LTR26 re
10847. 10958
/note="LTR26 re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.2%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 aacgagtgtcagctagaccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2058 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 88.2
Best Local Similarity 95.2
Matches 20; Conservative
                                                   pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                         Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCRA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct submission.

Submitted (24-0CT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes: clonerquest@sanger.ac.uk

On Aug 29, 2000 this sequence version replaced gi:9926454.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX RP4-808F24 is from the library RPCI-4 constructed at the Roswell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL139402 10959 bp DNA Human DNA sequence from clone RP4-808F24 on chromosome Xp11.23-11.4. Contains STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Length 3198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 22; DB E 100.0%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         916
                                                                                                                                                                                                                                                                                                                                                                                                                         б
                                                                                                                                                                                                                                                                                                                                                                                                                         900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 AACGAGTGTCAGCTAGACCAGC 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL139402
AL139402.11 GI:9944136
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 10959)
Clark, S.
Direct Submission
                                     1220. .1584
/gene="BnC1"
                                                                                                    1585. .2068
/gene="BnC1"
                                                                                                                                                                     2069. .2488
/gene="BnC1"
                                                                                                                                                                                                                                       2489. .2652
/gene="BnC1"
                                                                                                                                                                                                                                                                                                        2654. .>3057
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                     /number=4
3102. .3107
3176. .3181
                                                                                                                                                                                                                                                                                                                                                                                                                      2 069
                                                                                    number-2
                                                                                                                                                   'number=2
                                                                                                                                                                                                                       'number=3
                                                                                                                                                                                                                                                                                        'number-3
                  number-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eature key
                                                                                                                                                                                                                                                                                                                                                                            polyA_signal
BASE COUNT 992 a
ORIGIN
                                                                                                    intron
                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                       exon
                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT AL139402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
```

ð g ö

Gaps

; 0

```
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                    <196. .496
/note="12S storage protein CRAI"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Mol. Biol. 19 (6), 1049-1055 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cruciferin; cruciferin storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.8; DB
Pred. No. 7.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                     LETTLTHSSGPASYGRPRVAAA"
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 AACGAGTGCCAGCTCGACCAGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 3081)
                                                                                                                                                                                                                                                                                                                                                                                                                                       985. .1431
1432. .1546
                                                                                                                                                                                                                                                                                                                                                                                   623. .888
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                               /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breen, J.P.
Direct Submission
                                                                                                                                                                                                                                                                                                                    <196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92379259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
BNC2G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
               REFERENCE
                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
                                                                              FEATURES
                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M37247.1 GI:166675
12S storage protein.
A.thaliana, cDNA to mRNA.
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Core eudicots;
         Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 2346)
Pang, P.P., Pruitt, R.E. and Meyerowitz, E.M. Molecular cloning, genomic organization, expression and evolution of 12S seed storage protein genes of Arabidopsis thaliana Plant Mol. Biol. 11, 805-820 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                 .496,623. .888,985. .1431,1547. .1951)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.8; DB 8; Length 2346; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATHCRAIAA 2346 bp DNA PLN 27
A.thaliana 12S storage protein CRA1 gene, exons 1-4.
M37247
                                                                                                                                       /organism="Arabidopsis thaliana" /cultivar="Landsberg erecta" /db_xref="taxon:3702" /clone_lib="lambda EMBL4" | 138. .147 /note_laptara-box" | 196. .496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 7.8;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="alternative"
528 c 472 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 AACGAGTGCCAGCTCGACCAGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                 join(196. .496
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1432. .1546
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.5%;
90.9%;
 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1547. .1951
/number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     889. .984
/number=2
985. .1431
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             623. .888
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                      /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                               promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATHCRA1AA
LOCUS
                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                    JOURNAL
                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
```

```
/codol_start=1
//protein_id=1AAA3277.1"
/db.xref="d1:de"AAA32777.1"
/db.xref="d1:de"AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 2346)
Pang, P. P., Pruitt, R.E. and Meyerowitz, E.M.
Molecular cloning, genomic organization, expression and evolution
of 125 seed storage protein genes of Arabidopsis thallana
Plant Mol. Biol. 11, 805-820 (1988)

    (bases 1 to 3081)
    Breen, J.P. and Crouch, M.L.
    Molecular analysis of a cruciferin storage protein gene family of

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
join[196. 496,623. 888,985. 1431,1547. 1951)
/note="128 storage protein CRAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1432. .1546
/note="12S storage protein CRA1 intron C"
1547. .>1951
/note="12S storage protein CRA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497. .622
/note="12S storage protein CRA1 intron A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89. .984
'note="12S storage protein CRA1 intron B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BNC2G 3081 bp DNA PLN
B.napus BnC2 gene for cruciferin storage protein.
X59295
X59295.1 GI:17791
```

```
source
                             ORGANISM
                                                                                                                                                                                 TITLE
                                                                      REFERENCE
                                                                                  AUTHORS
                                                                                                                                                                        AUTHORS
                                                                                                                                                 MEDLINE
                                                                                                                                        JOURNAL
                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                       TITLE
                                                                                                                                                                                                                                        COMMENT
        SOURCE
                                                                                                                                                                                                                                         ö
                                                                                                          /clone="lambda Bnc2"
join(<665. .947,1320. .1701,1777. .2197,2381. .>2785)
gene="BnC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB005239 84544 bp DNA PLN 27-DEC-2000 Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MLN1. AB005239 BA000015 GI:2264311
                                                                                                                                                                      .2785)
Submitted (24-APR-1991) Breen J.P., Jordan Hall, Indiana University, Bloomington, IN 47401, USA
See also MIGBO & 52924 (for BDC1 gene).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                  join(665. .947,1320. .1701,177. .2197,2381.
/qene="BnC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                   /product="cruciferin storage protein"
/protein_id="CAA41985.1"
(db_xref="G1:762920"
/db_xref="SWISS-PROT:P33524"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                    /organism-"Brassica napus"
/db_xrefe-"taxon:3708"
/cell_line="EBS767"
/clone_lib="Ch4a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18.8; DB
Pred. No. 7.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=2
1777. 2197
/gene="BnC2"
                                                                                                                                                        'gene="BnC2"
                                                                                                                                                                                                                                                                                                                                                                                                 /number=1
1320. .1701
/gene="BnC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=2
1702. .1776
/gene="BnC2"
                                                                                                                                                                                                                                                                                                                                           <665. .947
/gene="BnC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2382. .>2785
/gene="BnC2"
                                                                                                                                                                                                                                                                                                                                                                           948. .1319
/gene="BnC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .2926
623 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2198. .2380
/gene="BnC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number-3
                                                                                                                                                                                                                                                                                                                                                                   /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyA_signal
BASE COUNT
ORIGIN
                                             Source
                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
AB005239/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
 JOURNAL
                                                                                                                       mRNA
                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                 CDS
                                FEATURES
                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
CORGANCE ACABLIGORS: Athliama (strain:Columbia) DNA, clone_lib:Hit:Hitsuip pl
ORGANISM
ATABLIGORS: Athliama
ATABLIGORS: Athliam
ATABLIGORS: A thliam
ATABLICATION
ATAB
```

CDS

CDS

```
join(41744. .41855,41947. .42360,42441. .42520,42621. .43001,43096. .43185,43267. .43341,43518. .43740,43847. .43947,4084. .44170,44251. .44403,44498. .44653,44728. .44937,45026. .45676,45764. .46294,46387. .46947,47129. .47233,
                                                                                                                                                          /colon-cont_experimental
/protein_id="BAB10982.1"
/db_xref="G1:979516"
/translation="MOSKSLAKSKRAHTLHHSKKSHSVHKPKVPGVSEKNPEKLQGNQ
rkSPVQSRRVSALPSNWDRYDDELDAAEDSSISLHSDVIVPKSKGADYLHLISEAQAE
                                                                                                                                                                                                                                                                                              SNSKIENNLDCLSSLDDLLHDEFSRVVGSMISSARGEGILSWMEDDNFVYEEDGSVKPG
FLSKLNVLAKTLENVDLLHDEFSTRVVGSMISSARGEGILSWMEDDNFVYEEDGSVKPG
FLSKLNVLAKTLENVDLHERLYIDPDLLPLPELNTSGTKVSRNEEPSHSHTAQNDPI
GKSSAFSTELDSLLKSHSSTROFNKFGNPSDQKIHMTGFNDVLDDLLESTPVSIIPQS
NQTSSKVLDPEDSWLDTI"
johi (31663. 31801, 32230. 33626, 33221. 34085)
//note="contains similarity to zinc finger protein IDI
gene_id:MLNI.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKFTDSPVIDLTVNGTKLSIQQDNGSMHVGTSVWPCSLILSKFA
/translation="MKFTDSPVIDLTVNGTKLSIQQDNGSMHVGTSVWPCSLILSKFA
ERWSTLDSSSSTTSNPYAELPDFRRRGIELGTGGCVAGMAFYLLGLTEIVLTDIAP
VWARLLIVARNGTALGKSLKTSIVYWNNRDQISALKPPFDLVIAADVVYIEESVGQL
VTAMBELLVADDGAVLLGYQIRSPEADKLFWELCDIVFKIEKVPHEHLHSDYAVEETDV
YIFRKKVKKNBAESVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei chromosome II clone RPC193-28H13, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 167645)
El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                               .22845,22924. .23036,23129. .23230,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC007864.4 GI:14787195
HTG; HTGS_PHASE2.
Trypanosoma brucei.
Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8; Length 84544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pir||T38261
similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/protein_id="BAB10984.1"
/db_xref="GI:9759518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.8;
Pred. No. 9.
                               complement(join(22369.
                                                            23307. .23673))
/note="gene_id:MLN1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 16719 AACGAGTGCCAGCTCGACCAGC 16698
                                                                                                                  unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC007864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
AC007864
                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/protein_id="BAB10980.1"
/db_xref="G1:9759514"
/db_xref="G1:9759514"
/translation="MATPELLILITAVELSTEITAQRAAPAPGPAGFINITAILEKG
GQFVTLIRLLNTTQIGNQINIQINSSSEGMTVLAPTDNAFQNIKPGTLNKLSPDDQVK
ILIXHVSKFYTLEDLLSVSNPVRTQASGRNVGGVYGLNFTGGGNQVNVSTGVVETRL
STSLRQBRPLAVYVVDMVLLPEEMFGERKISPMAPPPKSKSPDVSDDSESSKKAAAPS
ESEKSGSGEMNTGLGLGLIVVLCLKFL"
join (21063. ..21237,21296. ..21408,21497. ..21667,21741. .21953,
                                                                                                                                                                                                                                                                                                 GTKKQKYDRISEKKVSTPIEVLCKNQPSEFVSYFHYCRSLRFDDKPDYSYLKRĒFRDE
FIREGYQPDVYPDWYLKYPDIGSSGSSSRTRHHTTAKPGRNAPFIERQERILGKET
FIYKIPGAVEAFSRRHPTTSSPRDRSRSRNSDDGPFSKQTHGDSERANSSSRYRASS
SRKAVAASSSRPSSARGOFSESRTSSRLVSSGGGGGGGGGGGGRPSTSGRVQAGYESKTL
SFSRATAARNTREDQLRSFELLSLRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAEKNASAVDGAIRVSGWQFSYDVQDPIFFDFNLDLPAGSRCLL
VGANGSGKTTLLKILAGKHWVGGKNVVQVLDRSAFHDTELVCSGDLSYLGGSWSKTAG
SAGDIPLQGDFSAEHMIFGVEGIDPFRREKLIDLLDINLQWRMHKVSDGQRRRVQICM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="WarvSSLLSFCLTLILFHGYAAOQGQOGQQFPNECQLDQLNAL
EPSHVLKSEAGRIEVWDHHAPQLRCSGVSFARYIIESKGLYLPSFFNTAKLSFVAKGR
GLMGKVIPGCAETFQDSSEFQPRFEGQGGSQRFRDMHQKVEHIRSGDTIATTPGVAQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FYNDGGEPLVIVSVFDLASHONGLDRNPREATLAGNNROGGWALGGREQGPGKNIFNG
FGPRVIAGALKIDLGTAGQLGNGDDNRGNIVRYQGFFGVIRPPLRGGRPGEEEEEGR
FGRHGNGLEEFILCSARCTDNLDDPSRADVYKFOGLGYISTLNSYDLPILRFIRLSALRG
SIRQNAMAVLPQWNANANAILYYDGEAQIQIVNDNGNRYFDGGVSGGGLIAVPGGFSV
VKRATSNRFGWVEFKINANAQINTLAGRTSVLRGLPLEVITNGFQISPEEARRYKFNT
LETTLTHSSGPASYGRPRVAAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mnvkkvpnvpGSPALSALLkLGVIGGLGLyCIGSSMynvDGGHR
AIVFNRFYGIKDRYYPEGTHEKIPLEERALIYDVRSRPYVENSQTGSNDLQTYTIGLR
VLTRPMGDRLPEIYRTLGQUYGERVLDPSIINETLKAVVAQYNASHLITQREAVSREIR
KIVTERAARENIALDDYSTTNLKFGKEFTERIEKGOYAAQERERRAKTIVEKAEODKKS
AIIRAQGEAKSAQLIGQAIANNEAFITLRKIFAARELAQTIAKSANKVYLNSSDLLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLLHPFKVLLLDEVTVDLDVVARMDLLEFFKEECEQRCATIVYATHIFDGLETWÄSHL
AYINGGELKLSAKLDEIKDLKTSPNLLSVVEAWLRSETKVEKKTKKKPVVTSPPMSSR
                                                                                                                                                                                                                                             KTVLMLADQLLNRVEFMHTRGFLHRDIKPDNFLMGLGRKANQVYIIDFGLGKKKYRDLQ
THKHIPYRENKNLTGTARYASVNTHLGVEQSRRDDLESLGYVLMYFLKGSLPWGGLKA
                                                                                                                                                                                       /translation="MDLVIGGKFKLGKKIGSGSFGELYLGVNVQTGEEVAVKLENVKT
KHPQLHYESKLYMLLQGGSGIPNIKWFGVEGDYSVMVIDLLGPSLEDLFNYCNRKLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(12794 ...13054,13133 ...13219,13304 ...13440,
13520 ...13571,13656 ...13816,14094 ...14244))
/note="gb|AAD20643.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(15032. .15436,15552. .15998,16129. .16394,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains similarity to surface protein gene_id:MLN1.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="legumin-like protein"
/protein_id="BAB10979.1"
/db_xref="GI:9759513"
10646. .10686,10782. .10857))
/note="gene_id:MLN1.2"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/product="NBD-like protein"
/protein_id="BAB10978.1"
/db_xref="G1:9759512"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/product="prohibitin"
/protein_id="BAB10981.1"
/db_xref="G1:9759515"
                                                                                   /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
                                                                                                       /product="casein kinase I"
/protein_id="BAB10977.1"
/db_xref="G1:9759511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16518. .16818))
/note="gene_id:MLN1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="gene_1d:MLN1.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene_id:MLN1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .22201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19700. .20443
```

CDS

CDS

```
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAMPLING.
                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228
                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1:
AC039235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E 2 (bases 1 to 639)

S Eakin,N.Q., Morrison,H.G., McArthur,A.G., Nixon,J., Kim,U.,
Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
Direct Submission

Submitted (06-JUN-2000) Josephine Bay Paul Center for Comparative
Molecular Biology and Evolution, Marine Biological Laboratory, 7

NOTE: This record contains 1 individual

* Sequencing reads that have not been assembled into
* configs. Mans of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
                                                                                                                                                      SETS TO THE STATE OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Peterson, J., Hou, L., Zhao, H., Mason, T., Militscher, J., Pai, G., Van Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Melville, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Trypanosoma brucel GUTatio.1 RPC193-28H13 BAC genomic sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC070680 639 bp DNA HTG 06-JUN-2000 Glardia intestinalis clone EJ6926 strain WB-C6, LOW-PASS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia. (bases 1 to 639)
Morrison, H.G., McArth. A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.E. Glardia: a model for ancient eukaryotic genome analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.8; DB 2; Length 167645;
Pred. No. 9.5;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RPC193-28H13"
34626 c 40922 g 46529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /isolate="GUTat10.1"
/db_xref="taxon:5691"
/chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 151092 AACGAGTGTGAGCGAGACCAGC 151113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC070680
AC070680.1 GI:8276697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 85.5%;
1 Similarity 90.9%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE0.
Glardia intestinalis.
Glardia intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
AC070680/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                        JOURNAL
JOURNAL
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
```

à

```
E 2 (bases 1 to 957)

Eakin, N.Q., Morrison, H.G., McArthur, A.G., Nixon, J., Kim, U.,

Eakin, N.Q., Hinkle, G., Holder, M.E. and Sogin, M.L.

Direct Submission

L Submitted (10-ARR-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains 1 individual

* Sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* dentifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* vorces.
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC039235 957 bp DNA HTG 10-APR-2000 Glardia intestinalis clone EJ3094 strain WB-CG, LOW-PASS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Diplomonadida; Hexamitidae; Giardiinae; Giardia. 1 (bases 1 to 957)
Morrison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Cycoker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Giardia: a model for ancient eukaryotic genome analysis Unpublished
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                 Length 639;
the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 957;
22;
                                                                                                                                                                                                           others
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                           1 639: contig of 639 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 957: contig of 957 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                   1. 639
/organism="Giardia intestinalis"
/strain="WB-C6"
/db_xref="taxon:5741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 957
/organism="Giardia intestinalis"
                                                                                                                                                                                                                                                                                                 Score 18; DB 2;
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                           Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 18; DB
100.0%; Pred. No. 22;
ive 0; Mismatches
                                                                                                                                                                                                           155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:5741"
                                                                                                                                                                                                           147 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 g
                                                                                                                                                                                                                                                                           81.8%; Scc.
100.0%; Pre
0; }
                                                                                                                                                                                'clone="EJ6926"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="EJ3094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC039235
AC039235.1 GI:7531465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glardia intestinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                 359 GAGTGTCAGCTAGACCAG 342
                                                                                                                                                                                                                                                                                                                                                                                       4 gagtgtcagctagaccag 21
                                                                                                                                                                                                      165 c
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 gagtgtcagctagaccag 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
```

Search completed: February 25, 2002, 18:03:03 Job time: 18591 sec

THIS PAGE BLANK (USPTO)

```
hybrid seed; male-sterility gene;
barstar gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                    PCR primer for endogenous sequences in transgenic plants.
                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                   Transgenic plant; winter oilseed rape; fertility restorer gene; barnase gene;
                                                                                                                                                                                                                 AAX22769
AAF26304
AAV55840
AAQ31550
                                                                                                                                                                             AAQ31549
                    AAI39698
                                                                               AA158985
                                                                                                     AAF22283
                                                                                                                                                                                                          AAT91841
                                                                                                                                                                                            AAQ54681
                                                                                                                                                                AAX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0457037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Both G, De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-2000; 2000WO-EP12872.
22
                                                                                                                                                                                                                        1148
1548
1550
1550
                            AAH25457 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-381419/40.
WO200141558-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                     22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                      AAH25457;
AAH25457
RESULT
                              000000
                                                                                       00000000000
                                                                                                                                                                                                                                                                                                         PCR primer B03, to
Cruciferin A gene.
Enterococcus faeca
NLERK2 CDNA 3' reg
Pseudomonas aerugi
Pseudomonas aerugi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer for end
PCR primer B03, to
                                                         (without alignments)
26.322 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                 ; Search time 716.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqn/Na1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1990.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1990.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1992.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1994.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1994.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1994.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1994.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1994.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqn/Na1999.DAT:
                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
/SIDS2/gcgdatu/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdatu/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdatu/geneseq/geneseqn/NA1983.DAT:*
/SIDS2/gcgdatu/geneseq/geneseqn/NA1984.DAT:*
/SIDS2/gcgdatu/geneseq/geneseqn/NA1985.DAT:*
/SIDS2/gcgdatu/geneseq/geneseqn/NA1985.DAT:*
/SIDS2/gcgdatu/geneseq/geneseqn/NA1986.DAT:*
/SIDS2/gcgdatu/geneseq/geneseqn/NA1986.DAT:*
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                 930621 segs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                 February 25, 2002, 18:17:41
                                                                                             22
                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAO13870
AAX13213
AAT60974
AAF15388
AAO7552
AAH07552
AAH14119
AAH16554

    nucleic search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH25457
AAD07002
                                                                             US-09-698-903B-13
22
1 aacgagtgtcagctagaccagc
                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                                                                  N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3113
20633
1692
353
353
716
850
1790
1929
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1000.0
1000.0
1000.0
78.2
76.4
73.6
73.6
73.6
71.8
71.8
```

DB seq DB seq

Minimum Maximum Database

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Pseudomonas sp Typ Human IkappaB poly Encodes IkB NF-kap Human I-kappa-B-al

Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome

Example 5; Page 53; 98pp; English

cDNA clone (cDNA clone (cDNA sequenc

Human Human Human Human

22 22 22 17.2 16.8 16.2 115.8 115.8

Score

Result No.

Rat proteosome RIN Drosophila melanog Human inhibitory k Human SOCS14 CDNA

BAC containing rep BAC containing rep Human secreted exp DNA encoding a kap Mouse opioid recep DNA encoding a kap Mouse kappa-3 opio DNA encoding a kap Enterococus faeca Probe #2963 used MAD-3. Homo sapie Probe #10878 used

Arabidopsis thalia Arabidopsis thalia Human secreted pro Human polynucleoti Human polynucleoti Arabidopsis thalia

Aspergillus oryzae Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Probe #21465 used Probe #8384 used t Human secreted pro

Sequence

```
ö
                         The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene (e.g. barnase gene), and the other plant has an expression cassette comprising a fertility restorer gene (e.g. barstar gene), integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer B03, to recognise foreign DNA and flanking sequence of MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is PCR primer which is used to recognise foreign DNA and a flanking sequence of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to a transgenic Brassica plant or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 22; DB 22; Length 22; 100.0%; Pred. No. 0.043; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      transgenic plants of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS-B2 elite event; transgenic Brassi
male-sterility gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 33; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-2000; 2000WO-EP10680,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD07002 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-300517/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200131042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica napus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD07002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
*8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAMES OF COLOR OF PARTY PARTY
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The DNA is the genomic sequence of the seed storage protein gene cruciferin A (cruA). It can be used in the prodn. of transgenic plants expressing cruciferin in its seeds for use in an industrial process. The seeds conig. the cruciferin can be used without the need for first extracting and/or isolating the enzymes. The use of seeds for the storage of cruciferin provides a stable vehicle which is easily packaged and transported and easily handled during use.
                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Length 3113;
  Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Seeds contg. enhanced enzyme levels from transgenic plants for catalysing reactions, increasing nutritional values or treating digestive disorders.
                                                                                                                                                                                                                                                                                                                                                                                           Verwoerd
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3113 BP; 961 A; 685 C; 586 G; 881 T; 0 other;
 Score 22; DB 22;
Pred. No. 0.043;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         Van Ooyen AJJ, Rietveld K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 12
Pred. No. 0.09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX13213 standard; DNA; 20633 BP
                                                                                                                           BP
                       ô
                                                                                                                                                                                                                     ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
100.0%;
100.0%;
                                             1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Fig 3; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                           DNA; 3113
                                                         1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                            91EP-0200688
                                                                                                                                                                                                                     cruA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                                                 91EP-0200688
                                                                                                                                                                                                                                                                                                                                            90US-0498561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                  (KONN ) GIST-BROCADES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                  Seed storage protein;
                                                                                                                                                                                                                                                                                                                                                                                         Sijmons PC,
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-289815/40.
                                                                                                                          AAQ13870 standard;
                                                                                                                                                                                           Cruciferin A gene.
                                                                                                                                                                                                                                         Brassica napus.
                                                                                                                                                                                                                                                                                                            25-MAR-1991;
                                                                                                                                                                                                                                                                                                                                 25-MAR-1991;
                                                                                                                                                                                                                                                                                                                                            23-MAR-1990;
                                                                                                                                                                      09-DEC-1991
                                                                                                                                                                                                                                                                                    02-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1999
                                                                                                                                                                                                                                                              EP449376-A.
                                                                                                                                                AAQ13870;
                                                                                                                                                                                                                                                                                                                                                                                       Pen J, S
Quax WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX13213;
                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX13213/c
                                                                                                              AAQ13870
                                             οy
                                                                 g
                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXX
```

m

us-09-698-903b-13.rng

```
Smith TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200070086-A1
                                                                                                                                  (AMRA-) AMRAD
          WO9704091-A1
                                                      19-JUL-1996;
                                                                            05-FEB-1996;
                                                                                                             22-DEC-1995;
                                                                                        20-JUL-1995;
27-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-NOV-2000
                                06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barry TG,
                                                                                                                                                         Nicola NA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF15388;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF15388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                         982 nucleotide sequences isolated from the Enterococcus facealis genome.
AAX12938 to AAX13919 represent these nucleotide sequences which are
primary nucleotide sequences, also known as contigs. The computer-based
system can identify fragments of the Enterococcus facealis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus facealis in samples. They can also be used for
progression of disease, and for identifying agents which can be used
modulate the growth or pathogenicity of Enterococcus facealis, or
another related organism, in vivo or in vitro. In particular the
polypeptides encoded by the Enterococcus facealis nucleotide sequences
can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                   computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                    New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                               Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20633 BP; 5857 A; 4284 C; 3025 G; 7427 T; 40 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor protein tyrosine kinase; cell proliferation; cell differentiation; cell survival; nerve cell; ss.
          Enterococcus faecalis genome contig SEQ ID NO:276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17.2; DB 20;
Pred. No. 33;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LERK; ligand for eph-related kinase; ERK; NLERK2;
                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1284-1294; 2084pp; English.
                                                                                                                                                                                                                         Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 18911 AACGAGTATCATCTAAACCAGC 18890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT60974 standard; cDNA; 1692 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 aacgagtgtcagctagaccagc 22
                                                                                                                                                     97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                 98WO-US08985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLERK2 cDNA 3' region.
                                                                Enterococcus faecalis
                                                                                                                                                                                                                                             WPI; 1999-045171/04.
                                                                                                                                 04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                       14-NOV-1997;
                                                                                                                                                                            16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-1997
                                                                                                            12-NOV-1998
                                                                                                                                                                  06-MAY-1997
                                                                                                                                                                                                                                                                                                     Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT60974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detd. for a cDNA sequence (see also AAT60966) coding for NLERK2 (AAM10637), a novel human ligand for eph-related kinase (LERK). Th NLERK2 CDNA was obtd. from a human foetal brain cDNA library using probes (see also AAT60967-69) based on an expressed sequence tag previously isolated on the basis of homology to conserved regions
                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid mol. encoding ligand for eph-related kinase - useful for treatment of, pref. neuronal, cells to increase survival, proliferation and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The 3' region (AAT60974) and 5' region (AAT60975) sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ssrA gene; tmRNA; bacterium; chloroplast; diatom; detection; detection; identification; quantification; characterisation; nucleic acid array; DNA chip; drug design; treatment monitoring; contamination; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1692 BP; 316 A; 504 C; 385 G; 472 T; 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IRBI-) ENTERPRISE IRELAND T/A BIORESEARCH IRELA.
(UYNA-) UNIV NAT IRELAND GALWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa ssrA gene, SEQ ID NO:101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.4%; Score 16.8; 90.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of known LERKs (see also AAW10633-36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 43-45; 71pp; English
                                                                                                                                                                                                               OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1434 ACCACTGTCAGCTAGACCAG 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF15388 standard; DNA; 353 BP
                                                                                       95AU-0004263.
95AU-0006847.
95AU-0007299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 acgagtgtcagctagaccag 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2000; 2000WO-IE00066.
96WO-AU00460
                                                           96AU-0007890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                             WPI; 1997-132632/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 18; Conserv
```

ö

Found in all bacteria and is also round in chloroplasts and diatoms. It rescuing truncated minas which have lost stop codons. Sizh genes and rescuing truncated minas which have lost stop codons. Sizh genes and times a grant be used as target regions in nucleic acid probe assays for the detection, identification or quantification of a prokaryotic or eukaryotic organism. CDNA transcripts of tunkna molecules (corresponding to a region of high homology from the 5' end or the 3' end of the DNA molecule can be used as a universal target region in a nucleic acid probe assay, while a fraquent of the sizh gene or a mucleic acid probe assay, while a fraquent of the sizh gene or a nucleic acid probe assay, while a fraquent of the sizh gene or a nucleic acid probe assay, while a fraquent of the sizh gene or a nucleic acid probe assay, while a fraquent of the sizh gene or a nucleic acid probe assay, while a fraquent of the sizh gene or a sa a target region for the generation of genus specific probes. These regions in a safet region for the generation of genus specific probes. These regions corresponding to a region of low homology can be used as the basis for amplification primer design. The target regions may be used as the basis of an assay for distinguishing a prokaryotic or eukaryotic or euka The invention relates to the ssrA gene or tmRNA, an RNA transcript of the ssrA gene, or fragments thereof as target regions in a nucleic acid probe assay for the detection and identification of prokaryotic and/or eukaryotic organisms. The invention also relates to 38 novel ssrA sequences and their tmRNA transcripts (claimed), and to pan-bacterial, genus- and species-specific asrA gene/funRNA directed probes and PCR primers (claimed). tmRNA is a stable, high copy number RNA which is found in all bacteria and is also found in chloroplasts and diactoms. It for therapoutic purposes, and target regions may be used to monitor the efficacy of drug therapies against infectious agents. Target regions may also be used to monitor the viability and level of probiotic organisms in the gastrointestinal tract. The methods and nucleic acids and compositions of the invention have applications in medicine, and also in industry (e.g., for assessing bacterial contamination of a foodstuff or an environmental sample). Sequences AAFI5338-F15442 represent sera genes, or fragments thereof, from a wide variety of organisms. Use of sarA gene, tmRNA, or fragments of them, as target regions in probe assays for detection of prokaryotic or eukaryotic organisms, and for determination of species -Disclosure; Page 55; 221pp; English. WPI; 2001-025025/03.

Sequence 353 BP; 94 A; 94 C; 99 G; 66 T; 0 other;

Gaps ö Score 16.2; DB 22; Length 353; Pred. No. 57; 0; Mismatches 3; Indels 0 Query Match
Best Local Similarity 85.79
Matches 18; Conservative

ô

1 aacgagtgtcagctagaccag 21 ð

a

AAF15493 standard; RNA; 353 BP 09-MAR-2001 (first entry) AAF15493; AAF15493 RESULT EXPXPX

Pseudomonas aeruginosa tmRNA, SEQ ID NO:102.

ssrA gene; tmRNA; bacterium; chloroplast; diatom; detection;
detection; identification; quantification;
nucleic acid array; DNA chip; drug design; treatment monitoring; contamination; ss

Pseudomonas aeruginosa.

WO200070086-A1.

23-NOV-2000

15-MAY-2000; 2000WO-IE00066.

99WO-IE00043. 14-MAY-1999; (IRBI+) ENTERPRISE IRELAND T/A BIORESEARCH IRELA. (UYNA-) UNIV NAT IRELAND GALWAY.

Barry TG, Smith TJ;

WPI; 2001-025025/03.

Use of ssrA gene, tmRNA, or fragments of them, as target regions in probe assays for detection of prokaryotic or eukaryotic organisms, and for determination of species -

Disclosure; Page 55; 221pp; English.

The invention relates to the ssrA gene or tmRNA, an RNA transcript of the ssrA gene, or fragments thereof as target regions in a nucleic acid probe assay for the detection and identification of prokaryotic and/or eukaryotic organisms. The invention also relates to 38 novel ssrA sequences and their timeMa transcripts (claimed), and to pan-bacterial, csquences and their timeMa transcripts (claimed), and to pan-bacterial, genus - and species specific ssrA gene/tmRNA discreted probes and pcR primers (claimed). tmRNA is a stable, high copy number RNA which is confident in all bacteria and is also found in chloroplasts and distons. It has a dual function both as a tRNA and as an mRNA and is involved in rescuing truncated mRNAs which have lost stop codons. SsrA genes and transcripts of the sasays for the detection, identification, or quantification of assays for the detection, identification, or quantification of assays for the detection, identification, or quantification of assays for the detection or lower process. The sast and as a universal transcript or a region of high homology from the 5' end or the 3' end of the DNA molecule can be used as universal target region in corresponding to a region of 10w homology from the 5' end or the 3' end of the DNA molecule corresponding to a region of 10w homology and passay of the DNA molecule corresponding to a region of 10w homology and because or a target region to distinguish between species and as a target region of genus-specific probes. These regions may be used as the basis for amplification primer design. The crash of probe formmat for broad scale detection and/or identification of amultiple probe formmat for broad scale detection and identification of the broad scale high throughput detection and identification of the broad scale high throughput detection and identification of the broad scale high throughput detection and identification of an stable public organism and distinguish between strains of the sars gene or the tmRNA transcript can be used in a massay to ob efficacy of drug therapies against infectious agents. Target regions may also be used to monitor the viability and level of probiotic organisms in the gastrointestinal tract. The methods and nucleic acids and compositions of the invention have applications in medicine, and also in industry (e.g., for assessing bacterial contamination of a foodsfulf or an environmental sample). Sequences AAF15443-F15547 represent thrans, or fragments thereof, from a wide variety of organisms.

BP; 94 A; 94 C; 99 G; 66 U; 0 other; Sequence 353

us-09-698-903b-13.rng

```
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence of the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs and primers allow obtaining of the full-length cDNAs and primers allow obtaining of the full-length cDNAs and primers allow obtaining of the full-length cDNAs and PAH13613 to AAH13613 to AAH13613 to AAH13613 to represent human amino acid sequences; and AHH13612 to AAH13613 to represent contents allow which are used in the exemplification
                                               ö
                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto J;
                                               ö
         Length 353;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito K,
       Score 16.2; DB 22;
Pred. No. 57;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 2467; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                     Human cDNA clone (5'-primer) SEQ ID NO:2467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T, Nishikawa T,
                                                                                                                                                                                                                     BP
                                                                                                     21
         73.68;
71.48;
                                                                                                                                                                                                                   AAH05632 standard; cDNA; 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0248036
                                                                                 1 aacgagtgtcagctagaccag
                                                                                                                                                                                                                                                                                               (first entry)
Ouery Match 13.0.
Best Local Similarity 71.4:
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length cDNAs
                                                                                                                                                                                                                                                                                               26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2001
                                                                                                                                                                                                                                                       AAH05632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ota
                                                                                                                                                                                                 AAH05632
                                                                                                                                                                             RESULT
                                                                                 ò
                                                                                                                     셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAM103166 to AAM113628 and AAM13633 to AAM18742 represent human cDNA sequences; AAB92446 to AAM13693 represent human amino acid sequences; and AAM13629 to AAM13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length converges and the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 3' end sequence. Where the oligonucleotide comprises a 3' end sequence complementary to a polynucleotide comprises a 3' end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto
                                                                                                           ö
                                                                        Length 716;
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K,
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki
                 Sequence 716 BP; 165 A; 196 C; 217 G; 131 T; 7 other;
                                                                    Score 15.8; DB 22;
Pred. No. 1e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 4387; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA clone (5'-primer) SEQ ID NO:4387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi K,
                                                                                                             ö
                                                                                                                                                                                                                                                                              AAH07552 standard; cDNA; 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                        71.8%;
89.5%;
                                                                                                                                                                                    122 gagtggcagctggaccagc 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000EP-0116126
                                                 Query Match
Best Local Similarity 89.22,
The 17; Conservative
                                                                                                                                                 4 gagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2001.
                                                                                                                                                                                                                                                                                                                     AAH07552;
                                                                                                                                                                                                                                                             AAH07552
X os
                                                                                                                                                   δy
                                                                                                                                                                                    셤
```

us-09-698-903b-13.rng

```
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonuclectide complementary to comprise the complementary strand of a polynuclectide which comprises one of complementary strand of a polynuclectides; or (b) a combination of an oligonuclectide comprises a sequence complementary to the comprise and a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to the polynuclectide which comprises a 3'-end sequence complementary to a polynuclectide which comprises a 3'-end sequence of sequence of an oligonuclectide comprises a 3'-end sequence of the sequence of the comprises at least 15 nuclectides and the combination of the 5'-end sequence 15'-end sequence 16'-end sequence 1
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynuclectides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto J;
                                                                                                                                                                                        ö
                                                                                                                                           Length 850;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K, Ya
, Otsuki T;
                                                                    G; 160 T; 9 other;
                                                                                                                                    Score 15.8; DB 22;
Pred. No. 1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 11310; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA sequence SEQ ID NO:11310.
                                                                    Sequence 850 BP; 196 A; 227 C; 258
                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishikawa T,
1 T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                      AAH14119 standard; cDNA; 1790
                                                                                                                                       71.8%;
89.5%;
                                                                                                                                                                                                                                                        represent oligonucleotides,
                                                                                                                                                                                                                              4 gagtgtcagctagaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                          of the present invention.
                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogal T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH14119;
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shii S,
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                              AAH14119
                                                                                                                                                                                                                                                                                                                                                                                                         ន្តដូច្ន
                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                              à
```

```
The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonuclectide complementary
complementary strand of a polynuclectide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotide which comprises as the complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence. Where the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide comprises a 1-east 15 nucleotides and the combination of
the specification. The primer sets can be used in antisense therapy and
the specification. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95493 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto J;
                                                                                                                                                                            ö
                                                                                                                                             Length 1790;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi K, Saito K, Ya
A, Nagai K, Otsuki T;
                                                                                    Sequence 1790 BP; 398 A; 456 C; 504 G; 432 T; 0 other;
                                                                                                                                         Score 15.8; DB 22;
Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 15615; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequence SEQ ID NO:15615.
                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wakamatsu
                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa T,
                                                                                                                                                                                                                                                                                                                                  AAH16554 standard; cDNA; 1929
                                                                                                                                         71.8%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                            122 gagtggcagctggaccagc 140
                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001 (first entry)
                                                                                                                                                                          Conservative
                                                                                                                                                                                                             gagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                   AAH16554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishii S,
                                                                                                                                                                                                                                                                                                 1
                                                                                                                                                                                                                                                                                                                 AAH16554
 8x88888
                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                 δ
```

```
02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV69286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV69286/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                       ö
the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH054893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                         Human secreted protein-encoding gene 8 cDNA clone HSYA250, SEQ ID NO:49.
                                                                                                                                                                                                                                                                                          Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid athritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; anglogenic disorder; kidney disorder; endocrine disorder; infection; wound healing; vulnerary; gene therapy; cell culture; chemotaxis; food additive;
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encoding a human secreted protein is
                                                                                                                       ö
                                                                                                   Length 1929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Human secreted protein"
/note= "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Mature human secreted protein"
                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM;
                                                                      Sequence 1929 BP; 438 A; 489 C; 536 G; 466 T; 0 other;
                                                                                                  Score 15.8; DB 22;
Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               binding partner identification; ss
                                                                                                                                                                                                              AAD05091 standard; cDNA; 2096 BP.
                                                                                                  71.8%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                    01-NOV-2000; 2000WO-US30039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0164344.
2000US-0195296.
                                                                                                                                           4 gagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-2000; 2000US-0195296
27-JUL-2000; 2000US-0221367
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komatsoulis G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ç
                                                    the present invention.
                                                                                                            Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
5..838
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                .841
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-308780/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAE01202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200134768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                     17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen HS,
                                                                                                                                                                                                                                 AAD05091;
                                                                                                   Query Match
                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                 Ношо
                                                                                                                                                                                                  AAD05091
                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                        8888888888
                                                                                                                                                             q
                                                                                                                                           ò
```

```
AAEO1293-AABO1200 represent CDNARS COTRESPONDING TO 3 number secreted protein servered AAEO1218-AAEO1226 represent human secreted proteins they encode. AAEO1218-AAEO1226 represent human secreted proteins they encode. The secreted proteins and their genes are useful for preventing. The secreted protein in a sample or by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new protein in a sample or by determining the presence of mutations in the new protein in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, arking allergies, neurological disorders (e.g., alzhelmer's disease, atherosclerosis, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, astrointestinal disorders, prequency disorders, and infections. The proteins can also be used to aid wound canburn, to maintain organs before transplantation, for supporting contact ligands or binding partners, and in chemotaxis, and can be used to a sea food additive or preservative to modify storage properties.

Altibodies specific for a protein of the invention can be used in a sea food additive or preservative to modify storage properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liver activin; beta c; beta e; cell differentiation; haematopoiesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatopenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay; menstrual disorder; transgenic; modulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                      AAD05053-AAD05106 represent cDNAs corresponding to 15 human secreted
used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2096 BP; 476 A; 529 C; 584 G; 504 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.8; DB 22;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein-encoding cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= activin beta c" /note= "contains introns"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of mouse activin genetic loci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1147..2736
                                                                             Claim 1; Page 429; 474pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV69286 standard; DNA; 10708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.8%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tad=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
```

/note= "activin beta c exon 1"

```
This represents the sequence of mouse activin genetic loci. The invention relates to murine beta c and beta e polypeptides and the genes encoding them. Disorders of cell growth or differentiation (or susceptibility to them.) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene activity or by casemone secretion, neuronal survival, spermatogenesis of formation, hormone secretion, neuronal survival, spermatogenesis, bone formation, contains secretion or cardiac morphogenesis are some conditions that can be stimulated by treatment with an liver activin. Cell growth and differentiation can upregulates the compound's expression. Antagonists can be used to treat to liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or heamtopolesis, particularly erythropolesis, e.g. for treating chemophilia, cystic fibrosis or menstrual disorders. Antibodies which bind the mennoassays, to generate anti-idiotypic antibodies (which bind transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, modivisors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders
                              /number= 1
/note= "activin beta c partial intron (12-kb)"
                                                                                                                         /*tag= e
/note= "activin beta e promoter region"
                                                                                                                                                                                                                                                               'note= "activin beta e exon 1"
                                                                                                                                                                                                                                                                                                                            'note= "activin beta e intron"
1783..9533
                                                                                                                                                                                                                                                                                                                                                                                       /note- "activin beta e exon 2"
                                                                                                                                                                                    /product= "activin beta e"
/note= "contains introns"
8249..8546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4D-G; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US20882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0752919
                                                                                              /number= 2
2737..8248
                                                                                                                                                         8249..9536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-312408/27.
P-PSDB; AAW60617, AAW60618.
                                                              .2733
    1463..1994
                                                                                                                                                                                                                                                                               ..8782
                                                                                                                                                                                                                                                                                                               /number=
                                                                                                                                                                                                                                                  /number-
                                                                                                                                                                                                                                                                                                                                                                        /number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonadio J, Fang J;
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9822492-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1998
                                                                                                            promoter
   intron
                                                                                                                                                                                                                                                                             intron
                                                               exon
                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                         CDS
```

```
susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopolesis, erythroid differentiation, ovarian follicular maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and additions differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to compound may also induce bone growth (e.g. for treating osteoporosis or osteomatopolesis, particularly erythropolesis, e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which the liver activin containing liver activin activin also, the liver activin mans series and modified forms) proteins, madanistrators.
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #21465 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                               Length 10708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                           Sequence 10708 BP; 2651 A; 2844 C; 2607 G; 2546 T; 60 other;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                          71.8%; Score 15.8; DB 19;
89.5%; Pred. No. 1.5e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID No 21465; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1949 GAGTGTCTGCTCGACCAGC 1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-023659.
                                                                                                                                                                                                                                                                                                                                                                                                                     4 gagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI52779 standard; DNA; 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                   nodulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI52779;
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA152779
                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
    à
```

The present invention relates to single exon nucleic acid probes (SENP).

this cona encodes a murine liver activin beta c polypeptide. Sequences Berived from beta c cDNA clone is used for screening and cloning a liver ctivin beta e gene. Disorders of cell growth or differentiation (or

rhis cDNA

derived

```
ö
The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                          Probe #8384 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                   ö
                                                                                                          Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 578 BP; 145 A; 139 C; 145 G; 149 T; 0 other;
                                                                                                        22;
                                                                 Sequence 163 BP; 30 A; 44 C; 50 G; 39 T; 0 other;
                                                                                                       Score 15.6; DB 2
Pred. No. 1e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID No 8384; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
31-AUG-2000; 2000US-0633366.
21-SEP-2000; 2000US-0236369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                      Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                                                                                                                                                                                         AAI39698 standard; DNA; 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000GB-0024263
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000;
                                                                                                                                                                                                                                                                                                               17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                    AAI39698;
                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                           SSSSSXS
                                                                                                                                                                                     g
                                                                                                                                                             ò
```

ö

Gaps

;

Score 15.6; DB 22; Length 578; Pred. No. 1.2e+02; 0; Mismatches 4; Indels 0

Query Match
Best Local Similarity 81.8%;
Matches 18; Conservative

ò g

Search completed: February 25, 2002, 18:17:42 Job time: 16700 sec

Seguence

Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 134, App Sequence 114, App Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli

Sequence (Sequence] Sequence] Sequence]

OM nucleic

Run on:

Sequence:

Searched:

```
Sequence 20, Application US/08146422
Patent No. 5543576
GENERAL INFORMATION:
APPLICANT: VAN OOJJEN, ALBERT J. J.
APPLICANT: RIETVELD, KRIJN
APPLICANT: PEN, JAN
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
APPLICANT: VERWOERD, TEUNIS C.
APPLICANT: VERWOERD, PEDNIS C.
APPLICANT: VERWOERD, PENDIS J.
TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
TITLE OF INVENTION: ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 1;
Pred. No. 0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Nelson CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 02-NOV-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KENNEDY, BILL
REGISTRATION NUMBER: 33,407
REPERCNEKD/OCKET NUMBER: 44615-20011.23
REPERCNEKD/OCKET NUMBER: 44615-20011.23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
TELEX: 706141
TINFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 3113 base pairs
TYPE: nucleic acid
US-07-596-867C-10
US-08-445-463B-1
US-08-445-463B-1
US-09-060-756-634
US-09-060-756-634
US-09-060-756-422
US-09-060-756-422
US-09-060-756-422
US-08-611-757-50
US-08-611-757-50
US-08-611-757-50
US-08-611-757-50
US-08-11-8
US-09-195-868-11
US-09-195-868-11
US-08-678-01
US-09-418-540-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
100.0%;
    11506
11506
119506
119503
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
11970
1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
         ល់សស់សស់សស់សស់សស់សស់សំសំសំស
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-146-422-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-146-422-20
       00000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                           February 25, 2002, 18:05:52 ; Search time 301.6 Seconds
(without alignments)
16.520 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
Sednence
Sednence
Sednence
Sednence
Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/Packfiles1.seq:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/lna/5A_COMB.seq:*/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-349-627-2
US-08-46-337A-17
US-08-475-359-17
US-08-802-322-2
US-08-895-601-3
US-08-933-750C-73
US-09-234-613-73
US-08-920-857A-1
US-08-920-827-10
US-08-920-827-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-920-812-10
US-08-920-827-10
US-08-921-177-10
US-08-362-577C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-466-337A-16
US-08-475-359-16
US-08-465-887A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-920-828-10
US-08-247-901C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US94-03437-1
                                                                                                                                                                                                                                                                                                                                                                                                                          351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                          1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*
                                                                                                                                                                                                                                                       US-09-698-903B-13
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
```

Database :

٠ چ

00000000000000000000

g ð

```
Length 1330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Pasternak, Gavril W.

APPLICANT: Pasternak, Gavril W.

APPLICANT: Pan, Ying Xian

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING

TITLE OF INVENTION: RAPPA3 OPIOLD RECEPTORS, RECEPTORS

TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF

NUMBER OF SEQUENCES:

ADDRESSEE: Cooper & Dunham

STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                    COMPUTAT: UNITED STATES OI AMETICA
CUDWITKI: UNITED STATES OI AMETICA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: The PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUFFWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NAMBR: US/08/147,592A
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NAMBR: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/100,694
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATPORNEY/AGENT INFORMATION:
NAME: Wilson, MARK B.
REGISTRATION: WARK B.
NAME: Wilson, MARK B.
REGISTRATION NUMBER: 37,259
EPPERDENDANCE/ANDER: 37,259
EPPERDENDANCE/ANDER: NUMBER: 37,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                  TITLE OF INVENTION: Compositions and Methods NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.4;
Pred. No. 63
                                                                                                    ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas
                                                                                                                                                                                                                             United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARCD: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08147949A Patent No. 5747279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: ARTELECOMMUNICATION: TELECOMMUNICATION TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (512) 418-3000
(512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: N/A
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 AGTGTCAGCAAGACCAG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 agtgtcagctagaccag 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.0
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161..1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-147-949A-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-147-592A-5
                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
               Gaps
                                                                                                                                                                                                                                                Sequence 2, Application US/08626554
| Petent No. 5714474
| GENERAL INFORMATION:
| APPLICANT: VAN OOIJEN, ALBERT J.J.
| APPLICANT: RIETVELD, KRIJN
| APPLICANT: HOEKEMA, ANDREAS
| APPLICANT: HOEKEMA, ANDREAS
| APPLICANT: BIJMONS, PETER C. |
| APPLICANT: SIJMONS, PETER C. |
| APPLICANT: VERNORED, TEUNIS C. |
| TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
| TITLE OF INVENTION: USE
| NUMBER OF SEQUENCES: 3
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: MORRISON & FOERSTER |
| STREET: 2000 PENNSYLVANIR AVENUE NW GRAAFF. DO TENTER OF CONTY: NASHINGTON |
| CONTY: MASHINGTON |
| CONTY: 
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 22; DB 1; Length 3113;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 22; Conservative 0; Mismatches 0; Indels
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-147-592A-5/C
US-08-147-592A-5/C
Sequence 5, Application US/08147592A
FACTOR NO. 6096513
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I
APPLICANT: Relsine, Terry
APPLICANT: Yasuda, Kazuki
TITLE OF INVENTION: Opioid Receptor Genes,
         0; Mismatches
                                                                                              790 AACGAGTGTCAGCTAGACCAGC 811
                                                         1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    790 AACGAGIGICAGCIAGACCAGC 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-626-554-2
                                                                                                                                                                                                                                 JS-08-626-554-2
Matches
```

ö

Gaps

ð qq ö

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                              DB 2; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Haskill, John S.

APPLICANT: Haskill, John S.

APPLICANT: Baldwin Jr., Albert S.

APPLICANT: Baldwin Jr., Albert S.

TITLE OF INVENTION: Inhibitor of NF-kB Transcriptional

TITLE OF INVENTION: Activator and Uses Thereof

NUMBER OF SEQUENCES: 18

CORRESPONDENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Boru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower/ 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.1%; Score 15.2; DB 2;
85.0%; Pred. No. 71;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 0899.004.33514
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                            69.1%; Score 15.2;
85.0%; Pred. No. 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
10S-08-475-559-16/C
5 Sequence 16, Application US/08475359
Patent No. 5846714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 16:
                                                                        16:
                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-466-337A-16
                                                                                                                                                                                                                                                                                                                                                                                                 135 CTAGTGTCAGCTGGCCCAGC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-475-359-16
  TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEF: 25-3856
INPORMATION FOR SO ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                             3 cgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 cgagtgtcagctagaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 312/474-6300
312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.03
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: C
                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.0%; Score 15.4; DB 1; Length 2600; 94.1%; Pred. No. 66; 1; Indels 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower/ 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08466337A
Patent No. 5830756
GENERAL INFORMATION:
APPLICANT: Haskill, John S.
APPLICANT: Ralph, Peter
TITLE OF INVENTION: Inhibitor of NF-kB Transcriptional
TITLE OF INVENTION: Activator and Uses Thereof
NUMBER OF SQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/466,337A FILING DATE: 06-JUN-1995
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
CORNTER: TBM PC COMPATIBLE
CORNTER: TBM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,949A
FILING DATE: 05-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 44782/JPW/JKM
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 278-0400
TELEPAX: (212) 239-0555
TELECX: 42253 COOP UI
SEQUENCE CHARACTERISTICS:
LENGTH: 2600 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Pochopien, Donald J.
REGISTRATION UNMERS: 32,167
REFERENCE/DOCKET NUMBER: 0899,008/33518
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: United States
ZIP. 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600 AGTGTCAGCAAGACCAG 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 agtgtcagctagaccag 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.0
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 299..1
; OTHER INFORMATION
US-08-147-949A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: D
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 SCITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-466-337A-16/C
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

ö

a

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower/ 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/08466337A
Patent No. 5830756
GENERAL INFORMATION:
APPLICANT: Haskill, John S.
APPLICANT: Baldwin Jr., Albert S.
APPLICANT: Ralph, Peter
TITLE OF INVENTION: Inhibitor of NP-kB Transcriptional
TITLE OF INVENTION: Activator and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSER: Marshall, O'Toole, Gerstein, Murray & BADDRESSER: Masshall, O'Toole, Gerstein, Murray & B. STREET: 6300 Sears Tower/ 233 South Wacker Drive CITY: Chicago
STRATE: 1111nois
COUNTRY: United States
LID 60606-6402
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC COMPATIBLE
COMPUTER: PACHILIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,337A
FLING DATE: 06-JUN-1995
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAMME: POCLOPIEN. DORAIG J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 0899.008/33518
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.1%; Score 15.2; I Best Local Similarity 85.0%; Pred. No. 76; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PION APPLICATION:
PRIOR APPLICATION OF APPLICATION OF APPLICATION NUMBER:
PILING DATE:
ATTONREY/AGENT INFORMATION:
NAME: Peries, Rohan
REGISTRATION NUMBER: 35,572
REFERENCE/DOCKET NUMBER: 80002
TELEPHONE: 4115-855-5311
TELEPHONE: 414-855-532
                           ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 414-855-534
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERIZICS:
LENGTH: 819 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 cgagtgtcagctagaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO
US-09-349-627-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-466-337A-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                             RESULT 7
US-08-465-897A-16/C
US-08-465-897A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09349627
Petent No. 6194175
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Pello1,
TITLE OF INVENTION: Truncated Forms of Inhibitory Kappa B
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Bloscience
STREET 3401 Hillylew Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower/ 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: COLOGO SEALS TOWEY 433 SOUTH WACKET Drive CITY: Chloago STATE: Illinois COUNTRY: United States 2 IP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,887A FILING DATE: 06-JUN-1995
CLASSIFICATION: 455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.1%; Score 15.2; F
85.0%; Pred. No. 71;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0899.006/33516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATONNEY/AGENT INFORMATION:
NAME: POCHOPIEN, DOMAIG
REGISTRATION NUMBER: 32,167
REFERENCE/POCKET NUMBER: 0899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
135 CTAGTGTCAGCTGGCCCAGC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERA 3127,
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 base pairs
"YPE: nucleic acid
"YPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 cgagtgtcagctagaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.07
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-465-887A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-349-627-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: C.
```

õ g

ö

us-09-698-903b-13.rni

ö

Gaps

```
Sequence 2, Application US/08802322

Fatent No. 5932425

GENERAL INFORMATION:
APPLICANT: Alkalay, Irit
APPLICANT: Ben-Neriah, Yinon
APPLICANT: Manning, Anthony
APPLICANT: Manning, Anthony
APPLICANT: Marcon, Aracham
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: CELLULAR NF-(B ACTIVATION)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1550;
        Length 1550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Haskill, John S.
APPLICANT: Baldwin Jr., Albert S.
APPLICANT: RalDh, Peter
TITLE OF INVENTION: Inhibitor of NF-kB Transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUFTWARE: Patentin PC-DOS/MS-DOS
SUFTWARE: Patentin PC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NR/0^*
        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.2; DB
Pred. No. 80;
0; Mismatches
      69.1%; Score 15.2; D
85.0%; Pred. No. 80;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 860098.418 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/802,322 FILING DATE: 18-FEB-1997 CLESSIFICATION: 514 CLESSIFICATION: NAME: Maki, David J. REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/08465887A Patent No. 6001582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            917 CTAGTGTCAGCTGGCCCAGC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.1%;
85.0%;
                                                                                         3 cgagtgtcagctagaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 cgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1550 base pairs
TYPE: nucleic acid
                            Best_Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-802-322-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-465-887A-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98104
                                                                                                                                                                                           RESULT 11
US-08-802-322-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                           à
                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haskill, John S.
APPLICANT: Haskill, John S.
APPLICANT: Baldwin Jr., Albert S.
APPLICANT: Raldwin Jr., Albert S.
APPLICANT: Raldwin Jr., Albert S.
TITLE OF INVENTION: Inhibitor of NF-kB Transcriptional
TITLE OF INVENTION: Activator and Uses Thereof
NUMBER OF SEQUENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower/ 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Sarrs Tower/ 233 South Wacker Drive CITY: Chicago Sarrs Tower/ 233 South Wacker Drive STATE: 1111nois
COUNTRY: United States
2 IP: 6066-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE OFFRATIOS SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,359
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                     Ouery Match
69.1%; Score 15.2; DB 2;
Best Local Similarity 85.0%; Pred, No. 80;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/08475359 Patent No. 5846714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGIGSTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 0899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1550 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  917 CTAGTGTCAGCTGGCCCAGC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                          3 cgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: 95..1045
US-08-466-337A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
95..1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-08-475-359-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
US-08-475-359-17
                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
```

ö

```
Query Match

69.1%; Score 15.2; DB 3; Length 1550;
Best Local Similarity 85.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION
FILING DATE: 16-0...
CLASSIFICATION: 435
ATTORREY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-096.01
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-832-7000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1550 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-933-750C-73/C
i Sequence 73, Application US/08933750C
i Patent No. 5932442
i GENERAL INFORMATION:
i APPLICANT: Lal, Preeti
i APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/933,750C FILING DATE: September 23, 1997 CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         917 CTAGTGTCAGCTGGCCCAGC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 cgagtgtcagctagaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                               95..1045
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 95..
US-08-895-601-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-895-601-3/c
; Sequence 3, Application US/08895601
; Sequence 3, Application US/08895601
; Patent No. 6060262
; GENERAL INFORMATION:
APPLICANT: Beer-Romero, Peggy
APPLICANT: Glass, Susan J.
APPLICANT: Rolfe, Mark
; TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION,
TITLE OF INVENTION: AND METHODS AND REAGENTS RELATED THERETO
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 1550;
                     NUMBER OF SEQUENCES: 18

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower/ 233 South Wacker Drive STATE: 111inois
COUNTY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                  COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Bateniin Release #1.0, Version #1.30
SOFTWARE: Pateniin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/465,887A
FILING DATE: 06-JUN-1995
CLESSIFICATION NUMBER: US/08/465,887A
FILING DATE: 06-JUN-1995
ATTORNEY/AGENI INFORMATION:
NAME: POCHOPIEN, DORAIG J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 31,2474-6300
TELEPAN: 312/474-6300
TELEPAN: 312/474-6300
TELEPAN: 312/474-6300
TELEPAN: 312/474-6300
TELEPAN: 312/474-6300
TELEPAN: 11570-886 ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  TITLE OF INVENTION: Activator and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.1%; Score 15.2; D
85.0%; Pred. No. 80;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      917 CTAGTGTCAGCTGGCCCAGC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 cgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.03
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 95..1045
US-08-465-887A-17
```

g δ

ö

Gaps

ö

```
δ
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                          Query Match 66.4%; Score 14.6; DB 2; Length 2028; Best Local Similarity 81.0%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.

TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGNET INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-234-613-73/c
; Sequence 73, Application US/09234613
; Patent No. 6132973
                                                                                                                                                                                                                                                                                                                                                                                                        Db 1486 ATCCAGTGTCAGCAACACCAG 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 2028 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSNOTO5
CLONE: 1568361
                                                                                                                                                                                                                                                                                                                                                                                  1 aacgagtgtcagctagaccag 21
TELEX:
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 2028 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDUW TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
TELEX:
                                                                                                                                      TOPOLOGY: linear
| IMMEDIATE SOURCE:
| LIBRARY: UTRSNOTOS
| CLONE: 1568361
US-08-933-750C-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                  ò
```

ő

```
Michigan State University DNA Sequencing Facility Arabidopsis Biological Resource Center, The Ohio State University, 309 Botany & Zoology Bidg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 614202931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                             M9G6STM A
M6ZC12STM
M24D11STM
M56F1STM
M27C1STM
M36E1STM
M16F1STM
M15G11STM
M15G11STM
M15G11STM
M15G11STM
M15G11STM
M15G11STM
M15G11STM
M21B1STM
                                                                                                                                                                                                                                                                                                                                                                M8H2STM A
M9B4STM A
M15C12TTM
M20G5STM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 152)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new sexion of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                          M49C4STM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         M29E3STM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M33C7STM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M40A1STM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BES20593 152 bp mRNA EST 19-MAR-2001 M13F7STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M13F7 5', mRNA sequence.
BES20593 GI:9778571
                  BES 25454
BES 2543
BES 2543
BES 25432
BES 25432
BES 25432
BES 25432
BES 25432
BES 25432
BES 25403
BES 25403
BES 25403
BES 20017
BES 25401
BES 26401

    152
    /organism="Arabidopsis thaliana"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                   BE523398
BE524178
BE520917
BE520827
BE522480
                                                                                                                                                                                                                                                                                                                                                                                                                   BE521646
BE524379
BE522847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE523644
BE524918
BE520427
BE520918
BE520556
BE522759
                                                                                                                                                                                                                                                                                                                                                                BE525377
BE525401
BE520824
                                                                                                                                                                                                                                                                                                                              BE521713
BE523183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: benning@msu.edu
 Tel: 517 355 1609
Fax: 517 353 9334
 thale cress.

    30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30     30  
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20567808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
BE520593
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
 M43F11STM
M47A2STM
M40E7STM
M47G12STM
M43A1STM
M14H9STM
M62M3STM
M62M3STM
M62M3STM
                                                                                                                                            (without alignments)
28.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE520593 M13F7STM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           Search time 8261.74 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE523925
BE524190
BE525380
BE523695
BE52365
BE523306
BE520764
BE525569
BE525569
BE525503
                                                                                                                                                                                                                                                                                                                                                                22703874
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                          11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                           February 25, 2002, 17:21:20
                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE524190
BE524190
BE52580
BE523695
BE523695
BE523875
BE522306
BE522569
BE525569
BE525569
                                                                                       nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE520593
                                                                                                                                                                                                                                     1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_gss_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est1:*
gb_est2:*
gb_htc:*
gb_gss:*
em_gss_fun:*
                                                                                                                                                                                                   US-09-698-903B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
                                                                                                                                                                                                                                                                                                                                                                                                  DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_gss_inv:*
em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_gss_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_estfun:*
em_esthum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_estin:*
em_estom:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_estro:*
em_estov:*
em_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_estpl:*
em_estba:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match

    CO    C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Notal number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118.8
118.8
118.8
118.8
118.8
118.8
118.8
                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                         nucleic
                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                  Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum
                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
```

```
1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
                                                                                                                      RESULT
BE524190
                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
BE525280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                             g
                                á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 174)

White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning.

A new set of Arabidopsis expressed sequence tags from Geveloping seeds. The metabolic pathway from carbohydrates to seed oil

L Plant Physiol. 124 (4), 1582-1594 (2000)

Contact: Benning, C

Millian Contact: Molecular Biology
                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 517 355 1609

Fax: 517 353 934

Bmail: benningemsu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bidg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
/strain="Columbia"
/db_xref="taxon:3702"
/clone="Mu3F7"
/clone=lub=xrabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/note="0rgan: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"
a 47 c 42 g 34 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.col1"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: Ecor; Site_2: XhoII"
a 52 c 40 g 46 t
                                                                                                                                                                                                                                                                                                                                                                                                                                               BE523925 174 bp mRNA EST 19-MAR-2001 M43F11STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M43F11 5', mRNA sequence.
BE523925 GI:9781903
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                          85.5%; Score 18.8; DB 10; Length 152; 90.9%; Pred. No. 75; 1ve 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.8; DB 10; Length 174; Pred. No. 78; 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
/clone="M43F11"
/clone_llb="Arabidopsis developing seed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Arabidopsis thaliana"/strain-"Columbia"
                                                                                                                                                                                                                                                                                                                   1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                        57 AACGAGTGCCAGCTCGACCAGC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                                                                                                                                                           Local Similarity 90.9
mes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
                                                                                                                                                                     ø
                                                                                                                                                                     29
                                                                                                                                                                                                                                          Query Match
Best Local S:
Matches 20
                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                tches
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
BE523925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                   g
```

```
rel: 517 355 1609
Fax: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Natl Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
ES
Location/Qualifiers
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="M47A2"
/clone="M47A2"
                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

| (bases 1 to 182)
| White,J.a., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduya.O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil
| Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Benning, C
Dept. of Blochemistry & Molecular Biology
Michigan State University
224 Blochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoII" 58 c 49 g 42 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M61A10STM Arabidopsis developing seed Arabidopsis thallana cDNA BE525280 GI:9783258
                                                                                                                                HE524190 182 bp mRNA EST 19-MAR-2001
M47A2SIM Arabidopsis developing seed Arabidopsis thaliana cDNA
Clone M47A2 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib-"Arabidopsis developing seed"
/tissue_type-"seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.8; DB
Pred. No. 79;
0; Mismatches
                         104 AACGAGTGCCAGCTCGACCAGC 125
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE524190.1 GI:9782168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 85.5
Best Local Similarity 90.9
Matches 20; Conservative
```

m

```
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 517 355 1609
Fax: 517 353 9334
      Fax: 517 353 9334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE524251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE524251
                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dp
                                                                                                                                                                                                                                                                                                                                                       Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                         224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 212)
White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant physiol. 124 (4), 1382-1594 (2000)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissuc_type="seed"
/dev.stage="5-13 days after flowering"
/dev.stage="5-13 days after flowering"
/lab_host="E.coli"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"
58 c 54 g 50 t
                                                            1 (bases 1 to 206)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE523695 212 bp mRNA EST 19-MAR-2001
M40E75TM Arabidopsis developing seed Arabidopsis thaliana cDNA
clone M40E7 5', mRNA sequence.
BE523695
BE523695.1 GI:9781673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Arabidopsis developing seed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.8; DB 10;
Pred. No. 82;
0; Mismatches 2;
                                                                                                                                                                                                            Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dept. of Biochemistry & Molecular Biology Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3702"
/clone="M61A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AACGAGTGCCAGCTCGACCAGC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Benning, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 85.5'
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                              Tel: 517 355 1609
Fax: 517 353 9334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 517 355 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .206
                                                                                                                                                                                        20567808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                      MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
BE523695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
```

```
Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
Email: bening@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Nell Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 223)
White, J. A., Toddy, J. Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new set of Arabidopsis expressed sequence tags from developing Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                        /clone_lib-"Arabidopsis developing seed"
/tissuc_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host-"E.coli"
/note-"Organ: Developing seed; Vector: pBluescript SK-;
Site_l: EcoRi; Site_2: XhoII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE524251 223 bp nRNA EST 19-MAR-2001
M47G12STM Arabidopsis developing seed Arabidopsis thaliana cDNA
clone M47G12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                    1. 212
/organisme"Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="M40E7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .223
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.8; I
Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Columbia"
/db_xref="taxon:3702"
/clone="M47G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AACGAGTGCCAGCTCGACCAGC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE524251.1 GI:9782229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
```

ð g

```
·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                          BE522306.1 GI:9780284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE520764.1 GI:9778742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.5
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 517 355 1609
Fax: 517 353 9334
                                                                                                                             thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                        ACCESSION
                                                                                                          KEYWORDS
SOURCE
                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
BE520764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
            BE523306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                              TITLE
                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Blological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana Eukaryota; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 25)

White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Hhite, J.A., Todd, J., Ohlrogge, J. and Benning, C. Ilardya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
/note="Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoII"  
69 c 57 g 60 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoII" Site_1 52 g 56 t 1 others
                                                                                                                                                                                                                                                                                       BE523875 225 bp mRNA EST 19-MAR-2001 M43ALSTM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M43A1 5', mRNA sequence.
BE523875 GI:9781853
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                        Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 225;
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Arabidopsis developing seed"
/fissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E_col1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                        5
                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.8; DB 10;
Pred. No. 84;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
                                                                                                    Score 18.8; DE
Pred. No. 84;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain-"Columbia"
/db_xref-"taxon:3702"
/clone="M43A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                       99 AACGAGTGCCAGCTCGACCAGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 AACGAGTGCCAGCTCGACCAGC 139
                                                                                                                                                                    1 macgagtgtcagctagaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 aacgagtgtcagctagaccagc 22
                                                                                                   85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.5%;
90.9%;
                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 90.9 Matches 20; Conservative
                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            thale cress.
                                   43
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                   BE523875
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                               BASE COUNT
ORIGIN
                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
```

ð qq

```
Arabidopsis thallana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatorbyta; Magnollophyta; eudicotytedons; core eudicots;
Spermatorbyta; Magnollophyta; eudicotytedons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 231)
White, J.A., Todd, J.V., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant physiol. 124 (4), 1582-1594 (2000)

E 20567808
Contact: Benning, C.
Dept. of Biochemistry & Molecular Biology
Michigan State University
Total Blochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bening@mau.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Nell Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thale cress.

Arabidopsis thaliana

Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 232)

White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.

A new set of Arabidopsis expressed sequence tags from developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoII"
72 c 57 g 57 t
BE522306 231 bp mRNA EST 19-MAR-2001 M25A1STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M25A15', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE520764 232 bp mRNA EST 19-MAR-2001 MA449STM Arabidopsis developing seed Arabidopsis thaliana cDNA BE520764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .231. / corganism="Arabidopsis thaliana" |
/organism="Arabidopsis thaliana" |
/strain="Columbia" |
/db xref="taxon:3702" |
/clone="M25A1" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.8; DE
Pred. No. 85;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
```

Gaps

```
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

( (bases 1 to 238)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de
Illarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: benning@msu.edu
Clones were originally prepared at Michigan State University.
Arabidopsis Biological Resource Center, The Ohio State University,
309 Botany & Zoology Blig., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 TEL: 6142929371.
                                                       /strain-"Columbia"
/db_xref="taxon:3702"
/db_xref="taxon:3702"
/clone="600014455R1"
/clone=lib="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.col1"
/note="Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoR1; Site_2: XhoII"
a 72 c 56 g 63 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoII" 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE525596 238 bp mRNA EST 19-MAR-2001
M62C23STM Arabidopsis developing seed Arabidopsis thaliana cDNA
clone 600014490Rl 5', mRNA sequence.
BE525596
                                                                                                                                                                                                                                                                                                                                                      Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                    Score 18.8;
Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.5%; Score 18.8;

    .232
    /organism="Arabidopsis

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="600014490R1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE525596.1 GI:9783497
                                                                                                                                                                                                                                                                                                                                                    85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rel: 517 355 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 517 353 9334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thale cress.
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20567808
                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
BE525596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                           Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Benning, C
Dept. of Blochemistry & Molecular Biology
Michigan State University
224 Blochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viriliplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; eurosidas II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 232)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones were originally prepared at Michigan State University.

Arabidopsis Biological Resource Center, The Ohio State University,
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 61429220603 TEL: 614292371.

Location/Qualifiers
                                                                                                                                                                                                                                                          Michigan State University DNA Sequencing Facility Arabidopsis Biological Resource Center, The Ohio State University, 309 Botany 2001ogy Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoII"
73 c 57 g 58 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE525569 232 bp mRNA EST 19-MAR-2001
M62M13STM Arabidopsis developing seed Arabidopsis thaliana cDNA
clone 600014458R1 5', mRNA sequence.
BE525569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
20567808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Arabidopsis developing seed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
;;
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.8; DB
Pred. No. 85;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref-"taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 AACGAGTGCCAGCTCGACCAGC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: benning@msu.edu
                                                                                                                                                                                                                                        Email: benning@msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="M14H9'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE525569.1 GI:9783470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 517 355 1609
Fax: 517 353 9334
                                                                                                                                                                                            517 355 1609
                                                                                                                                                                                                                 Fax: 517 353 9334
                                                                                                                                                                                                                                                                                                                                                                    1. .232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20567808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44
                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                              ľel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                    JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE525569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

9

Matches

g ð

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

MEDLINE COMMENT

JOURNAL

TITLE

DEFINITION

BE523203

```
Contact: Benning, C
Dept. of Blochemistry & Molecular Biology
Michigan State University
224 Blochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                       Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Sosidae; eurosidas II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 243)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Phat Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bening@msu.edu
Lones were originally prepared at Michigan State University.
Arabidopsis Biological Resource Center, The Ohio State University,
309 Boctany & Zoology Blidg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 TEL: 6142929371.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 244).
White J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE525454 244 bp mRNA EST 19-MAR-2001 M62G03STM Arabidopsis developing seed Arabidopsis thallana cDNA clone 600014412R1 5', mRNA sequence. BE5245454 GI:9783432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .243
/organism="Arabidopsis thaliana"
/organism="Arabidopsis thaliana"
/stran="columbia"
/db.xref="taxon.3702"
/clone="600014450R1"
/clone="600014450R1"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Developing seed;
Site_1: EcoRI; Site_2: XhoII"
69 c 65 g 59 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.8; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.5%;
90.9%;
                                      Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AACGAGTGCCAGCTCGACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 517 355 1609
Fax: 517 353 9334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
These 20; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thale cress
                                                                                                                                                                                                                                                                       20567808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20567808
                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                REFERENCE
                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                       MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE525454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bening@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Soology Bidg., 1735 Nail Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371
                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dept. of Blochemistry & Molecular Biology
Michigan State University
224 Blochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana Eukaryota, Embryophyta; Eracheophyta; Braryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Varidiplantae; Streptophyta; Eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 239)
White, J.A., Todd.J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.

Anew Set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib-"Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="seed"
/dev_stage="seed"
/lab_host="E.coli"
/nab_host="E.coli"
/note="Coran: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRi; Site_2: XhoII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M62Ci3STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone 600014450R1 5', mRNA sequence. BES25564
BES25564.1 GI:9783465
                                                                                                                                                                                                                                     BE523203 239 bp mRNA EST 19-MAR-2001 M35C7STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M35C7 5', mRNA sequence.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 239;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
       ed. No. 85;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18.8;
Pred. No. 85;
       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Columbia"
/db_xref="taxon:3702"
/clone="M35C7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                             ö
                                                                      laacgagtgtcagctagaccagc 22
                                                                                                                 24 AACGAGTGCCAGCTCGACCAGC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AACGAGTGCCAGCTCGACCAGC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                    BE523203.1 GI:9781277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 aacgagtgtcagctagaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benning, C
                        20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517 355 1609
517 353 9334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
                                                                                                                                                                                                                                                                                                                                                                            thale cress.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20567808
Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
```

BASE COUNT ORIGIN

FEATURES

RESULT 13

ð g BE525564

DEFINITION

ACCESSION VERSION KEYWORDS

ö

Gaps

```
Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Email: benning@msu.edu
Clones were originally prepared at Michigan State University.
Arabidopsis Biological Resource Center, The Ohio State University,
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 614920603 TEL: 6142929371.

1. 244

//cration/Qualifiers
1. 244
//craniam="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; thaliana Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Core eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicacea; Arabidopsis. (Dases 1 to 244)
White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Clones were originally prepared at Michigan State University.
Arabidopsis Blological Resource Center, The Ohio State University,
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: Developing seed; Vector: pBluescript SR-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M62K03STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone 600014414R1 5', mRNA sequence.
BES25533
BES25533.1 GI:9783434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="columbia"
/db_xref="taxon 3702"
/clone="60014414R1"
/clone_lib="Arabidopsis developing seed"
/tissue_type="seed"
                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
/clone="600014412R1"
/clone=11b="Arabidopsis developing seed"
/tlssue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.col1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.8; DB 10;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .244
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                         Site_1: EcoRI; Site_2: XhoII"
74 c 66 g 57 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                       /strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 aacgagtgtcagctagaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 AACGAGTGCCAGCTCGACCAGC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
BE525533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
ö
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRi; Site_2: XhoII"
14 c 60 g 67 t
                                                                                                                                       Gaps
                                                                                                                                       ö
                                                                                                             Length 244;
                                                                                                                                       Indels
                                                                                                            DB 10;
                                                                                                                                     ,;
;
                                                                                                         Score 18.8; Di
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                Search completed: February 25, 2002, 17:21:21 Job time: 16174 sec
                                                                                                                                                                                          91 AACGAGTGCCAGCTCGACCAGC 112
                                                                                                                                       ö
                                                                                                                                                                1 aacgagtgtcagctagaccagc 22
                                                                                                            85.5%;
90.9%;
                                                                                                                                       Conservative
                                                                                                            Query Match
Best Local Similarity
                                                        43
                                                        BASE COUNT
ORIGIN
                                                                                                                                     Matches
                                                                                                                                                                  δ
                                                                                                                                                                                          qq
```

	Ltd
4.5	Compugen
version	- 2000
GenCore	(c) 1993
	opyright

: GenEmbl:*

1: 9b_ba:*
2: 9b_htg:*
3: 9b_ln:*
4: 9b_om:*
5: 9b_pat:*
7: 9b_ph:*
8: 9b_pt:*
10: 9b_pt:*
11: 9b_pt:*
11: 9b_pt:*
12: 9b_pt:*
13: 9b_pt:*
13: 9b_pt:*
13: 9b_pt:*
13: 9b_pt:*
14: 9b_pt:*
15: em_pat:*
16: em_pat:*
17: em_ph:*
18: em_ph:*
18: em_pt:*
19: em_pt:*
21: em_pat:*
22: em_pat:*
23: em_pat:*
24: em_pt:*
25: em_pat:*
25: em_pat:*
26: em_sts:*
27: em_pat:*
28: em_pt:*
29: em_vi:*
31: em_htgo_rod:*
31: em_htgo_rod:*
33: em_htgo_rod:*
34: em_htgo_rod:*
35: em_htgo_rod:*
36: em_htgo_rod:*
37: em_htgo_rod:*
38: em_htgo_rod:*
38: em_htgo_rod:*
38: em_htgo_rod:*
38: em_htgo_rod:*
38: em_htgo_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AX127761 Sequence AX172482 Sequence 124540 Sequence 20	1835/3 Sequence 2 X14555 Brassica na	X59294 B.napus BnC AC021599 Homo sapi	AC092613 Homo sapi AC005047 Homo sapi	AF142615 Equus cab	AF190914 Escherich	156101 Sequence 9	X05952 Shigella so	N24352 S.dysenteri	AF081284 Escherich U81136 Shigella fl	U82621 Shigella fl	AF177050 Shigella	AE007213 SINGENIZO AE005271 Escherich	AF139396 Snigella AE005307 Escherich	AF051097 Balanoglo	AF335540 Shigella	AF141323 Shigella AF153317 Shiqella	AJ278144 Escherich	AF200692 Shigella AC020099 Drosophil	AF074613 Escherich	AB011549 Escherich	AX191725 Sequence AC093096 Drosophil	AL391753 Shigella	AL391/33 SNIGELIA AC019337 Homo sapi	AF348706 Shigella AF348706 Shigella		15-MAY-2001 producing same
																											PAT 3s for
qi	AX127761 AX172482 124540	1836/3 BNCRUA	BNC1G AC021599	AC092613 AC005047	AF142615 T56095	AF190914	156101	SSIS600	SFU9/492 SHFSHTA	AF081284 SFU81136	SFU82621 SDY271153		AE00713 AE005271	AF139596 AE005307	AF051097 AF335540	AF335540	AF153317	ECO278144	AF200692 AC020099	AF074613	AB011549	AX191725 AC093096	SFPWR100	SFPWK100 AC019337	AF348706 AF348706	ALIGNMENTS	Patent W00131042. 1134408 cct. ict. ict. ict. ict. ict. ive. iv
DB	9999		(7)																								22 bp om Paten; :1413440; truct. truct. truct. dence. 22) de Beuck 1042-A 1; ience N.; ion/Qual. 0:sm="syi
Length 1	22 22 3113	3113	4	151210 154016	287	646	1188	1264	1433 3294	3715 3719	5430	7150	10040	11058	15708	20962	32094	37710	51334 77283	92077	92721				221851 221851		from GI:14 GI:14 Onstru onstru to 22 to 22 to 23 to 23 to 22 to 23 to 24 to 23 to 24 to 24
Query Match	100.0																								78.2		AX127761 Sequence 14 AX127761 AX1277761 AX127761 AX127761 AX127761 AX127761 AX127761 AX127761 AX1277761 AX1277761 AX1277761 AX1277761 AX1277761 AX1277761 AX1277761 AX1277761 AX12777761 AX12777777 AX127777 AX127
core	222	22	22 17.4															•							17.2 17.2		٥
Result No. So	- 12 E	ດ ດ 4 ເບ	9 /					16		o 0	7 7	23	25	٥,	28	. 0 .	32 32	۳,	3 3 5	9 2	. 00 1	o 0	41	n r	44		RESULT 1 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TILLE JOURNAL FEATURES SOURCE

10-AUG-1998

BASE COUNT ORIGIN

DEFINITION

RESULT AX172482

õ g ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS JOURNAL

FEATURES

REFERENCE

BASE COUNT ORIGIN

```
Ryan,A.J.
Direct Submission
Submitted (02-MAR-1989) Ryan A.J., Department of Biological
Sciences, University of Durham, South Road, Durham, DHI 3LE, United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica napus Brassica napus Brassica napus Brassica napus Brassica Spermatophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3113)
Ryan, A.J., Royal, C.L., Hutchinson, J. and Shaw, C.H.
Genomic sequence of a 12S seed storage protein from oilseed rape (Brassica napus c.v. jet neuf)
Nucleic Acids Res. 17 (9), 3584 (1989)
                                                                                                                                                                                                                                                                                                                                                                       Tobases 1 to 3113)
Van Ooijen, A.J.J., Rietveld, K., Hoekema, A., Pen, J.,
Sijmons, P.Christian, Verwoerd, T.Cornelis and Quax, W. Johannes.
Production of enzymes in seeds and their use
Patent: US 5714474-A 2 03-FEB-1998;
Location, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Length 3113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .313

/organism="Brassica napus"

/strain="Jet Nouf"

/db_xref="taxon:3708"

/tissue_type="leaf"

644. .650

600. .3010

/note="primary transcript"

join(709. .991,1220. .1581,2049. .2870)

/codon_strain="retrial forms of the product of the pr
                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica napus cruA gene for cruciferin.
X14555
X14555 GI:17810
CruA gene; cruciferin; seed storage protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 22; DB 6; Best Local Similarity 100.0%; Pred. No. 0.27; Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų
                                                                                                                                                        I83673 3113 bp DNA
Sequence 2 from patent US 5714474.
I83673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
. 684 c 586 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
             1183 CGCAGTTCTGTGAACATCGACC 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 1183 GGCAGTTCTGTGAACATCGACC 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 egcagttetgtgaacategaee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3113 bp
                                                                                                                                                                                                                                                I83673.1 GI:3407203
                                                                                                                                                                                                                                                                                                                                 Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               961 a
                                                                                                                                                                                                                                                                                                     Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BNCRUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                              RESULT (
183673/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BNCRUA/c
                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 3113)
van Ooijen,A.J.J., Rletveld,K., Hoekema,A., Pen,J., Sijmons,P.C.,
varwoerd,T.C. and Quax,W.J.
Production of enzymes in seeds and their use
Patent: US 5543576-A. 20 06 AUG-1996;
Location/Qualifiers
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct.
synthetic construct
synthetic construct
artificial sequence.
1 (bases 1 to 22)
de Both, G. and de Beuckeleer, M.
Hybrid winter oilseed rape and methods for producing same Patent: WO 041558-A 43 14-JUN-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

Query Match

100.0%; Score 22; DB 6; Length 3113;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                           Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 6; Length 22; 
Pred. No. 0.17; 
; Mismatches 0; Indels
                                                                                                      ; Score 22; DB 6; Length 22; Pred. No. 0.17; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/db_xref="texon:32630"
/note="primer BNA06"
7 c 5 9 5 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ų
  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124540 3113 bp DNA
Sequence 20 from patent US 5543576.
124540 GI:1604410
                                                                                                                                                                                                                                                                                                                                                                                           AX172482 22 bp DNA
Sequence 43 from Patent WO0141558.
AX172482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 22;
Best Local Similarity 100.0%; Pred. No. (
Matches 22; Conservative 0; Mismatche
     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
1 685 c 586 g
  S
                                                                                                                                                                                                            1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                1 CGCAGTTCTGTGAACATCGACC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX172482.1 GI:14597594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 cgcagttctgtgaacatcgacc 22
  Ö
                                                                                                Query Match
Best Local Similarity 100.(
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified.
ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
```

DEFINITION ACCESSION VERSION

RESULT 124540/c LOCUS

ð 셤 ORGANISM

KEYWORDS

REFERENCE AUTHORS

source

FEATURES

TITLE JOURNAL

BASE COUNT

ORIGIN

à

ö

Gaps

ö

Indels

m

```
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           GFRDMHQKVEHIRTGDTIATHCGVAQMFYNDGNQPLVIVSVLDLASHONDLDRPRPFYLAGNNPPGGGOWTEGREGQPQKNILLNGFTPEVLAKAFKIDVRTAQQLQNQQDNRGNIT
YQGPFSVIRPPLRSQRPGFTEVNGLEETICSAFCTDNLDDFSNADVYKPQLGYISTL
NSYDLPILRFLLSALRGSIRQNAMVLPQWNANAVLYYTDGEAHVQVVNDNGBNVF
DGQVSQGQLLSIPQGFSVVKRATSEQFRWIEFKTNANAQINTLAGRTSVLRGLPLEVI
SNGYQISLEBARRVKFNIIETTLIHSSGPASYGGPRKADA"
                   /db_xref="SWISS-PROT:P33523"
/translation="WARLSSLLSFSLALLIFLHGSTAQOFPNECQLDQLNALEPSHVL
KAEAGRIEVWDHHAPQLRCSGVSFVRYIIESKGLXLPSFFSTAKLSFVAKGEGLMGRV
                                                                                            VPGCAETFODSSVFQPSGGSPSGEGQGQGQGQGQGGGGGGGQGQGQGQGQGQGQGQSQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens clone RP11-189E18, WORKING DRAFT SEQUENCE, 29 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Length 3198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2000 (Rel. 62, Created)
21-SEP-2000 (Rel. 65, Last updated, Version 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 8;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-143830
Birren B., Linton L., Nusbaum C., Lander E.;
"Homo sapiens, clone RP11-189E18";
Onpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; HTG; 143830 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                       /number=1
992. .1219
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                       /number=1
1220. .1584
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2069. .2488
/gene="BnC1"
/number=3
                                                                                                                                                                                                                                                           <709. .991
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_DRAFT; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /number=2
1585 .2068
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2489. .2652
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2654. .>3057
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /number=4
3102. .3107
3176. .3181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o 069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyA_signal
polyA_signal
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC021599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC021599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pieces.
                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
AC021599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELL REPAREMENT OF THE REPAREM
                                                                                     /db_xref="SWISS-PROT:P11090"
/translation="MARLSSLLSFSLALLTFLHGSTAQQFPNECQLDQLNALEPSHVL
KAEAGRIEVWDHHAPQLRCSGVSFVRYIIESKGLYLPSFFSTARLSFVAKGEGLMGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosidas II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 3198)
Breen,J.P. and Crouch,M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="lambda Bnc1"
join(<709. .991,1220. .1584,2069. .2488,2653. .>3057)
/gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(709. .991,1220. .1584,2069. .2488,2653. .3057)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (24-APR-1991) Breen J.P., Jordan Hall, Indiana
University, Bloomington, IN 47401, USA
See also M16860 & X59295 (for BnC2 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Length 3113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BNC1G 3198 bp DNA PLN
B.napus BnC1 gene for cruciferin storage protein.
X59284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="cruciferin storage protein"
/protein_id="CAA41984.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Mol. Biol. 19 (6), 1049-1055 (1992) 92379259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 8;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cruciferin; cruciferin storage protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Brassica napus"
/strain="c.v Tower"
/db_xref="taxon:3708"
/cell_line="ED8767"
/clone_lib="CH4a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              881
                                                                                                                                                                                                                                                                                         1582 . . 2048
/note="intron II"
2915 . . 2920
/note="polya signal"
2989 . . 2994
/note="polya signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .3198
db_xref="GI:17811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="BnC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 3198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.(
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X59294.1 GI:17790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breen, J.P
                                                                                                                                                                                                                                                                                                                                                                                                                                           961
                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rape.
                                                                                                                                                                                                                                                                                                     intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
BNC1G/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
```

a õ

```
11895: gap of
14229: cont
                              Center code: WIBR
                                                         preserved.
                                                            931
2471
2571
                                                                 4444
5566
5666
                                                                        11796
                                                           831
```

```
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101824
116519
116619
                                                                                                                                                                                                                                                                                                                           52254
52354
57552
57652
64109
64209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
RA Birren B., Linton L., Nusbaum C., Lander E., Abraham H., Allen N.,
RA Adderson S., Baldwin J., Barna N., Beckerly R., Beda F., Boguslavkiy L.,
Boukhgalter B., Brown A., Burkett G., Castle A., Choepel Y., Colangelo M.,
RA Collins S., Collymore A., Cooke P., DeArcellano K., Dowino M.,
RA Doyle M., Fenestor J., Ferreira P., FitzHugh W., Forrest C., Gage D.,
RA Howland J., Gardyna S., Grant G., Hagos B., Headrond A., Horton L.,
RA Howland J.C., Johnson R., Jones C., Kann L., Karatas A., Klein J.,
RA Mandand P., Marquis N., McEwan P., McGurk A., McKernan K., McPheeters R.,
RA Macdonald P., Marquis N., McEwan P., McGurk A., McKernan K., McPheeters R.,
RA Moldrim J., Meneus L., Morrow J., Naylor J., Norman C.H., O'Connor T.,
RA Rymond C., Riley R., Rothman D., Roy A., Santos R., Severy P., Spencer B.,
Raymond C., Riley R., Rothman D., Roy A., Santos R., Severy P., Spencer B.,
Raymond C., Riley R., Rothman D., Roy A., Santos R., Severy P., Spencer B.,
Raymond C., Riley R., Rothman D., Roy A., Santos R., Yo A., Wu X., Wyman D.,
RA Ye W.J., Zimmer A., Zody M.;
                                                                                                                                                                                                                                                                                                              Submitted (16-JAN-2000) to the EMBL/GenBank/DDBJ databases.
Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                 On Sep 20, 2000 this sequence version replaced gi:9152655. All repeats were identified using RepeatMasker:
Smit, A.F.A. 6 Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: This was seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project neme: L5793
Center clone name: L89_E_18
Center clone name: 189_E_18
Sequencing vector: M13, M78815; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Consensus quality: 137518 bases at least Q30
Consensus quality: 137518 bases at least Q30
Insert size: 150000; agarose-fp
Insert size: 150000; agarose-fp
Insert size: 141030; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830: contig of 830 bp in length
930: gap of 100 bp
2570: gap of 1540 bp in length
2570: gap of 100 bp
4343: contig of 1773 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14229: contig of 2334 bp in length
14329: gap of 100 bp
16423: contig of 2094 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16523: gap of 100 bp 19064: contig of 2541 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14230
14330
16424
16524
```

```
note="assembly_fragment clone_end:SP6 vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116618: gap of 100 bp 129081: contig of 12463 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9181: gap of 100 bp
143830: contig of 14649 bp in length
                             21384: gap of 100 bp
23749: contig of 2365 bp in length
23849: gap of 100 bp
27606: contig of 3757 bp in length
                                                                                                                                                                                                                                                         47908: gap of 100 bp 52233: contig of 4345 bp in length 52353: gap of 100 bp 57551: contig of 5198 bp in length 57651: gap of 100 bp 64108: contig of 6457 bp in length 64108: contig of 6457 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ap of 100 bp contig of 14695 bp in length
                                                                                                                                                                                             501: gap of 100 bp 44277: contig of 4676 bp in length 377: gap of 100 bp 47808: contig of 3431 bp in length
                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95030: gap of 100 bp 101723: contig of 6693 bp in length
                                                                                                                                                  in length
                                                                                                                                                                                 in length
                                                                                                                                                                                                                                                                                                                                                             08: gap of 100 bp 71334: contig of 7126 bp in length
                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp contig of 7977 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11: gap of 100 bp 94930; contig of 8219 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444. .5565
/note-"assembly_fragment"
5666. 7543
/note-"assembly_fragment"
7644. .9898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
21385. 23749
/note="assembly_fragment"
23850. 27666
/note="assembly_fragment"
27707. 31136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7644. .9898
/note="assembly_fragment"
999. .11795
/note="assembly_fragment"
11896. .14229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2571. 4343
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14330. .16423
/note="assembly_fragment"
1654. .19064
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
14330. .16423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"/clone="RP11-189E18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       931. .2470
/note="assembly_fragment
                                                                                                                                                  ф
                                                                                                                                                              55: gap of 100 bp 39501: contig of 4046 bp
                                                                                                                                                                                                                                                                                                                                                                                                                          p of 100 bp contig of 7100 bp
                                                                                                100 bp
3430 b
                                                                                                                                35355; contig of 4119 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .143830
/db_xref~"taxon:9606"
64: gap of 100 bp 21284: contig of 2120 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                           06; gap of 1
31136: contig of
                                                                                                                                                                                  cont. ...: gap of 44277:
                                                                                                                                                                                                                                                                                                                                                                               con.
gap of
79411:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101823: gap of
116518: cont
                                                                                                                                                                                                                                                                                                                                                                                                                          511: gap of
86611: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129082 129181:
129182 14383(
                                                                                                                             31236:
                                                                                                                                                                                                                                                                                                                                                             64208:
                                                                                                                                                            35455:
                                                                                                                                                                                                                                                                                                                                                                                           71434:
                                                                                              27706:
                                                                                                                                                                                              39601:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         86711
                                                                                                                                                                                                                               44377
                                                                                                                                                                                                                                                                                                                                                                                                                            79511
```

us-09-698-903b-14.rge

```
Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC005047 154016 bp DNA PRI 07-OCT-2000
Homo sapiens BAC clone CTB-14E15 from 7q22-q32, complete sequence.
AC005047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 154016)
Sulston, J. E. and 154016
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Courtney, L., Gillam, B., Stoneking, T., Elliott, G. and Langston, Y. The sequence of Homo sapiens BAC clone CTB-14E15
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of I contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.1%; Score 17.4; DB 2; Length 151210; 94.7%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
              Sequencing vector: plasmid; 37%
Sequencing vector: plasmid; 37%
Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-terminator Big Dye; 63% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149642 bases at least Q40
Consensus quality: 149695 bases at least Q30
Consensus quality: 151204 bases at least Q20
Insert size: 143000; agarose-fp
Insert size: 151210; sum-of-contigs
Quality coverage: 8.04 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                     1 151210: contig of 151210 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector_side:right"
a 28928 c 30068 g 47041 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .151210
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="7"
/clone="RP11-189E18"
      Sequencing vector: M13; 26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 17340 GCAGTTCTGTGAACATAGA 17322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC005047.3 GI:10716665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 154016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  % (bases 1 to 154016)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (bases 1 to 154016)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 gcagttctgtgaacatcga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .151210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99063792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AC005047
                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
MO 03109, 199, 2001 this sequence version renland minimaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG. HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jul 19, 2001 this sequence version replaced gi:10198499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 143830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .----- Summary Statistics -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H_NH0189E18
Drafting center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.4; DB 33;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- Genome Center --
                                                                                                               /note="assembly_fragment"
44378. 47808
/note="assembly_fragment"
47909. .52253
/note="assembly_fragment"
52354. .57551
/note="assembly_fragment"
57652. .64108
                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
79512. 86611
/note="assembly_fragment"
86712. 94930
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                               64209. .71334
/note="assembly_fragment"
71435. .79411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
101824. .116518
/note="assembly_fragment"
116619. .129081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of Homo sapiens clone Unpublished
/note="assembly_fragment"
31237, .35355
                      /note="assembly_fragment"
35456. .39501
                                                                 /note="assembly_fragment"
39602. .44277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
129182. .143830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 83635 GCAGTTCTGTGAACATAGA 83653
                                                                                                                                                                                                                                                                                                                                                                                                                                                            95031. .101723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 151210)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.18;
94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 gcagttctgtgaacatcga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                      misc_feature
                                                           misc_feature
                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                  misc_feature
                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
AC092613/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
```

ò

COMMENT

/rpt_family-"MBR99" 6319. .6516 /rpt_family-"CR1" 8583. .8761 /rpt_family-"Alu" 7rpt_family-"Alu" 9218. .9514

/rpt_family="MaLR" 4849. .5153

/rpt_family="Alu"

'rpt_family="Alu"

/rpt_family="L1" 5740. .6039

9238 .9514 /rpt_family="Alu" 10478 .1077

Ly="ERVL"

.11523

/rpt_famil

/db_xref="Gī:6120582" 12056. .12181 /rpt_family="MalR" 12256. .12482

mily-"MIR" 12625

/rpt_famil 12500. 19

```
/rpt_family="ERV1"
21148. 21458
/rpt_family="Alu"
21459. .21613
                                                                                   repeat_region
                                     repeat_region
                                                                                                                                    repeat_region
                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STS
Direct Submission
Submitted (07-OCT-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 7, 2000 this sequence version replaced gi:7631121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of this clone was established as part of a mapping and sequencing collaboration between the NEGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE INFORMATION:
Clone CTB-14E15 is from the first release of the human BAC library
CLIDB-9788K-B. The library ochtains cloned DNA from the male
fibroblast cell line 9788K. See: Shizuya et al., Proc. Mari.
Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8
(1996). This clone is available from Research Genetics, Inc.
                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (1.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repetts; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Due to low quality, the fidelity of the sequence from 130932 to 130982 can not be guaranteed.
Location/Qualifiers
1. .154016
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is GSI-34D21, 200 base pair overlap. Actual start of this clone is at base position 1 of CTB-14E15; actual end is at base position 7330 of GSI-34D21.
                                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC WUGSC WILL CONTENT WORL STATE: Attp://genome.wustl.edu/gsc Contact: Saplens@watson.wustl.edu Center project name: H_RG014E15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="7q22-q32"
/clone="CTB-14E15"
/clone_lib="CITB-978SK-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     903. .2491
/rpt_family="ERV1"
2495. 2700
/rpt_family="L1"
2720. .2838
/rpt_family="Alu"
2839. .3289
/rpt_family="L1"
3411. 3476
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selection: chloramphenicol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'rpt_family-"L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.resgen.com).
VECTOR: pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
        TITLE
JOURNAL
```

/rpt_family="L1" 14509, 14900 /rpt_family="MaLR" 14901, 15114

rpt_family="ERV1" 14352. .14508

/rpt_family="CR1" 12717. .12750 /rpt_family="CR1" 12817. .12901

18305. 18622 100.xref="G1:485206" 18833. 19179 /rpt_family="MER2_type" 19215. 19509

rpt_family="Alu" 9983. .20033

'rpt_family="L2" :0109. .20370

/rpt_family="L2" 20708. .20760 /rpt_family="MalR" 20933. .21089

/rpt_family="Malk" ?1094.

'rpt_family="MER103" 8305, 18622

/rpt_family="L2" 18099. .18221

FEATURES

/rpt_family="ERVK" 17710. .17806 /rpt_family="ERV1" 17850. .17908

/rpt_family="L1" 16147. 16636 /rpt_family="ERV1" 16640. 17690

.17690

'rpt_family="ERV1" 5626. .16096

rpt_family="L1" 5152. .15625

```
ö
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           To compare the state of the sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 646)
Schlock.S., Radl.S., Blass,J. and Reidl.J.
Genetic rearrangements of the regions adjacent to genes encoding
heat-labile enterotoxins (eltAB) of enterotoxigenic Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF190914 646 bp DNA BCT 16-JAN-20
Escherichia coli strain K2 eltB gene, 3' flanking sequence.
AF190914
                                                                                                ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 587;
                                                    Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclusified.
Unclusistied.
1 (bases 1 to 587)
Parcdos K. and McCarty, J.
Nucleic acid probes for the detection of shigella Patent: US 5648481-A 3 15-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appl. Environ. Microbiol. 66 (1), 352-358 (2000)
20087561
                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.2; DB 6;
Pred. No. 1.1e+02;
0; Mismatches 3;
                                                 Score 17.2; DB 4;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .646
/organism="Escherichia coli"
/plasmid="Ent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                          156095 587 bp DNA
Sequence 3 from patent US 5648481.
156095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="K2"
/db_xref="taxon:562"
<1. .>646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
149 c 139 g
                                                                                                                                          566 CGCAGTACTGTGAACCTCGATC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
Plasmid Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF190914.1 GI:6694242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1. .>646
/gene="eltB"
                                                                                                                                                                                                                                                                                                                                                                                      I56095.1 GI:2476889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia,
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10618247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
AF190914
                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                  RESULT 11
156095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
PUBMED
                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

1 (bases 1 to 287)

Tallmadge R.L., Hopman, T.J., Schug, M.D., Aquadro, C.F.,
Bowling, A.T., Murray, J.D., Caetano, A.R. and Antczak, D.F.
Aquine dinucleotide repeat loci COR061-COR080
20078362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 287)
Tallmadge,R.L., Hopman,T.J., Schug,M.D., Aquadro,C.F.,
Bowling,A.T., Murray,J.D., Caetano,A.R. and Antczak,D.F.
Direct Submission
Submitted (13-APR-1999) Cornell University, J.A. Baker Institute,
Hungerford Hill Rd., Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 79.1%; Score 17.4; DB 9; Length 154016; Best Local Similarity 94.7%; Pred. No. 1.5e+02; Matches 18; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF142615 287 bp DNA MAM
Equus caballus microsatellite COR078 sequence.
AF142615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="microsatellite COR078"
/rpt_type=tandem
/rpt_unit=gt 102 g 92 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 287
/organism="Equus caballus"
/db_xref="taxon:9796"
/chromosome="2"
                                                                21985. .22223
/rpt_family" ERV1"
22241. .22647
/rpt_family-"Alu"
22613. .22860
/rpt_family-"MaLR"
22919. .23389
                                                                                                                                                                                                                                 /rpt_family="ERV1"
23390. 23579
23680. 23805
2456_family="ERV1"
2456_family="ERV1"
24451. 24460
/rpt_family="MR"
24491. 24642
/rpt_family="MalR"
25010. 25099
/rpt_family="MalR"
25230. 25647
/rpt_family="ERV1"
21626. .21980
/rpt_family="MaLR"
21985. .22223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MaLR" 25939. .26236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
28723. .29014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF142615.1 GI:6318588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10612238
                           repeat_region
                                                                       repeat_region
                                                                                                                    repeat_region
                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF142615/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
```

```
RESULT 15
156099
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                               ORGANISM
                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                             δ'n
                                                                                                                                                                                                                                                                                                                                  g
                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                          07-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-0CT-1997
                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

Query Match

96.4%; Score 17.2; DB 6; Length 1174;

Best Local Similarity 86.4%; Pred. No. 1.2e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0
                                                          Score 17.2; DB 1; Length 646;
Pred. No. 1.2e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1188;
               others
                                                                                                                                                                                                                                                                                                                                                                20 others
                                                                                                                                                                                                                                                                              1 (bases 1 to 1174)
Parodos, K. and McCarty, J.
Nucleic acid probes for the detection of shigella
Patent: US 5648481-A 5 15-JUL-1997;
Location, Qualifiers
1. .1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.2%; Score 17.2; DB 6; Length 1
86.4%; Pred. No. 1.2e+02;
Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1188)
Parodos, K. and McCarty, J.
Nucleic acid probes for the detection of shigella
Patent: US 5640481-A 9 15-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                          PAŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT
/note="3' flanking sequence"
134 c 149 g 175 t
                                                                                                                                                                                                                                                                                                                                                                330 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 t
                                                                                                                                                                                     156097 1174 bp DNA
Sequence 5 from patent US 5648481.
156097 1 GI:2476891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156101 1188 bp DNA
Sequence 9 from patent US 5648481.
156101
156101.1 GI:2476895
                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
296 c 276 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
                                                                                                    Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1188
                                                                                                                                                                                                                                                                    Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 19; Conserv
             182 a
                                                                                                                                                                                                                                                                                                                                                              252 a
                                                                                                                                                                                                                                             Unknown.
                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156101
                                                                                                                                                                                  LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
            BASE COUNT
ORIGIN
                                                                                                                                                              RESULT 13
156097
                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                              JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
I56101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
ö
       07-0CT-1997
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                           Length 1196;
                                                                                         Unknown.
Unclassified.
1 (bases 1 to 1196)
Parodos,K. and McCarty,J.
Nucleic acid probes for the detection of shigella Patent: US 5648481.A 7 15-JUL-1997;
                                                                                                                                                                                                                                   others
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                    Query Match 78.2%; Score 17.2; DB 6; Best Local Similarity 86.4%; Pred. No. 1.2e+02; Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                ų
                                                                                                                                                                                                                                353
156099 1196 bp DNA
Sequence 7 from patent US 5648481.
156099
                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 25, 2002, 18:03:11 Job time: 18599 sec
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                          /organism="unknown"
1 298 c 272 g
                                                                                                                                                                                                                                                                                                                                                 I56099.1 GI:2476893
                                                                                                                                                                                                                             259 a
                                                                         Unknown,
```

THIS PAGE BLANK (USPTO)

5.8 71.8 319608 21 AAH51601 Human chr. 5.8 71.8 319608 22 AAS09301 Human sch. 5.6 70.9 545 20 AAX24719 Tobacco 1.5.6 70.9 769 18 AAX30779 Streptoco 5.6 70.9 769 19 AAT98688 DNA encod 5.6 70.9 2108 22 AAF56464 Neisseria	15.6 70.9 2109 22 AAF56463 15.6 70.9 2111 22 AAF56458 15.6 70.9 2112 21 AAA75745 15.6 70.9 2112 21 AAZ54329 15.6 70.9 2112 21 AAZ564329	15.6 70.9 2112 22 15.6 70.9 2112 22 15.6 70.9 2112 22 15.6 70.9 2112 22 15.6 70.9 2112 22	15.6 70.9 2112 22 AAF56467 15.6 70.9 2582 7 AAN60610 15.6 70.9 2585 8 AAN70629	30 12:0 /0.9 830; 21 AAA814893 31 15:6 70:9 21185 21 AAA63350 32 15:6 70:9 63164 21 AAA63348	33 15.6 70.9 349980 21 AAF21544 Neisseria menir 34 15.6 70.9 349980 21 AAF21607 Neisseria menir 35 15.6 70.9 1437668 21 AAA81490 N. meningitidi 36 15.7 0.9 1437668 21 AAA81490 N. meningitidi	15.4 70.0 140 21 15.4 70.0 256 21 15.4 70.0 429 22 15.4 70.0 429 22	40 15.4 70.0 42.9 22 AAF5340 42 15.4 70.0 947 22 AAF5595 43 15.4 70.0 947 22 AAF5595 44 15.4 70.0 1131 22 AAF55405 45 15.4 70.0 1131 22 AAF55596 ABIGNMENTS	SUL H25	(C AAH25458; X T 05-SEP-2001 (first entry)		S Synthetic. N W0200141558-A1.	. 0	A 08-DEC-1999; 99US-0457037.	A (AVET) AVENTIS CROPSCIENCE NV. X I De Both G, De Beuckeleer M;	X R WPI; 2001-381419/40. X	T Transgenic winter oilseed rape plants suited for producing hybrid seed T with improved qualities, comprises a male-sterility gene and fertility T restorer gene, integrated into the genome -	S Example 5; Page 53; 98pp; English.
re version 4.5 33 - 2000 Compugen Ltd. sw model	, 18:17:42 ; Search time 716.55 Seconds (without alignments) 26.322 Million cell updates/sec	atcgacc 22	000	coostal residues cooken parameters: 1861242		O% summaries c	geneseq/geneseqn/Na1980.DAT:* geneseq/geneseqn/Na1981.DAT:* geneseq/geneseqn/Na1982.DAT:* geneseq/geneseqn/Na1983.DAT:* geneseq/geneseqn/Na1984.DAT:* geneseq/geneseqn/Na1985.DAT:* geneseq/geneseqn/Na1985.DAT:* geneseq/geneseqn/Na1986.DAT:*	RESUI AAH25 ID XX	AC AA XX XX DT 05	XX KW KW KW XX	a XX XX Inted, XX XX XX	90	08	AAH25458 PCR primer for end PAAD07003 PCR primer B04, to XX AAQ13870 Cruciferin A gene. PI	AAQ37508 Shigella specific XX AAQ37510 E. coli repeat 1. DR AAQ37514 S. flexneri repeat XX	AAQ37512 E. coli repeat 2 (PT AAV38672 Mus musculus SOCS7 PT AAH21115 C. glutanicum LP-6 PT AAC770136 Human ORFY ORFY541 xx	AAC12754 Human secreted pro PS
GenCo. Copyright (c) 199	Run on: February 25, 200	score: e:		mber of hits satisfying	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45	Database : N_Geneseq_1101:* 1: /SIDSZ/gcgdata/ 2: /SIDSZ/gcgdata/ 3: /SIDSZ/gcgdata/ 4: /SIDSZ/gcgdata/ 5: /SIDSZ/gcgdata/ 6: /SIDSZ/gcgdata/ 7: /SIDSZ/gcgdata/ 7: /SIDSZ/gcgdata/ 8: /SIDSZ/gcgdata/	9: /SIDSZ/gcgdat 10: /SIDSZ/gcgdat 11: /SIDSZ/gcgda 12: /SIDSZ/gcgda 13: /SIDSZ/gcgda	14: /SIDSZ/gcgdz 15: /SIDSZ/gcgdz 16: /SIDSZ/gcgdz 17: /SIDSZ/gcgdz	18: /SIDSZ/95454 19: /SIDSZ/959da 20: /SIDSZ/959da 21: /SIDSZ/959da 22: /SIDSZ/959da	Pred. No. is the number of r score greater than or equal and is derived by analysis o	90	Score Match Length DB	22 100.0 22 22 100.0 22 22 100.0 3113	17.2 78.2 587 17.2 78.2 1174 17.2 78.2 1188	7 17.2 78.2 1196 14 8 16.8 76.4 2019 19 c 9 16.8 76.4 2019 19 c 10 16.4 76.5 4961 21	11 15.8 71.8 226

Length 22;

~

```
ö
            The specification describes a pair of transgenic winter oilseed rape expression cassette comprising a male-sterility gene (e.g. barnase gene), and the other plant has an expression cassette comprising a fertility restorer gene (e.g. barstar gene), integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed, plants developed from the hybrid seed have agronomic performance. PCR primers AAHS157-98 were used to amplify endogenous sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer B04, to recognise foreign DNA and flanking sequence of MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic plant with a male-fertile Brassica genome. Transgenic the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is PCR primer which is used to recognise foreign DNA and a flanking sequence of elite event MS-B2.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characterized by ly by presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MS-B2 elite event; transgenic Brassica plant; transformation event; male-sterility gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                    100.0%; Score 22; DB 22; Length 22; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                    Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                     from transgenic plants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 33; 53pp; English.
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                       cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD07003 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200131042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD07003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
*5555555555555*&
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The DNA is the genomic sequence of the seed storage protein gene cruciferin A (cruA). It can be used in the prodn. of transgenic plants expressing cruciferin in its seeds for use in an industrial process. The seeds contg. the cruciferin can be used without the need for first extracting and/or isolating the enzymes. The use of seeds for the storage of cruciferin provides a stable vehicle which is easily packaged and transported and easily handled during use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seeds contg. enhanced enzyme levels from transgenic plants - used for catalysing reactions, increasing nutritional values or treating digestive disorders.
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                      Verwoerd TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22; DB 12; Length 3113;
Pred. No. 0.049;
); Mismatches 0; Indels 0
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3113 BP; 961 A; 685 C; 586 G; 881 T; 0 other;
                         ö
 Score 22; DB 22;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                    Rietveld K,
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Sijmons PC, Van Ooyen AJJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                        ö
                                              22
                                                                   22
                                                                                                                                                                                                                       Seed storage protein; cruA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 3; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uvery Match 100.0%;
Best Local Similarity 100.0%;
Matches 22; Conservative 0;
                                                                                                                           AAQ13870 standard; DNA; 3113
                                             1 cgcagttctgtgaacatcgacc
                                                          91EP-0200688
                                                                                                                                                                                                                                                                                                                                                      90US-0498561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 cgcagttctgtgaacatcgacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ37508 standard; DNA; 587
                                                                                                                                                                         09-DEC-1991 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-1993 (first entry)
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                           (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-289815/40.
Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                               Cruciferin A gene
                                                                                                                                                                                                                                               Brassica napus.
                                                                                                                                                                                                                                                                                                                  25-MAR-1991;
                                                                                                                                                                                                                                                                                                                                        25-MAR-1991;
23-MAR-1990;
                                                                                                                                                                                                                                                                                           02-0CT-1991
                                                                                                                                                                                                                                                                    EP449376-A.
                                                                                                                                                   AAQ13870;
                                                                                                                                                                                                                                                                                                                                                                                                              Quax WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ37508;
                                                                                                                                                                                                                                                                                                                                                                                                  Pen J,
                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ37508
                                                                                                                                      á
                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXX
```

m

us-09-698-903b-14.rng

```
The sequences given in AAQ37510-14 are fragments which represent repeat repeat is highly conserved and has characteristics of a transposable element. Over 20 copies of the repeat sequence are found in the chromosome and virulence plasmid of Shigella. The repeat occurs in 1 to 3 copies in some E. coli competitors, but not in other bacterial species. These fragments were used to design probes which are specific to Shigella and Enteroinvasive E. coli (EIEC). The probes are specific to a stable region of the Shigella or E. coli genome, and not the unstable virulence plasmid, which means that they are more reliable than previous probes in the detection of dysentry causing microbes. See also AAQ37506-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sonnel; flexner1; probe; Enteroinvasive; EIEC; element; virulence plasmid; detection; dysentry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid probes for detection of shigella and other pathogens - used to diagnose dysentery in non-isotopic test format and have utility in non-isotopic test formats requiring amplification for high sensitivity
                                                                                                            Nucleic acid probes for detection of shigella and other pathogens - used to diagnose dysentery in non-isotopic test format and have utility in non-isotopic test formats requiring amplification for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14; Length 1174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1174 BP; 252 A; 295 C; 277 G; 330 T; 20 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.2; DI
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                          Disclosure; Page 91; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 cgcagtactgtgaacctcgatc 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ37514 standard; DNA; 1188 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US06617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 cgcagttctgtgaacatcgacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0738800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 86.4
nes 19; Conservative
                                     χ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCarty JM, Parodos K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosome; Shigella;
E. coli; transposable

 S. flexneri repeat 2.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-076542/09.
                                                                        WPI; 1993-076542/09
(STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shigella flexneri.
                                                                                                                                                                       high sensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-1993
                                     McCarty JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9303187-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Si
Matches 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ37514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ37514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosome; Shigella; sonnei; flexneri; probe; Enteroinvasive; EIEC; E. coli; transposable element; virulence plasmid; detection; dysentry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAQ37506-09 fragments which were derived from the chromosome of Shigella sonnei. These fragments were used to design probes which are specific to Shigella and Enteroinvasive E. coll (EIEC). The probes are specific to a stable region of the Shigella or E. coll genome, and not the unstable virulence plasmid, which means that they are more reliable than previous probes in the detection of dysentry causing microbes. See also AAQ37506-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                     Chromosome; Shigella; sonnei; probe; Enteroinvasive E. coli; EIEC; virulence plasmid; detection; dysentry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid probes for detection of shigella and other pathogens - used to diagnose dysentery in non-isotopic test format and have utility in non-isotopic test formats requiring amplification for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 587 BP; 138 A; 149 C; 139 G; 161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.2; DE
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 89-90; 129pp; English
                 Shigella specific fragment NT15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ37510 standard; DNA; 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 cgcagttctgtgaacatcgacc
                                                                                                                                                                                                                          92WO-US06617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566 cgcagtactgtgaacctcgatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US06617
                                                                                                                                                                                                                                                               91US-0738800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0738800
                                                                                                                                                                                                                                                                                                                                          Parodos K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1993 (first
                                                                                                                                                                                                                                                                                                    (STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-076542/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. coli repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           high sensitivity
                                                                                                            Shigella sonnei
                                                                                                                                                                                                                                                               31-JUL-1991;
                                                                                                                                                                                                                          28-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-1991;
                                                                                                                                                                                                                                                                                                                                          McCarty JM,
                                                                                                                                               WO9303187-A
                                                                                                                                                                                    18-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat; ss.
```

AAQ37510;

2

g

ò

AAQ37510 RESULT

ő

Gaps

; 0

4

ô

```
not the unstable virulence plasmid, which means that they are more reliable than previous probes in the detection of dysentry causing microbes. See also AAQ37506-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2019 BP; 427 A; 510 C; 545 G; 528 T; 9 other;
                                                                                                                                                                                                                     œ
                                                                                                                                                                                                                                 AAV38672
                                                                                                                                                                                                                    RESULT
        8
                                                                                                                                                      à
                                                                                                                                                                            q
                                                                                                                                                                                                                                              ö
                      The sequences given in AAQ37510-14 are fragments which represent repeat sequences derived from the chromosome of E. coli and S. flexneri. The repeat is highly conserved and has characteristics of a transposable element. Over 20 copies of the repeat sequence are found in the chromosome and virulence plasmid of Shigella. The repeat occurs in 1 to 3 copies in some E. coli competitors, but not in other bacterial species. These fragments were used to design probes which are specific to Shigella and Enteroinvasive E. coli (EIEC). The probes are specific to a stable region of the Shigella or E. coli genome, and not the unstable virulence plasmid, which means that they are more microbes. See also AAQ37506-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences given in AAQ37510-14 are fragments which represent repeat sequences derived from the chromosome of E. coli and S. flexneri. The repeat is highly conserved and has characteristics of a transposable element. Over 20 copies of the repeat sequence are found in the chromosome and virulence plasmid of Shigella. The repeat occurs in 1 to 3 copies in some E. coli competitors, but not in other bacterial species. These fragments were used odesign probes which are specific to Shigella and Enteroinvasive E. coli (ELEC). The probes are specific to a stable region of the Shigella or E. coli genome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosome; Shigella; sonnel; flexneri; probe; Enteroinvasive; EIEC; E. coli; transposable element; virulence plasmid; detection; dysentry;
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid probes for detection of shigella and other pathogens - used to diagnose dysentery in non-isotopic test format and have utility in non-isotopic test formats requiring amplification for high sensitivity
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                      Score 17.2; DB 14; Length 1188;
Pred. No. 15;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                             Sequence 1188 BP; 258 A; 311 C; 273 G; 330 T; 16 other;
Disclosure; Page 93; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 92; 129pp; English.
                                                                                                                                                                                                                                                                                                                 195 cgcagtactgtgaacctcgatc 216
                                                                                                                                                                                                                                                                                                                                                                                  AAQ37512 standard; DNA; 1196 BP
                                                                                                                                                                                                                                                                                         1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                       78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US06617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0738800.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                  Best Local Similarity 86.4 Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parodos K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. colt repeat 2 (2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-076542/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9303187-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCarty JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          AAQ37512;
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                         RESULT
AAQ37512
ð
```

```
The sequence is that of a gene encoding a suppressor of cytokine signalling protein (SOCS). SOCS can be used to screen for naturally occurring antibodies to SOCS, which may occur, e.g. in some autoimmune diseases. Alternatively, specific antibodies can be used to screen for SOCS, which is useful as a knowledge of SOCS levels may be important for the diagnosis of certain cancers. Soluble SOCS polypeptides can be used to treat disease, injury or abnormality involving cytokine mediated cellular responsiveness, e.g. hyperimmunity, immunosuppression, allergies and hypertension.
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suppressor of cytokine signalling proteins - useful to treat disease, injury or abnormality involving cytokine mediated cellular responsiveness e.g. hyperimmunity, immunosuppression, allergies and
                                                                                                                              .
0
                                                                              Length 1196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOCS; suppressor of cytokine signalling; PCR primer; autoimmune disease; diagnosis; cancer; treatment; cytokine mediated cellular responsiveness; hyperimmunity; immunosuppression; allergies; hypertension; ss.
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholson SE;
Viney EM, Willson
Sequence 1196 BP; 259 A; 298 C; 272 G; 353 T; 14 other;
                                                                            DB 14;
                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                      Score 17.2; DB
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= SOCS7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 143-144; 325pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metcalf D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Starr R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
2..1054
                                                                                                                                                                                                AAV38672 standard; DNA; 2019 BP.
                                                                                                                                                                       1 cgcagttctgtgaacatcgacc 22
                                                                         78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97AU-0005117.
96AU-0003384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-AU00729
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i, Hilton DJ,
Richardson RT,
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus SOCS7 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-286854/25.
                                                                      Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW62621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alexander WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicola NA,
                                                                                                                                                                                                                                                                                                                                                                                       AAV38672;
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes the novel plasmids pTPT3 and pCRY4, isolated from Corynebacterium glutamicum DSM 5816. pTET3 contains about 27.8 kb; includes a replication region of 4539 bp (1) and a 7136 bp antibiotic resistance region (6) containing the teth gene (resistance to tetracycline) and the aadA gene (resistance to streptomycin and spectinomycin. pCRY4 contains about 48 kbp and includes a replication region of 1856 bp (4). Restriction maps and sequences for (1), (4) and (6) are reproduced. Composite plasmids derived from pTET3 and pCRY4 are used to produce strains of coryneform bacteria that produce vitamins (especially D-panthothenic acid); nucleotides, or L-amino acids (particularly lysine and threonine), which are useful in animal nutrition; the food and pharmaceutical industries, and human medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New plasmids pTET3 and pCRY4, and their composites, useful for expressing genes in coryneforms for production of amino acids, vitamins and nucleotides
                                                                                                                                                                                                                                                                                             L-amino acid production; replication region; antibiotic resistance; tetA; terracycline resistance; aadA; streptomycin resistance; vitamin; spectinomycin resistance; coryneform bacterium; D-panthothenic acid; lysine; threonine; animal nutrition; food industry; medicine;
                                           Gaps
                                          ö
              Length 2019;
                                          Indels

    C. glutamicum LP-6 DNA encoding tetR, tetA and aadA.

            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tauch A, Kalinowski J, Puehler A, Thierbach G;
                                        5
          Score 16.8; DE
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1 (1.3); Page 29-35; 46pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (1444..2013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB86252, AAB86253, AAB86254.
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
76.4%; Scor.
90.0%; Pred
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "tetR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product- "tetA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "aadA"
                                                                                                                                                                          ВÞ
                                                                                  124 gcagttctgtgaccatccac 143
                                                                                                                                                                        AAH21115 standard; DNA; 7316
                                                                      21
                                                                                                                                                                                                                                                                                                                                                          pharmaceutical industry; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5882..6721
/*tag= c
/product= "a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2000; 2000EP-0122056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DE-1053206
                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2124..3275
                                                                                                                                                                                                                                     (first entry)
                                                                      gcagttctgtgaacatcgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag- b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-391631/42
                        Local Similarity es 18: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEGS ) DEGUSSA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1097998-A1
                                                                                                                                                                                                                                   05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-2001
                                                                                                                                                                                                      AAH21115;
            Query Match
                                                                    ~
                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                g
```

```
ò
Expression plasmids based on pTET3 or pCRY4 provide high productivity and have unexpectedly good compatibility with known plasmids. This sequence represents a DNA sequence containing a fragment which encodes the Corprebacterium glutamicum LP-6 tetR, tetA and aadA proteins described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antidiated to antidiament; antibacterial; antifungal; antirheumatic; antithyroid; antidiaria; gene therapy; cancer; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria, autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinuia; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acids and peptides derived from open reading frame I for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                  ;
                                                                                                                                                                Length 7316;
                                                                                                           Sequence 7316 BP; 1485 A; 2116 C; 2164 G; 1551 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF2591 polynucleotide sequence SEQ ID NO:5181.
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating e.g. cancers, proliferative disordeneurodegenerative disorders and cardiovascular disease
                                                                                                                                                                DB 22;
                                                                                                                                                                                                    ;;
                                                                                                                                                              76.4%; Score 16.8; E 90.0%; Pred. No. 31; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 4360-4363; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                   AAC77036 standard; cDNA; 4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis; contraceptive; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1999; 99US-0127728, 30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating
                                                                                                                                                                Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB42827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                     AAC77036;
                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel
                                                                                                                                                                                                                                                                                                                                 RESULT
   8888888
                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

```
osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiabatic; hypotensive; dermatological; immunosuppressive;
antidiabatic; hypotensive; dermatological; anticheumatic;
antithyroid; and antianaemic. The sequences can be used for determining
the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treating
the product conditions associated with an ORFX-associated disorder. The
nucleic acids can be used to express ORFX proteins in gene therapy
vectors. The proteins and nucleic acids may be used to treat cancers,
proliferative disorders, neurodegenerative disorders, osteoarthritis,
graft vs host disease, cardiovasular disease, diabetes mellitus,
hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
the present or fungal infection, melaria, autoimmune disorders, asthma,
allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
concturnal haemoglobinaria, antiinflammatory disease; to, enhance
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                        74.5%; Score 16.4; DB 21; Length 4961; 94.4%; Pred. No. 48;
                                                                                                                                                                                                                                                         coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                     Sequence 4961 BP; 1411 A; 1065 C; 1123 G; 1362 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein 5' EST, SEQ ID NO: 16829,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giordano J;
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC12754 standard; cDNA; 226
                                                                                                                                                                                                                                                                                                                                                                                                                       2639 AGTTCTGTGAACATTGAC 2622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                   4 agttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC12754;
```

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT prinade ODNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

Claim 1; SEQ ID 16829; 71pp + CD-ROM; English.

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH51601 represents a human genomic nucleotide sequence comprising sbg1, 934665, sbg2, 935017 and 935018 nucleic acid sequences located on the human chromosome 13431 acus. The nucleotide sequences contrain biallelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and AAB62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and protein products. AAH51631 and AAB62916 - AAB65918 represent 935018 cDNA sequences and protein products. Primers AAH5163 - AAH51699 are used to sociate sbg1 cDNAs, while sbg1 exons from different primates are represented by sequences AAH51642 - AAH51699. Nucleotide sequences of amplicons which comprise biallelic markers located on the chromosome 13431-433 locus are represented in AAH51700 -AAH51817. Biallelic markers
cDNA sequences have been obtained, the full 5' UTR is rarely included.
5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides comprising sequences from sbgl and g35018 biallelic markers are used for genotyping and detecting schizophrenia or bipolar disorder and predisposition to these disorders -
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sbg1; g34665; sbg2; g35017; g35018; chromosome 13g31-g33; haplotype;
biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
                                                                                                                                                                                                               ;
0
                                                                                                                                                                              Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bihain
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human chromosome 13q31-q33 genomic nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blumenfeld M, Chumakov I, Bougueleret L,
                                                                                                                      Sequence 226 BP; 75 A; 29 C; 51 G; 67 T; 4 other;
                                                                                                                                                                              DB
                                                                                                                                                                       71.8%; Score 15.8; D
89.5%; Pred. No. 62;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 409-493; 737pp; English.
                                                                                                                                                                                                                                                                                                                                                                AAH51601 standard; DNA; 319608 BP.
                                                                                      expression and secretion vectors.
                                                                                                                                                                                                                                                                   138 CAGTTCTGTGAATTTCGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0131971.
990S-0132065.
990S-0143928.
990S-0145915.
990S-0146452.
990S-0162288.
                                                                                                                                                                                                                                           3 cagttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000; 2000WO-IB00435
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                         Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-619082/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200058510-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-1999
14-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999
29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Essioux L;
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 AAH51601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen D,
                                                                                                                                                                                                                                                                                                                                                AAH51601/c
   88888888
                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
/*tåg= w
/note= "Binds primer 99-31960-363.mis complement"
complement (95543..95563)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= ab
//note= "Biallelic marker A5"
complement (107282..107300)
/*tag= ac
/note= "Binds primer 99-24656-260.mis complement"
/*tag= ad /*tag= a
                      /note= "Binds primer 99-27935-193.mis complement"
complement (21845..21864)
                                                                                                                                                                                                                                                                                                                                   /*tåg- q
/note= "Binds primer 8-128-33.mis complement"
complement (65856..65874)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note = "Binds primer 99-24656.rp complement" (60279..160298
                                                           /noté= "Binds primer 99-27935.pu complement"
65463..65471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= x
note= "Binds primer 99-31960.rp complement"
07022..107040
                                                                                                                                                                                                                                                                                                                                                                                          /*tag= r
/note= "Binds primer 8-128.rp complement"
95034..95053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /noté= "Binds primer 99-31960-363.mis"
95384.,95408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= z
note= "Binds primer 99-24656-260.mis"
.07269..107293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note "Binds primer 99-24639-163.mis"
60628..160652
                                                                                                                                                                                     note= "Binds primer 8-128-33.mis"
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Binds primer 99-31960.pu"
95377..95395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= aa
'bound_moiety= Probe_99-24656-260
107281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bound_moiety- Probe_99-31960-363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bound_moiety~ Probe_99-24639-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= y
note= "Binds primer 99-24656.pu"
[07262..107280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **tag= ae
note= "Binds primer 99-24639.rp"
.60621..160639
                                                                                                                                  /note= "Binds primer 8-128.pu"
65466..65484
                                                                                                                                                                                                                                             bound_moiety- Probe_8-128-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Biallelic marker A6"
complement (160641..160659)
/*tag= a1
                                                                                                                                                                                                                                                                             /*tag= p
/note= "Biallelic marker A3"
complement (65486..65504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= v
/note= "Biallelic marker A4"
complement (95397..95415)
                                                                                                                                                                                                        65473..65497
/*tag= o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                    *tag=
                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95396
                                                                                                                                                                                                                                                                65485
                                                                                                                                                                                                          misc_binding
                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                               primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer_bind
                                             primer_bind
                                                                                                 primer_bind
                                                                                                                                                     primer_bind
                                                                                                                                                                                                                                                                                                                      primer_bind
                                                                                                                                                                                                                                                                                                                                                                         primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer_bind
         ö
are represented in the sequences by degenerate/undefined base codes. PCR the Invention. The bialibelic marker containing nucleotide sequences of the Invention. The bialibelic marker containing nucleotide sequences are used to determine the identity of the nucleotide at a bialibilic marker in a sample DNA sequence. The nucleotide sequences may be labelled and used for genotyping by determining the identity of a nucleotide at a Region D-related bialibilic marker in a biological sample from single or multiple subjects. By determining the frequency of a bialibilic marker in a population an association between a genotype and a trait, a haplotype and a trait can be detected. The sequences can be used to determine a predisoposition to or early onset of schizophrenia or bipolar disorder or a beneficial response to or side effects related to treatment against schizophrenia or bipolar disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human schizophrenia associated gene g35030 and biallelic markers Al-A71.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                        Sequence 319608 BP; 101600 A; 56677 C; 58335 G; 102722 T; 274 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tâg= e
/note= "Binds primer 99-27943-150.mis complement"
complement (8446..8465)
                                                                                                                                                                                                                                                                                                                  Score 15.8; DB 21; Length 319608;
Pred. No. 1.8e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; 935030; biallelic marker; Al-A71; chromosome 13q31-q33; schizophrenia; bipolar disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Binds primer 99-27943.pu complement"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Binds primer 99-27943-150.mis"
8304..8328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Binds primer 99-27935-193.mis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "Blnds primer 99-27943.rp"
/*tag= b
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bound_moiety= Probe_99-27943-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dound_moiety= Probe_99-27935-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= g
/note= "Binds primer 99-27935.rp"
21653..21671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= j
/note= "Biallelic marker A2"
complement (21673..21691)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Biallelic marker Al"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (8317..8335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
7938..7958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS09301 standard; DNA; 319608 BP.
                                                                                                                                                                                                                                                                                                                                                                                                          Db 164729 GCAGTTCTCTGAACATCTA 164711
                                                                                                                                                                                                                                                                                                                  Query Match 71.8%;
Best Local Similarity 89.5%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21365..21385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21660..21684
                                                                                                                                                                                                                                                                                                                                                                                         2 gcagttctgtgaacatcga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag≃
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS09301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS09301/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
     SSSSSSSSSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
/*tag- ao
/note- "Binds primer 99-24634-108.mis complement"
complement (161240..161257)
/note- "Binds primer 99-24639-163.mis complement"
160770..160787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- ba
/note= "Binds primer 99-16100-147.mis complement"
complement (171153..171173)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag- au
/note- "Binds primer 99-7652-162.mis complement"
complement (169331.169351)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= bg
/note= "Blnds primer 99-5862-167.mis complement"
                                                                                                   /note= "Binds primer 99-24639.pu complement"
160857..160875
                                                                                                                                                                                                                                                                                                                                                   **tag= ap
'note= "Binds primer 99-24634.rp complement"
:68813.,168830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "*tag= bb
note= "Binds primer 99-16100.rp complement"
.73065..173085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= av
note= "Binds primer 99-7652.rp complement"
70666..170686
                                                                                                                                                    'note= "Binds primer 99-24634-108.mis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag- ax
/note- "Binds primer 99-16100-147.mis"
170798..170822
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= ar
/note= "Binds primer 99-7652-162.mis"
168962..168986
/*tag= ....- nrohe 99-7652-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Binds primer 99-5862-167.mis"
                                                                                                                                                                                                        /bound_molety= Probe_99-24634-108
160876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= aw
/note= "Binds primer 99-16100.pu"
170791..170809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= ay
/bound_molety= Probe_99-16100-147
170810
                                              /note= "Binds primer 99-24634.pu"
complement (160785..160802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /bound_moiety= Probe_99-7652-162
168974
                                                                                                                                                                                                                                                                                                                                                                                              *tag~ aq
note~ "Binds primer 99-7652.pu"
168955..168973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'bound_moiety= Probe_99-5862-167
73358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Binds primer 99-5862.rp".73339..173357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Biallelic marker A10" complement (173359..173377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= at
/note= "Biallelic marker A8"
complement (168975..168993)
                                                                                                                                                                                                                                                         /note= "Biallelic marker A7"
complement (160877..160895)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= az
/note= "Biallelic marker A9"
complement (170811..170829)
                                                                                                                                                                         .60864..160888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73346..173370
                                                                                                                                     /*tag=
                                                                                                                                                                                           /*tag≔
                                  /*tag=
                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                      misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
            primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                  primer_bind
                                                                                                                   primer_bind
                                                                                                                                                                                                                                                                           primer_bind
                                                                                                                                                                                                                                                                                                                             primer_bind
                                                                                                                                                                                                                                                                                                                                                                              primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                               primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer_bind
```

```
This partial cDNA clone, termed TOBPPO6, encodes a polyphenol oxidase (PPO) polypeptide of tobacco (see also AAM97990). The clone was obtained by PCR amplification of young tobacco leaf cDNA using primers (see AAX24708-12) based on conserved copper binding sites of plant PPOs, and identified on the basis of homology to known plant PPO genes. PPO is the major enzyme responsible for browning and spoilage of fruits and vegetables after damage or injury. Sense PPO nucleic acids can be used to increase the levels of PPO in a plant. Optionally modified sense sequences and antisense sequences can be used to reduce PPO levels (by co-suppression in the case of sense sequences). Transgenic plants including antisense PPO sequences, and a plant vaccine including a nucleic acid encoding banana, tobacco or pineapple PPO or an antisense sequence are
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding polyphenol oxidase from banana, tobacco and pineapple - useful for, e.g. increasing levels of the enzyme expression, which is responsible for browning and spoilage of fruits after injury or damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyphenol oxidase; banana; tobacco; pineapple; transgenic plant; vaccine; browning; spoilage; ds.
                                                                                                                                                         Length 319608;
                                                                                                                                                                                           0;
        /*tag= bh //note= "Binds primer 99-5862.pu complement" 189753..189771
                                                                                                                                                                                           Indels
                                                                                                                         /note= "Binds primer 99-5919-215.mis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 545 BP; 171 A; 115 C; 115 G; 144 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Tobacco leaf polyphenol oxidase cDNA clone TOBPP06.
                                                                                                                                                     71.8%; Score 15.8; DB 22;
89.5%; Pred. No. 1.8e+02;
live 0; Mismatches 2;
                                                            /*tag= bi
/note= "Binds primer 99-5919.pu'
189938..189956
 complement (173495..173514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                        Db 164729 GCAGTTCTCTGAACATCTA 164711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 5; 47pp; English.
                                                                                                                                                                                                                                                                                                                               AAX24719 standard; cDNA; 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97AU-0006849.
                                                                                                                                                                                                                      2 gcagttctgtgaacatcga 20
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                              /*tag= b.
                                                                                                                                                                      trocal Similarity 89.5 ches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-070152/06.
P-PSDB; AAW97990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9853080-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAY-1997;
primer_bind
                                          primer_bind
                                                                                          primer_bind
                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robinson SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                              AAX24719;
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claimed.
                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                    AAX24719
                                                                                                                                                                                                                      δ
```

σ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX30724 to AAX30946 represent genomic DNA sequences isolated from Streptococcus pneumoniae strain 0100993. These genomic DNA sequences encode the novel proteins given in AAY11114 to AAY11367. The proteins, isolated from Streptococcus pneumoniae, can be used in vaccines against streptococcal infections and in assays for identifying compounds that inhibit or activate the activity of the proteins. The antagonists can be used to treat an individual having need to inhibit a bacterial protein. Vectors expressing the proteins can be used to induce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                            Gaps
                                                                                                                                                                                                                                                             Streptococcus pneumoniae strain 0100993; vaccine; immune response; streptococcal infection; pneumococcal; ss.
                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding pneumococcal polypeptide(s) - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.9%; Score 15.6; DB 18; Length 769; 81.8%; Pred. No. 95;
  Length 545;
                                                                                                                                                                                                                                    Streptococcus pneumoniae genomic DNA sequence SEQ ID NO:56.
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 769 BP; 204 A; 202 C; 140 G; 223 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hodgson JE, Knowles DJC, Nicholas RO;
 DB 20;
Score 15.6; DE
Pred. No. 90;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protective immune response in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 91; 354pp; English.
                                                                    (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                           ö
                                                    1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                 AAX30779 standard; DNA; 769 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccines, drug screening, etc
Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        97WO-US05306.
                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0025788.
96US-0014690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-503111/46.
P-PSDB; AAY11181.
                                                                                                                                                                                                                                                                                                                                 WO9737026-A1
                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1996;
02-APR-1996;
                                                                                                                                                                                                        20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                            09-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stodola RK;
                                                                                                                                                                             AAX30779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                   ô
                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
```

Search completed: February 25, 2002, 18:17:54 Job time: 16712 sec

.

.

56

Feb

Tue

```
(without alignments)
16.520 Million cell updates/sec
                                                                           ; Search time 301.6 Seconds
                                                                                                                                                                                                                                            702406
4.5
Compugen Ltd
                                                                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                                                                                   351203 seqs, 113238999 residues
  version -
                                                                           February 25, 2002, 18:05:55
                                                                                                                                                     1 cgcagttctgtgaacatcgacc 22
                                                   sw model
                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
 GenCore
Copyright (c) 1993
                                                  nucleic search, using
                                                                                                                         US-09-698-903B-14
22
                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
                                                                                                                                                                                                                                           Total number of
                                                                                                                                                                                                                                                                     sed
                                                                                                                          Title:
Perfect score:
                                                                                                                                                                            Scoring table:
                                                  OM nucleic -
                                                                                                                                                                                                                                                                    08
08
                                                                                                                                                     Sequence:
                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                  Minimum I
Maximum I
                                                                           Run on:
```

Issued_Patents_NA:*
.: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 9, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 20, Appl Description US-08-626-554-2 US-08-375-241-3 US-08-375-241-3 US-08-375-241-9 US-08-375-241-9 US-08-375-241-9 US-08-375-241-7 US-08-375-241-7 US-08-375-241-7 US-08-375-241-7 US-08-31-189-9 US-08-23-06617A-7 US-08-23-06617A-7 US-08-281-9 US-09-058-376-2 US-09-058-316-2 US-09-058-316-2 US-09-058-316-1 US-08-261-578-1 US-08-261-578-1 US-08-261-578-1 US-08-261-578-1 US-08-261-578-1 US-08-261-578-1 US-08-261-578-1 US-08-328-111-19 US-08-146-422-20 SUMMARIES 3113 3113 3113 587 587 11174 11196 11196 11196 11196 11196 1195 2048 2048 2158 2158 310 1062 3330 3330 3656 3656 Length Query Match Score Result Š ပပ 000000000 00000

Appli Appli Appli

Sequence 1, 1 Sequence 1, 1 Sequence 1, 1

-08-393-734-1 -08-894-489-1

Patent No. 5183745 Squence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 20, Appli Sequence 21, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 14, Appli Sequence 14, Appli Sequence 15, Appli Sequence 16, Appli Sequence 3, Appli Sequence 3, Appli Sequence 99, Appli	SEEDS AND THEIR	Length 3113;
5183745-1 5183745-5 US-08-39345-3 US-08-894-489-3 US-09-036-987A-1 US-09-370-01 PCT-US93-00031-18 PCT-US93-00031-22 PCT-US93-00031-12 PCT-US93-00031-12 PCT-US93-00031-14 PCT-US93-00031-14 PCT-US93-00031-16 US-08-481-073-3 US-08-441-155C-99 US-08-441-155C-99 US-09-009-490A-90	ALIGNMENTS 422 J. J. N. OF ENZYMES IN 46,422 46,422 615-20011.23	k; Score 22; DB 1; k; Pred. No. 0.012;
66.4 4649 666.4 6649 666.4 9592 1 959	TO THE THE TO THE	100.0%; Similarity 100.0%;
28 14.6 C 330 14.6 C 331 14.6 C 332 14.6 G 33.3 33.3 14.6 G 33.4 14.6 C 33.4 14.6 C 33.4 14.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4	US-08-146-422-20/c Sequence 20, Applicatio Patent No. 5543576 GENERAL INFORMATION: APPLICANT: RIETVELD APPLICANT: HOEKBAA, APPLICANT: PEN, JAN TITLE OF INVENTION: TREET OAIGOUNTRY: BAIO ALTO CONRESPONDENCE PAID STATE: California CONPUTER READABLE FO MEDIUM TYPE: Flop COMPUTER: PAID COMPUTER: PAID APPLICATION NUMBER FILING DATE: O2'N CLASSIFICATION: S ATTORNEY/AGENT INFOR MAME: KENEEDY, BI REGISTRATION INVENTION: S ATTORNEY/AGENT INFOR TELEFAX: (415) 49 TELEFAX: 100141 INFORMATION FOR SEQ 10 SEQUENCE CHARACTERIS LENGTH: 3113 base TYPE: INCLES: ain CONFORMATION FOR SEQ 10 SECUENCE: 1001612 au TELEFAX: 100141 TELEFAX: (415) 49 TELEFAX: 100141 TELEFAX: (415) 49	Query Match Best Local Sim

```
APPLICANT: Parodos, Kyriaki
APPLICANT: McCarty, Janice
TITLE OF INVENTION: Nucleic Acid Probes for the Detection of
TITLE OF INVENTION: Shigella
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.2; DB 1; Length 587; Pred. No. 3.1; 0; Mismatches 3; Indels
                                                            Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06617A FILLING DATE: 19920728
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/738,800
FILLING DATE: 31-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Amoco Corporation
STREET: 200 East Randolph Drive, P.O. Box
CITY: Chicago
STATE: 1111nois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                           PPLICALION
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 31-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granaban, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: GTR90-04
TELECOMMUNICATION INFORMATION:
TELEPRAX: 617-861-6240
TELEPRAX: 617-861-6540
TELEPRAX: 617-861-6540
TELEPRAX: 617-861-6540
TELEPRAX: 617-861-6540
SEQUENCE CHARACTERISTICS:
TENGRATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application PC/TUS9206617A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUFER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 CGCAGTACTGTGAACCTCGATC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cgcagttctgtgaacatcgacc 22
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 587 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.2
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-375-241-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
PCT-US92-06617A-3
                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
           Gaps
                                                                                                                                                                                         Sequence 2, Application US/08626554
Patent No. 5714474
GENERAL INFORMATION:
APPLICANT: VAN OOIJEN, ALBERT J.J.
APPLICANT: RIETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: BIN, JAN
APPLICANT: SIMONS, PETER C.
APPLICANT: VERMORED, TEUNIS C.
APPLICANT: VERMORED, TEUNIS C.
APPLICANT: UNENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 3.
CORRESPONDENCE ADDRESS:
           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kyriaki
Janice
Nucleic Acid Probes for the Detection of
Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 22; Conservative 0; Mismatches 0; Indels
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/626,554
FILING DATE: 02-APR-1996
CLASSIFICATION: 514
CLASSIFICATION: 514
         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISSTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 26192-20011.10
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-0763
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORTSON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE NW
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-375-241-3
US-08-375-241-3
Sequence 3, Application US/08375241
Setent No. 564841
GENERAL INFORMATION:
APPLICANT: Parodos, Kyriaki
APPLICANT: McCarty, Janice
TITLE OF INVENTION: Nucleic Acid if
TITLE OF INVENTION: Shigelia
                                                                                 Db 1183 CGCAGTTCTGTGAACATCGACC 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1183 CGCAGITCIGIGACATCGACC 1162
                                              1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 egcagitetgigaacategace 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3113 base pairs
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                      -08-626-554-2/c
22;
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
RESULT 7
US-08-375-241-9
US-08-375-241-9
| Sequence 9, Application US/08375241
| Patent No. 5648481
| GENERAL INFORMATION:
| APPLICANT: Parcodos, Kyriaki
| TITLE OF INVENTION: Nucleic Acid Probes for the Detection of TITLE OF INVENTION: Shigella NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS: 30
| CORRESPONDENCE ADDRESS: 30
| STREET: Two Militia Drive CITY: Lexington
                                                                                                                                           Sequence 5, Application PC/TUS9206617A
GENERAL INFORMATION:
APPLICANT: Parodox, Kyriaki
APPLICANT: McCarty, Janice
TITLE OF INVENTION: Nucleic Acid Probes for the Detection of
TITLE OF INVENTION: Shigella
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCES Anco Corporation
STREET: 200 East Randolph Drive, P.O. Box 87703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.2; DB 5; Length 1174; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06617A
FILING DATE: 19920728
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/738,800
FILING DATE: 31-7UL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, Norval B.
REGISTRATION NUMBER: 33.595
REGISTRATION NUMBER: 33.595
REFERENCE/DOCKET NUMBER: GTR90-04 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                               322 CGCAGTACTGTGAACCTCGATC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 CGCAGTACTGTGAACCTCGATC 343
            1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 312-856-4972
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 1174 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.4*
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEIC ACID
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 60680
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear PCT-US92-06617A-5
                                                                                                                                                                                                                                                                                                                                                                Illinois
                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                        RESULT 6
PCT-US92-06617A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
            δ
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Parodos, Kyriaki
APPLICANT: McCarty, Janice
TITLE OF INVENTION: Nucleic Acid Probes for the Detection of
TITLE OF INVENTION: Shigella
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.2; DB 1; Length 1174; Pred. No. 3.6; 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                     Score 17.2; DB 5; Length 587; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Galloway, Norval B.
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: GT90-04 PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-856-7180
TELEFAX: 312-856-4972
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 587 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
STANDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08375241
Patent No. 5648481
                                                                                                                                                                                                                                                                                                                                                                                                     566 CGCAGTACTGTGAACCTCGATC 587
                                                                                                                                                                                                                                                                                                                                                                                1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                     Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1174 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.2
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: double
                                                                                                                                                                                                                         ; TOPOLOGY: linear
PCT-US92-06617A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-375-241-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-375-241-5
                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                ŏ
```

Gaps

ó

3; Indels

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08375241
| Patent No. 5648481
| GENERAL INFORMATION:
| APPLICANT: Parodos, Kyriaki
| APPLICANT: McCarty, Janice | TITLE OF INVENTION: Nucleic Acid Probes for the Detection of TITLE OF INVENTION: 30
| CONRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive | STREET: Lexington | STATE: Massachusetts | COUNTRY: U.S. COUNTRY: U.S
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                         DB 5; Length 1188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.2%; Score 17.2; DB 1; Length 1196; 86.4%; Pred. No. 3.6; 11ve 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOURE: FILDHY GISTER
COMPOURE: INDM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,241
FILING DATE:
FLING DATE:
APPLICATION NUMBER: US 07/738,800
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/738,800
FILING AATOMEY AGENT INFORMATION:
NAME: GRADAIN PATICIA:
REGISTERATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: GTR90-04
TELECOMMUNICATION INFORMATION:
MANE: GRADAIN NUMBER: GTR90-04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      Score 17.2; DB
Pred. No. 3.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         195 CGCAGTACTGTGAACCTCGATC 216
                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                   1 egcagttetgtgaacategaee 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 CGCAGTACTGTGAACCTCGATC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                            Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
1 TOPOLOGY: linear
PCT-US92-06617A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617-861-6240
617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1196 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
TELEFAX: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
PCT-US92-06617A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-375-241-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                තු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
PCT-US92-06617A-9
; Sequence 9, Application PC/TUS9206617A
; GENERAL INFORMATION:
    APPLICANT: Parodos, Kyriaki
; APPLICANT: McCarty, Janice
    TITLE OF INVENTION: Nucleic Acid Probes for the Detection of
    TITLE OF INVENTION: Shigella
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Anoco Corporation
    STREET: 200 East Randolph Drive, P.O. Box 87703
    STREET: Lilinois
    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READDBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06617A
FILING DATE: 19920728
PRIOR APPLICATION NUMBER: US 07/738,800
FILING DATE: 31-UUL-1991
ATPONEY/AGENT INFORMATION:
                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.2; D:
Pred. No. 3.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: GALLOWAY, NOTVAL B.
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: GTR90-04 PCT
                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/738,800
FILIAG DATE: 31-010-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: GTR90-04
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-6240
      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 CGCAGTACTGTGAACCTCGATC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 egeagttetgtgaacategaee 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-856-7180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 1188 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-856-4972
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 86.4<sup>3</sup>
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-375-241-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
```

ô

S

```
APPLICATION NUMBER: US/08/158,189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 CACAGTTCAGTGAGCATCGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cgcagttctgtgaacatcga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08158189
Patent No. 5641497
GENERAL INFORMATION:
APPLICANT: Bevins, Charles L.
APPLICANT: Jones, Douglas E.
TITLE OF INVENTION: Gastrointestinal Defensin Peptides,
TITLE OF INVENTION: CDNA Sequences, Methods for Production and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and No. 5641497ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
Sequence 7, Application PC/TUS9206617A
GENERAL INFORMATION:
APPLICANT: Parodos, Kyriaki
APPLICANT: Parodos, Kyriaki
APPLICANT: Parodos, Kyriaki
APPLICANT: Naciary Janice
TITLE OF INVENTION: Nucleic Acid Probes for the Detection of
TITLE OF INVENTION: Shigella
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Amoco Corporation
STREET: 200 East Randolph Drive, P.O. Box 87703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.2%; Score 17.2; DB 5; Length 1196; 86.4%; Pred. No. 3.6; 1ive 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                       COMPUTE: TOTO COMPUTE FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC COMPATIAL
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: PCT/US92/06617A
FILING DATE: 19920728
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/738,800
FILING DATE: 31-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: GALLOWAY, NORVAL B.
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: GTR90-04 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-856-7180
INFORMATION FOR SEG 1D NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 CGCAGTACTGTGAACCTCGATC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1196 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEIC ACID
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US92-06617A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-158-189-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-233-788A-48/C
Sequence 48, Application US/08233788A
Sequence 48, Application US/08233788A
Sequence 48, Application US/08233788A
GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouplier, Sharon C.
APPLICANT: Clouplier, Sharon C.
APPLICANT: OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZONTRY: U.S.A.
ZONTRY: U.S.A.
ZONTRY: U.S.A.
ZONTRY: U.S.A.
ZONTRY: U.S.A.
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION: UNMBER: 35,570
FURNING NUMBER: 35,570
FURNING NUMBER: 35,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.2; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION: 433

PRIOR APPLICATION NUMBER: US/07/886,232
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSON, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/POCKET NUMBER: CH-0219
TELECOMMUNICATION INFORMATION:
TELEPAX: 215-568-3409
INFORMATION FOR SEQ ID NO: 9: SEQUERA: 195-568-3409
INFORMATION FOR SEQ ID NO: 9: SEQUENE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STAPE: TYPE: nucleic acid
STAPE: TYPE: unknown
US-08-158-189-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.1%; Sco.
85.0%; Pred
0;
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                    69.1%; Score 15.2; DB 1; Length 1126; 85.0%; Pred. No. 41; tive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: NOVEL HUMAN INDUCED TUMOR PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE PAIRMSCENTICELS, Inc.
STRESSE: 1007te Pharmaccuticals, Inc.
STREE: 3174 Porter Drive
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 85.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 3;
                                      ) NAME/KEY: CDS
; LOCATION: join(3..23, 27..944, 948..1124)
US-08-233-788A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUMPUTER READABLE FORM:

MEDIUM TYPE: DISKELTE
COMPUTER: IDSKELTE
COMPUTER: IDSKELTE
COMPUTER: PASTEM: DOS
SOFTWARE: PASTEM: DOS
TILING DATE: FILE HO HEREWITH
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REJERENGE/DOCKET NUMBER: PF-0113 US
REJERENGE/DOCKET NUMBER: PF-0113 US
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: SINGIE
                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08689974
Patent No. 5776732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-058-376-2/c
; Sequence 2, Application US/09058376
                                                                                                                                                                                                                                        492 GCTGTTCGGTGAACATCGCC 473
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                2 gcagttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               893 CAGCTCGGTGAACATCGTCC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 cagiticigitgaacategace 22
                                                                                                                                  Query Match
Best Local Similarity 85.07
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; IMMEDIATE SOURCE:
; LIBRARY: BRAINOTO3
; CLONE: 530522
US-08-689-974-2
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                              US-08-689-974-2/C
                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/07602608
| Patent No. 538224
| Patent No. 538224
| Patent No. 538224
| Patent No. 538224
| APPLICANT: Besnick, Robert J. APPLICANT: Bishop, David F. APPLICANT: Bishop, David F. APPLICANT: Wang, Anne M. TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGALACTOSAMINIDASE NUMBER OF SEQUENCES: 24
| CORRESPONDENCE ADDRESS: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: STREET: 1155 Avenue of the Americas
| CITX: New York | COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 1576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
Patent No. 6080841
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Murray, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN INDUCED TUMOR PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174, Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.2; 1
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                         ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,376
FILING DATE:
APPLICATION NUMBER: US/08/689,974
FILING DATE:
APPLICATION NUMBER: US/08/689,974
FILING DATE:
APPLICATION NUMBER: US/08/689,974
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATJORDAY POLICY
NAME: BIllings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0113 US
TELECOMMUNICATION: TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.1%; Scor.
85.0%; Pred
0; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     893 CAGCTCGGTGAACATCGTCC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 cagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.1
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRAIN0T03
530522
                                                                                                                                                                                              STREET: 3174 POI
                                                                                                                                                                                                                                                              u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: BRAIN
                                                                                                                                                                                                                                                            COUNTRY: UZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-07-602-608-11/C
                                                                                                                                                                                                                                            CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
                                                                                                                                                                                                                  CITY: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; CLONE: !
```

```
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: POLECATION DATA:
COURRENT PAPELICATION DATA:
APPLICATION NUMBER: US/07/602,608
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COULZEL' LAULE A.
RECIERRE/DOCKET NUMBER: 6923-008
TELECHONE: (212) 790-9090
```

Search completed: February 25, 2002, 18:05:56 Job time: 18604 sec

THIS PAGE BLANK (USPTO)

AA813570 ab5469.s
AA843570 ab5469.s
A1084952 cw86605.s
A1658711 tu22f10.x
BF066458 st15b08.y
A49544 yy83f09.s1
AA957411 z129b11.s
AA673411 z129b11.s
AA45087 zv52503.x
A149964 qf38901.x
A1802194 tx25503.x
AAA71463 zu06a09.s
AA70220 zj44h06.s

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

```
BE377681 653 bp mRNA EST 21-JUL-2000 60122924F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3594076 5', BE377681
                                                                                                                                                                                                                                                                                                                                                                                                        Manufalia; Butherla; Robentia; Sciurognath; Muridae; Murinae; Mus. B. I (bases 1 to 653)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Lu Onpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8767 row: o column: 05
High quality sequence stop: 612.
Location/Qualifiers
I. .653
//strain="FVB/N"
//strain="FVB/N"
//db.xref="Laxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                              AA421463
AA700220
AW235369
                                                                                                                                                                     AW952652
AA868429
AI680857
AZ717353
AI740628
AI637690
AL041092
                                                                                                                                                                                                                             BE412370
BG989620
AQ852470
                                                                AA679411
AA426087
AI149964
                                                                                                                                                      BH121721
AA700001
                                BF066458
                 AI084952
                                                        BF483372
                                                                                                                             AI631483
                                                                                                                                                                                                                                                             AV655742
                         AI658711
                                                                                                                                      AW013257
F03921
                                                                                                                                                                                                                                                                                                                                                            BE377681.1 GI:9323046
  679
706
758
768
804
                                                                                                                                                                                                                             833
122
400
406
431
                                                                                                                                                                                                                                                                                                                                                                            house mouse.
 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                            RESULT
BE377681
                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
  LOCUS
                                 υ
                                                                                                                                                        O
                                                                                                                                                                                               ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1561687 vw88f09.x
A277264 2M0011K06
A1019782 ua90h12.r
AL026437 Fugu rubr
A277336 Eugu rubr
A277336 2M0011108
AK006515 Mus muscu
AM086177 xc77e11.x
AA701011 255604.s
F02043 HSCOMGO n
AA569516 nf23e01.s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE377681 601229824
                                                                (without alignments)
28.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      February 25, 2002, 17:21:21; Search time 8261.74 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                             22703874
                Compugen Ltd
                                                                                                                                             11351937 seqs, 5372889281 residues
                                                                                                                                                            Total number of hits satisfying chosen parameters:
     GenCore version 4.5
Copyright (c) 1993 - 2000 Comm
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                      1 cgcagttctgtgaacatcgacc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIS61687
AZ777264
AI019782
FR0030063
FR0730058
                                                                                                                                                                                                                    summaries

    nucleic search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE377681
                                                                                                                     IDENTITY_NUC Gapor 1.0
                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                            em_gss_other:*
                                                                                  US-09-698-903B-14
                                                                                                                                                                                                                                                                                                                                                                                   em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
                                                                                                                                                                             seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                            em_gss_hum:*
                                                                                                                                                                                                                                                                                                                                                                    em_gss_inv:*
                                                                                                                                                                                                                                                                                                                                                     em_gss_fun:*
                                                                                                                                                                                                                                                                                                                                                                            em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                            em_estfun:*
em_esthum:*
                                                                                                                                                                                                                                                                   em_estom:*
em_estpl:*
em_estba:*
                                                                                                                                                                                                                                                                                                   em_estov:*
em_htc:*
                                                                                                                                                                                                                                                                                                                   gb_est1:*
gb_est2:*
gb_htc:*
gb_hts:*
                                                                                                                                                                                                                                                             em_estin:*
                                                                                                                                                                                                                                                                                             em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                    EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.4
4.76.4
4.76.4
4.76.4
7.44.5
7.44.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.9
```

/clone="IMAGE:3594076" /clone_lib="NCI_CGAP_Mam1" /tissue_type="tumor, biopsy sample"

F02043 AA569516

AA701011

AK006515 AW086177

17.8 16.8 16.8 16.8 16.8 16.8 16.4 16.4

110087654321

Score

Result

source

FEATURES

AA700001 2169007.5 AA8684252 EST364737 AA8680857 tx42001.8 A171353 RPCI-24-1 A1740628 wg23f08.x A1741092 tt29e11.x A1641092 DKFZp434 BE412370 JJLO-HT17 A0852470 LMA-HT17 AV655742 AV655742

W91993 zh47d10.s1 BH121721 RPCI-24-2

Gaps

; 0

90.0%; Pred. No. 5.3e+02; tive 0; Mismatches 2; Indels

```
85 CAGTTCTTTGAACATCTACC 104
                                                                      3 cagttctgtgaacatcgacc 22
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                   Mus musculus
            Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                             DEFINITION
                            Matches
                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                   RESULT
AZ777264
                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                      ò
                                                                                                         셤
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="3 months, virgin"
/lab_host="DHIOB"
/nab_host="Drgan: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
181 c 195 g 145 t
                                                                                                                                                                                                                                                                                                                                                                                                                 AI561687 244 bp mRNA EST 25-MAR-1999 vw88#f09.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1262057 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone was previously sequenced on the 5' end only, this new data is from the 3' end
High quality sequence stop: 229.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:664609
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fat: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                              Score 17.8; DB 10; Length 653;
Pred. No. 2.18+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1262057"
/clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"

    244
    /organism="Mus musculus"
/strain="C57BL/6"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                          193 CGCAGTTCTGTGAGCTTCGAC 213
                                                                                                                                                                                                                                                                        1 egcagttetgtgaacategae 21
                                                                                                                                                                                          Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI561687.1 GI:4513032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex-"females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse. Mus musculus
                                                                                                                   132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                          AI561687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                            g
```

```
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (qil4732114 qipl48129072.1), a copy-number of pMD42 (qil4732114 qipl48129072.1), a copy-number of pMD42 (qil4732114 qipl48129072.1), a copy-number of pMD42 complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
2M001IK06R Mouse 10kb plasmid UUCCIM library Mus musculus genomic clone UUGC2M001IK06 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGClM library" /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: K column: 06
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 279.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0011K06"
                                                                                               AZ777264.1 GI:12905692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
```

Query Match

```
182 GCAGTTCTGTGACCATCCAC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 90.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             V_type: pha
PRIMER: KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sednence.
                                                                                       FR0030063
                                                                                                                           seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 18
                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                         LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                      FR0030063
                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FR0030058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                        RESULT
     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 346)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 3'); double-stranded conn was lighted to Eco RI adaptors (Pharmacia), digested with Not I and cloned into RNH brot I and Eco RI sites of the modified pt/T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:898027
                                                                                                                                                                                     ua90h12.rl Soares_mammary_gland_NbWMG Mus musculus cDNA clone IMAGE:1344807 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, W. Waterston, W. Waterston, W. Waterston, W. Washu-HHMI Mouse EST Project
Unpublished (1990)
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                    ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
   Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 346;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="TMAGE:1364807"
/clone_lib="Soares_mammary_gland_NbMMG"
//sex="male"
76.4%; Score 16.8; DB 13;
ilarity 90.0%; Pred. No. 5.5e+02;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 10;
Pred. No. 5.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 285.
Location/Qualifiers
1. .346
/organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 g
                                                                                                                                                                                                                                            A1019782
A1019782.1 GI:3234118
                                                                   76.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcagttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo."
1 95 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer [5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.4
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                    house mouse.
Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                          RESULT
AI019782
                                                                                                                                                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
```

```
Takifugu rubripes.
Takifugu rubripes.
Takifugu rubripes.
Takifugu rubripes.
Takifugu rubripes.
Takifugu rubripes.
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa: Chordata; Teleostei; Neoteleostei;
Acathhomorpha; Acathhopterygii; Teleostei; Euteleostei; Neoteleostei;
Acathhomorpha; Acathhopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
El (bases 1 to 611)
Elgar, G., Clark, M.; Smith, S., Meek, S., Warner, S., Umrania, Y.,
Williams, G. and Brenner, S.
Direct Submission
Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CBIO 1SB, UK. Email:
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                        GSS; genome survey sequence.
Takifugu rubripes.
Takifugu rubripes.
Takifugu rubripes
Takifugu rubripes
Takifugu rubripes
Takifugu rubripes
Takifugu rubripes
Actinopterygii: Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
I (bases I to 605)
I (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR0030058 611 bp DNA GSS . 25-JUN-19:
Fugu rubripes GSS sequence, clone 072H16aG6, genomic survey
FR0030063 605 bp DNA GSS 25-JUN-19:
Fugu rubripes GSS sequence, clone 072H16aE4, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One pass dye-terminator sequencing of cosmid cloned genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 13; Length 605;
Pred. No. 6.3e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .605
/organism="Takifugu rubripes"
/db_xref="taxon.31033"
/clone_lib="cosmid 072H16"
/clone="072H165E4"
a 147 c 173 g 132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
                                                                                                                                                              AL026432
AL026432.1 GI:3263775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL026427
AL026427.1 GI:3263770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.4%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 cgcagttctgtgaacatcga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 CCCAGTTTGTGAACATCGA 48
```

ç

```
Mus musculus
                                                                                                                                                                            æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11042159
                                                                                                                                                                          174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11076861
                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                              ထ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
AK006515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                      DNA GSS 16-FEB-2001
plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/note="Wector: PWD42nv; Purified genomic DNa from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                              Gaps
pass dye-terminator sequencing of cosmid cloned genomic
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0011108"
/clone_llb="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                          Length 611;
                                                                                                                                                    others
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308, Blomedical Polymers Research Bldg., 20
                                                                                                                                                  16
                                                                                                                                                                                                                  76.4%; Score 16.8; DB 13;
90.0%; Pred. No. 6.3e+02;
tive 0; Mismatches 2;
                                                                    /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_11b="cosmid 072H16"
/clone="072H16a6"
144 c 169 9 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                  ų
                                                                                                                                                                                                                                                                                                                                                                                                                AZ777336 613 bp DNA
2M0011108R Mouse 10kb plasmid UUGCIM
clone UUGC2M0011108 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 0011 row: I column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .613 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 613.
Location/Qualifiers
                                     Location/Qualifiers
                                                                                                                                                169 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain-"C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ777336.1 GI:12905813
                                                                                                                                                                                                                                                                                         1 cgcagttctgtgaacatcga 20
                                                                                                                                                                                                                                                                                                                         19 CCCAGTTTTGTGAACATCGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                     Local Similarity 90.0 es 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                        1. .611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
                    sednence.
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                              RESULT
AZ777336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                               ORIGIN
```

```
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb]ART29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptorent E. coli XL10-Gold (Stratagene) cells and selected for ampleillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1301)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
20499374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Shibata, K., Itoh, M., Aizawa, K., Kitsunai, T., Tashiro, H., Takiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watchiki, M., Yondeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Riken integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer ceasarch. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409, 685-690 (2001)
5 (Dases 1 to 1301)
Adachi,J., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakwa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,
Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (bases 1 to 1301)
The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK006515 1301 bp mRNA HTC 05-JUL-2001 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700029008, full insert sequence.
AK006515 GI:12839656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAP trapper.

Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1700029008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 13; Length E
Pred. No. 6.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1301)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 CTCAGTTCTGTGAATATCGA 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 cgcagttctgtgaacatcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 90.0°
Matches 18; Conservative
```

us-09-698-903b-14.rst

```
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA701011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                      human.
                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
AA701011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                   AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
     KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                      REFERENCE
                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                           Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Sano, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shibagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADVDVNHHLIPDTRPPFSRRLTSLVVCPLYISAAYHNLQCFRLLLQAGANPDFNCNGP
VNTQBFYRGSPGCVMDAVLRHGCEAAPVSLLVVERGANLNUVKWESLGPEARGRRKMDP
ELLQVFKEARSIPRTLLSLCRVNRALGKYRLHLVPXAAARPHKEVFAL"
345 c 318 g 313 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLRNLLQEESYRSRINEKSVWCCGWLPCTPLRIAATAGHGNCVDFLIRKGAEVDLVDV
KGQTALYVAVVNGHLESTEIILEAGADPNGSRHHRSTPVYHASRVGRDDILKALIRYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MGFGSSSAGPNLKEWLREQFCDHPLEHCDDTRLHDAAYVGDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AWUB6177 206 bp mRNA EST 14-OCT-1999 xc77ell.xl NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:2590316 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.4%; Score 16.8; DB 12; Length 1301; 90.0%; Pred. No. 7.3e+02; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
/db_xref="taxon:10090"
/db_xref="MGD:MGI:1902349"
/db_xref="MGD:MGI:1917320"
/clone="1700029008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/protein_id="BAB24628.1"
/db_xref="GI:12839657"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1301
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 GCAGTTCTGTGACCATCCAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW086177.1 GI:6041251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 gcagttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.4
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
AW086177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
```

```
Tumor Gene Index
Interport Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium, LINL
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming.

Non-directionally cloned. Size-selected on agarose gel, and carrent size 500 bp. Non-amplified library. " 24 c 24 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 234)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 206)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zg55d04.sl Soares_pineal_gland_N3HPG Homo sapiens cDNA_clone
IMAGE:397255 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 10; Length 206;
Pred. No. 8e+02;
); Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Ov32"
/clone_lib="NCI_CGAP_Ov32"
/tissue_type="papillary serous carcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .206
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA701011
AA701011.1 GI:2704176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.5%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 agttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 AGTICTGTGAACATIGAC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 270)
4 (Mases 1 to 270)
4 (Mases 1 to 270)
5 (Maffray, C., Behar, G., Bols, F., Bouchier, C., da Silva, C., Devignes, M. D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamm, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Rabaktchis, C. and Tessier, A.

Sebastiani-Rabaktchis, C. and Tessier, A.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: 40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F02043 270 bp mRNA EST 01-FEB-1995
HSCOMG102 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: generation.fr
Single read. removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: alc-Omg10
Seq primer: (-21)M13_universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.4; DB 10; Length 234;
Pred. No. 8.2e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                      89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="total brain"
/dev_stage="3 months old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .270
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-0mg10"
                                                                                                                                                                                                                                                                                                                                                 M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c-0mg10 3', mRNA sequence.
F02043
F02043.1 GI:645600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 agttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
COMMENT
                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F02043
```

à g

```
L (Uabes 1 LO 290)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),
Upublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Www-bio.llnl.gov/Dbptphage/finage.html
Seq primer: 40ml3 fwd. ET from Amersham
High quality sequence stop: 263.
Location/Qualifiers
/note="Organ: brain; Vector: lafmid BA, Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: a 38 c 39 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA569516 290 bp mRNA EST 25-AUG-1997 nf23e01.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:914616, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote—"Vector: pamplo; site_1: Not1; site_2: EcoRI; lst strand CDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor specific primer, and the resulting PCR product subcloned into pAMPl0 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not David Krizman, "Inharry was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 290)
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                Query Match

Query Match

A4.5%; Score 16.4; DB 11; Length 270;
Best Local Similarity 94.4%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:6606"
/clone="IMAGE:914616"
/clone_lib="NCI_CGAP_Fr1"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA569516.1 GI:2343496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AGTICTGTGAACATTGAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 agttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 a
                                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA569516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
AA569516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

DEFINITION

RESULT

g

F03921

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL MEDLINE

COMMENT

TITLE

FEATURES

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1394153"
/clone="IMAGE:1394153"
/clone="IMAGE:1394153"
/clone="IMAGE:1394153"
/clone="IMAGE:1394153"
/clone="IMAGE:1394153"
/lab_host="bold"
/lab_hos
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
AAB43570 304 bp mRNA EST 31-DEC-1998
aj54f09.si Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394153
3', mRNA sequence.
                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 304)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 335)
NCI-CSAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ow86c05.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:1653704 3', mRNA sequence.
AI084952
AI084952.1 GI:3423375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.5%; Score 16.4; DB 10; Length 304; 94.4%; Pred. No. 8.7e+02; tive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                      AA843570.1 GI:2930088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 agttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111111111111 111 26 AGTTCTGTGAACATTGAC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sonrce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                           DEFINITION
                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                             ACCESSION
                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI084952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 303)
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Walage-Samson, R., Pietu, G., Poullot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                         FO3921 303 bp mRNA EST 19-FEB-1995
HSC2DF112 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genexpress@genethon.fr
Single read. removed at sequence 5'end
Genexpress=lbrary_idt: C; Genexpress_sequence_idt: alc-2df11
Seq primer: (-21)M13.universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humain
Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                             ô
                                                                           Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_cref="taxon:9606"
/clone="to-ref11"
/clone=lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4; DB 11;
Pred. No. 8.6e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genethon Centre de recherche sur le Genome
1, rue de l'Internationale, BP60 91002 EVRY
Tel: 33169472800
                                                                     Score 16.4; DB 10;
Pred. No. 8.6e+02;
); Mismatches 1;
                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.5%;
94.4%;
                                                                     74.5%;
ilarity 94.4%;
Conservative
                                                                                                                                                                         F03921
F03921.1 GI:670548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genexpress-Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 agttctgtgaacatcgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AGTICTGTGAACATTGAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.5
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 33160778698
                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. R. Aca
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
```

ö

Gaps

ö

BASE COUNT ORIGIN

RESULT 14 AA843570

õ

Sequencing Center information can be

```
BASE COUNT
ORIGIN
 JOURNAL
COMMENT
          FEATURES
```

Search completed: February 25, 2002, 17:21:24 Job time: 16177 sec

ö

Gaps

ó

Score 16.4; DB 10; Length 335; Pred. No. 8.8e+02; 0; Mismatches 1; Indels 0;

Query Match 74.5%; Best Local Similarity 94.4%; Matches 17; Conservative (

à qq

```
February 25, 2002, 12:53:12 ; Search time 2331.3 Seconds (without alignments) 148.604 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                         1472140 seqs, 8248589755 residues
                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        US-09-698-903B-2
21
1 gtaacatagatgacaccgcgc 21
                                  OM nucleic - nucleic search, using sw model
                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_htgo_hum:*
em_htgo_inv:*
em_htgo_rod:*
em_htg_inv:*
em_htg_iv:*
em_htg_rod:*
em_htg_rod:*
                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                   9b_ba:*
9b_htg:*
9b_htg:*
9b_on:*
9b_ov:*
9b_pt:*
9b_pt:*
9b_pr:*
9b_pr:*
9b_sr:*
9b_sr:*
9b_vi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_or:*
em_ov:*
em_pat:*
em_ph:*
em_pl:*
em_ro:*
                                                                                                                                                                                                                                                                                                                                                                                                               em_fun:*
em_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_sy:*
em_un:*
em_v1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                 em_in:*
em_om:*
                                                                                                                                                                                                                                                            GenEmb1:*
                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                            Database :
                                                                                                                                                         Searched:
                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derlived by analysis of the total score distribution.

SUMMARIES

scrip	AX127749 Sequence AR152423 Sequence AR152423 Sequence AR152423 Sequence AR152429 Sequence AR152429 Sequence AR152429 Sequence AR152429 Sequence B01312 3' Untrans1 D25449 Rice genomi AJ007623 Agrobacte AJ007623 Agrobacte AJ007623 Agrobacte AJ007623 Agrobacte AJ007624 Agrobacte AJ007624 Agrobacte AJ007624 Agrobacte AJ007624 Agrobacte AJ007624 Agrobacte AJ08765 Sequence AX019188 Sequence AJ08795 Sequence AJ08795 Sequence AJ08795 Sequence AZ01239 Sequence AZ01239 Sequence AZ01239 Sequence AZ01239 Sequence AZ0176 Sequence AZ01775 Sequence AZ01776 Sequence AZ01777 Sequence AZ01777 Sequence AZ0177 Sequence AZ017 Sequence AZ0	<u>u</u>
ID	AX11277 AX112774 AX112704 AX1151059 AR1152421 AR1152421 AR1152421 AR1152421 AR1152421 AR1152421 AR1152421 AR16231 AX019416 AX019416 AX019416 AX019416 AX019416 AX019416 AX01923 AX019317	2145 6 AR019221 2256 8 AB003140 2215 6 AR104331 2319 6 AR118422 2319 6 AR118422 2319 DNA 2 from Patent W00131042. 1 GI:14134396 construct. construct. 1 sequence. 1 L0 21 1 nd 31042 - A 2 03 -MAY - 2001; 1 copposince N.V. (BE) Location/Qualifiers 1.Cotation/Qualifiers
DB	25 26 27 28 28 28 28 28 28 28 28 28 28 28 28 28	6 A A 6 A A 6 A A 6 A A 6 A A 6 A A 6 A A 6 A A 13439 A 13439 A 13439 A 142-A 5 S S i C a S i C a S
Length	22 4 5 6 6 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6	1. 2145 6 AR012 1.0 2356 8 AB00 2319 6 AR111 2.0 2319 6 AR111 2.0 2315 6 AR111 2.0 2315 6 AR111 2.1 Dp Dp 2.2 from Patent WO 3.1 GI:14134396 3.1 GI:14134396 3.1 GI:14134396 3.1 GONSTRUCT. 3.1 CONSTRUCT. 3.2 construct. 3.3 Construct. 3.4 GI:14134396 3.6 CONSTRUCT. 3.6 CONSTRUCT. 3.7 CONSTRUCT. 3.8 AND 0131042-A 2 03 3.8 COPSCIENCE N.V. 4.0 0131042-A 2 03 5.0 CONSTRUCT. 6.1 CONSTRUCT. 6.1 CONSTRUCT. 1. 21 7. CONSTRUCT. 7. CONST
Query Match		27749 27749
Score		
Result No.	00000000 000 00000000 000000 000000 0000	9 HO 8 H OK & 87

08-AUG-2001

õ

```
Unclassilteu.

1 (bases 1 to 249)
Mettler,I.J., Plaisted,D.C., Grier,S.L., Houghton,W. and Gardiner,M.
Inbred maize line R372H
Patent: US 6232533-A 8 15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 249)
Mettler,I.J., Plaisted,D.C., Grier,S.L., Houghton,W. and Gardiner,M.
Inbred maize line R660H
Patent: US 6232534-A 8 15-MAY-2001;
Location/Qualifiers
1. 249
                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 21; DB 6; Length 249; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 100.0%; Score 21; DB 6; Length 249; 1.1 Similarity 100.0%; Pred. No. 0.22; 21; Conservative 0; Mismatches 0; Indels
                                                                PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
                                                                                                                                                                                                                                                                                     85 t
                                                           AR152423 249 bp DNA
Sequence 8 from patent US 6232533.
AR152423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AR152432 249 bp DNA
Sequence 8 from patent US 6232534.
AR152432
AR152432.1 GI:15118482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR110597 261 bp DNA
Sequence 4 from patent US 6114608.
AR110597
AR110597.1 GI:12826873
                                                                                                                                                                                                                                                                      /organism="unknown"
1 38 c 47 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism≃"unknown"
. 38 c 47 q
                                                                                                      AR152423.1 GI:15118473
                                                                                                                                                                                                                                                                                                                                                                                           247 GTAACATAGATGACACCGCGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gtaacatagatgacaccgcgc 21
                                                                                                                                               Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                     79 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 a
                                                                                                                                 Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                      DEFINITION
                                RESULT 4
AR152423/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
AR152432/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
AR110597/C
LOCUS
                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                         REFERENCE
                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                 1 (Dases I to 249)
Mettler, I.J. Dietrich, P.S and Sinibaldi, R.M.
Nucleic acid construct comprising bacillus thuringiensis crylAb
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                               14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassined.
Unclassined.
Unclassined.
Unclassined.
Mettler,I.J., Plaisted,D.C., Grier,S.L., Houghton,W. and Gardiner,M.
Inbred maize line R412H
Patent: US 6229075-A 8 08-MAX-2001;
                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 21; DB 6; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 6; Length 249; 100.0%; Pred. No. 0.22; tive 0; Mismatches 0; Indels
                                                      100.0%; Score 21; DB 6; Length 21; 100.0%; Pred. No. 0.17; 0; Mismatches 0; Indels
                                                                                                                                                                                                               PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      ų
                                                                                                                                                                                                                                                                                                                                                                          Patent: US 6114608-A 8 05-SEP-2000;
Location/Qualifiers
1. .249
  m
                                                                                                                                                                                                         ARI10601 249 bp DNA
Sequence 8 from patent US 6114608.
ARI10601. GI:12826877
                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARISIOOO 249 bp DNA Sequence 8 from patent US 6229075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
38 c 47 g
    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
38 c 47 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 GTAACATAGATGACACCGCGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AR151000.1 GI:15115591
                                                                                                                          1 GTAACATAGATGACACCGCGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 GTAACATAGATGACACCGCGC 227
                                                                                                            1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gtaacatagatgacaccgcgc 21
  U
                                                                                   21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
 φ
                                                                                                                                                                                                                                                                                           Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
                                                      Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 21; Conserv
7 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 a
                                                                                                                                                                                                                                                                            Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
                                                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                             RESULT 2
AR110601/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
AR151000/c
LOCUS
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
```

BASE COUNT

ð

ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS

BASE COUNT ORIGIN

셤

TITLE JOURNAL

FEATURES

AUTHORS TITLE

REFERENCE

JOURNAL

FEATURES

ö

Gaps

ö

08-AUG-2001

ö

Gaps

; 0

14-FEB-2001

Gaps

ö

```
A01H5/00, A01H1/00, C12N1/20, C12N15/00//A01N65/00, C07K13/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1997
                                                                                                                                                                                                                                                                                                08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 261)
Mettler,I.J., Plaisted,D.C., Grier,S.L., Houghton,W. and Gardiner,M.
Inbred maize line R660H
Patent: US 623234-A 4 15-MAY-2001;
Location/Qualifiers
1. 261
                                              100.0%; Score 21; DB 6; Length 261; 100.0%; Pred. No. 0.22; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 6; Length 261; 100.0%; Pred. No. 0.22; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      792389, 27-MAR-1986 US 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E01312 280 bp DNA PAT 3' Untranslated region of nopalin synthetase gene. E01312. GI:2169571 JP 1987201527-A/4. unidentified unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Control | Cont
                                                                                                                                                                                                                                                                                                PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                             AR152428 261 bp DNA
Sequence 4 from patent US 6232534.
AR152428
AR152428.1 GI:15118478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strandedness: Single;
                                                                                                                                                                253 GTAACATAGATGACACCGCGC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        topology: Linear;
hypothetical: No;
anti-sense: No;
                                                                                                                                      1 gtaacatagatgacaccgcgc 21
                                                Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (C12N1/20,
PC C12R1:01);
CC strandedness
CC topology: Li
CC hypothetical
CC anti-sense:
FH Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 a
                                                                                                                                                                                                                                                                                                                                                                                                           Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                    RESULT 9
AR152428/c
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E01312/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Unclassified.

1 (bases 1 to 261)
Mettler,I.J, Dietrich,P.S and Sinibaldi,R.M.
Nucleic acid construct comprising bacillus thuringiensis crylAb
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 261)

Wettler,I.J., Plaisted,D.C., Grier,S.L., Houghton,W. and Gardiner,M.
Inbred maize line R372H
Patent: US 6232533-A 4 15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 261)
Mettler,I.J., Plaisted,D.C., Grier,S.L., Houghton,W. and Gardiner,M.
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 6; Length 261; 100.0%; Pred. No. 0.22; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB 6; Length 261;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                        Patent: US 6114608-A 4 05-SEP-2000, Location/Qualifiers 1.261 / Crganism="unknown" 83 a 41 c 50 g 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR150996 261 bp DNA
Sequence 4 from patent US 6229075.
AR150996.1 GI:15115587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR152419 261 bp DNA
Sequence 4 from patent US 6232533.
AR152419
AR152419.1 GI:15118469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taraince, maize line R412H
Patent: US 6229075-A 4 08-MA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 GTAACATGACACCGCGC 233
                                                                                                                                                                                                                                                                                                                                                                                      1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                             Ouery Match 100.0
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
AR150996/c
LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
AR152419/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                AUTHORS
                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                      ò
```

ö

Gaps

ö

ዋ

```
Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                               SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                              terminator
                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                            source
                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                            FEATURES
     ABA7623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA7624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-NOV-1993) to the DDBJ/EMBL/GenBank databases. Yuzo Minobe, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondal 2-1-2, Tsukuba, Ibaraki 305, Japan (E-mail:MINOBE@trcs0.riken.go.jp, Tel:0298-38-7441, 2059-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Enhartoideae; Oryzae; Oryza.
1 (bases 1 to 288)
Minobe,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of sequence tagged site from japonica rice Nipponbare as an RFLP marker Unpublished (1993) Submitted (1893) to DDBJ by:
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                             06-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                     Query Match 100.0%; Score 21; DB 6; Length 280; Best Local Similarity 100.0%; Pred. No. 0.23; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                       RICL429B 288 bp DNA STS
Rice genomic DNA, L429B, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 21; DB 11; Similarity 100.0%; Pred. No. 0.23; 21; Conservative 0; Mismatches 0;
                                                                                   ų
                                                                                                                                                                                                                                                                                                                                D25449.1 GI:436695
STS: Not I linking clone; RFLP; Rice.
Oryza sativa (strain:Nipponbare) DNA.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ب
                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dept. Rice Genome Research Program
              /A_signal >1. .<281.
Location/Qualifiers
1. .280
/organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .288
/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
                                                                   /db_xref="taxon:32644"
49 c 58 q
                                                                                  58 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 9
                                                                                                                                                                                                                 246 GTAACATAGATGACACCGCGC 226
                                                                                                                                                                                          1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 GTAACATAGATGACACCGCGC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phone: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
C
              polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROJECT - 'RGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yuzo Minobe
                                                                                  ಪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National
                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minobe, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Japnan
FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                         source
                                                                                                                                                                                                                                                                       RICL429B/c
LOCUS
                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                           à
                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

12

RESULT

```
ö
                                                                                                                                                                                                                                             1 (bases 1 to 31).

Hardegger, M.R., 380 and Herrmann, A.

Quantitative detection of the 35S promoter and the NOS terminator as 31ng quantitative empetitive PCR

Z. Lebensm.-Unters. -Forsch., A Eur. Food Res. Technol. 209, 83-87 (1999)
ABA7623 318 bp DNA BCT 18-FEB-2000
Agrobacterium tumefaciens nos terminator with artifical insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens.
Agrobacterium tumefaciens.
Agrobacterium tumefaciens.
Agrobacterium tumefaciens.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
1 (bases 1 to 358)
Hardegger,M.R., Brodmann,P. and Herrmann,A.
(unantitative detection of the 355 promoter and the NOS terminator using quantitative cmpetitive PCR
Z. Lebensm. Unters. -Forsch., A Bur. Food Res. Technol. 209, 83-87 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA7624 358 bp DNA BCT 18-FEB-2000
Agrobacterium tumefaciens nos terminator with artifical insert of
                                                                       AJ007623
AJ007623.1 GI:3319860
AJ007623.1 GI:3319860
nos gene; terminator
Agrobacterium tumefaciens.
Agrobacterium tumefaciens
Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 318)

Hardegger, M.R.

Direct Submissor, 2011

Submitted (03-JUL-1998) Hardegger M.R., Lebensmittel, Kantonales
Laboratorium Basel-Stadt, Kannenfeldstrasse 2, CH/4012 Basel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 358)

Hardegger, M. R.

Direct Submission

Submitted (03-JUL-1998) Hardegger M.R., Lebensmittel, Kantonales
Laboratorium Basel-Stadt, Kannenfeldstrasse 2, CH/4012 Basel,
SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 1; Length 318; llarity 100.0%; Pred. No. 0.23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .318 /organism="Agrobacterium tumefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Agrobacterium tumefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="nos"
/note="insert location 142-181"
64 c 55 g 97 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /plasmid="Ti"
/db_xref="taxon:358"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ007624
AJ007624.1 GI:3319861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="nos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
```

```
Search completed: February 25, 2002, 17:59:54 Job time: 18402 sec
                 terminator
BASE COUNT
ORIGIN
                                                                                                                                                   ŏ
                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic construct.

Synthetic construct
artificial sequence.

artificial sequence.

artificial sequence.

E 1 (bases 1 to 838)

S Lamberty, M., Hofmann, J., Bulet, P. and Brookhart, G.L.
Gene coding for heliomicine and use thereof
L Patent: WO 9953053-A 19 21-0cT-1999,
IAMBERTY MIREILLE (FR); HOFMANN JULES (FR); BULET PHILIPPE (FR);
RHONE POULENC AGROCHIMIE (FR); BROOKHART GARY LEE (US)

Location (Volganisme Synthetic construct")

/db xref="taxon:32630"
moter 7.532
                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-2000
                                                                                                                                                                                                                                                                                                                                 07-MAY-1999
          /db_xref="taxon:358"

1. 358

1. 358

1. 358

/gene="nos"

/gene="nos"

/note="insert location 142-221; direct repeat"

a 75 63 g 106 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 21; DB 6; Length 563; Best Local Similarity 100.0%; Pred. No. 0.25; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                            Ouery Match 100.0%; Score 21; DB 1; Length 358; Best Local Similarity 100.0%; Pred. No. 0.23; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 563)
Michiels, F. and Williams, M.
IMPROVED BARGTAR GENE
PATENT: WO 9810081-A 6 12-MAR-1998;
MICHIELS FRANK (BE)
LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX014764 838 bp DNA
Sequence 19 from Patent W09953053,
AX014764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
/db_xref="taxon:32644"
133 c 145 g 133
                                                                                                                                                                                                                                                                                                                    A/1436 563 bp DNA
Sequence 6 from Patent WO9810081.
A71436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX014764.1 GI:10041035
                                                                                                                                                                                                                       /plasmid="Ti"
                                                                                                                                                                                                                                                                                                                                                                         A71436.1 GI:4775049
                                                                                                                                                                                                                                                                                                                                                                                                     unidentified.
unidentified
unclassified.
                                                                                                       ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 a
                                                                                                      114
                                                            terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
AX014764/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                              LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                RESULT 14
A71436/c
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
Gaps
                                                                                                                                     ;
;
                                                                                                    6; Length 838;
                                                                                                100.0%; Score 21; DB 6; Length 83
100.0%; Pred. No. 0.26;
.ive 0; Mismatches 0; Indels
                                   233
                                 175 g
                                                                                                                                                                                       822 GTAACATAGATGACACCGCGC 802
                                                                                                                                                                   1 gtaacatagatgacaccgcgc 21
misc_structure 533..568
terminator 569..832
COUNT 296 a 134 c
                                                                                               Query Match
Best Local Similarity 100.0
Matches 21; Conservative
```

NOS terminator seq Tomato spotted wil Part of plasmid pL Vector plasmid pSI PMABI DNA sequence Plasmid pMJBI used Plasmid PMJBI ECOR

Nucleotide sequenc Nucleotide sequenc Nopaline synthase

AAT66536 AAX86467 AAC89659

nopaline

35S CaMV promoter-Sequence of chimer Tomato-tobacco end OBPILT sequence.

AAD01014 AAX60384 AAQ29293 AAQ21191 AAQ74261 AAQ57524

Expression cassett Nematode-responsiv

Arabidopsis thalia

AAT59713 AAX78852 AAV64071

Nucleotide sequenc Oleosin-hirudin fu Raspberry drul gen Oligonucleotide #1 Arabidopsis thalia

Nucleotide sequenc T-DNA sequence of

AAF86440 AAV64070 AAV54016 AAX08450 AAC68664

AAV44279 **AAT86752** AAD01016 AAD01018

AAV44284

Agrobacterium tume

Expression cassett Expression cassett DNA construct codi Oleosin-protein A Raspberry drul gen PND3018 repression PND3008 activation

SAG12-1 promoter,

```
\begin{array}{c} \texttt{11} \\ \texttt{11} \\ \texttt{12} \\ \texttt{13} \\ \texttt{14} \\ \texttt{15} \\ \texttt{16} \\ \texttt{16} \\ \texttt{17} \\ \texttt{17} \\ \texttt{17} \\ \texttt{17} \\ \texttt{18} \\
      (without alignments)
25.126 Million cell updates/sec
                                                                                                                                                                                                                            ; Search time 716.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                **Single-State Ageneseq/geneseqn/NA1980.DAT:**

**SIDSZ/gcgdata/geneseq/geneseqn/NA1981.DAT:**

**SIDSZ/gcgdata/geneseq/geneseqn/NA1982.DAT:**

**SIDSZ/gcgdata/geneseq/geneseqn/NA1982.DAT:**

**SIDSZ/gcgdata/geneseq/geneseqn/NA1989.DAT:**

**SIDSZ/gcgdata/geneseq/geneseqn/NA1989.DAT:**

**SIDSZ/gcgdata/geneseq/geneseqn/NA1989.DAT:**

**SIDSZ/gcgdata/geneseq/geneseqn/NA1989.DAT:**

**SIDSZ/gcgdata/geneseq/geneseqn/NA1999.DAT:**

**SIDSZ/gcgdata/geneseq/genese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1861242
                           4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930621 seqs, 428662619 residues
                           GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                            February 25, 2002, 13:39:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                               1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                               US-09-698-903B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                             1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08
08
                                                                                                                                                         OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum |
Maximum |
                                                                                                                                                                                                                            Run on:
```

RESULT

ALIGNMENTS

AAT86755 AAD11579 AAD11578 AAT42919

Plasmid pTC0113; transgenic Brassica plant; transformation event; male-sterility gene; tobacco; PCR primer; probe; ss. PCR primer MDB355 to amplify a fragment of pTCO113. Chimeric - Bacillus amyloliquefaciens. Chimeric - Nicotiana tabacum. ž BP. 26-OCT-2000; 2000WO-EP10680. (AVET) AVENTIS CROPSCIENCE 99US-0430497 De Beuckeleer M; 21 AAD06991 standard; DNA; WPI; 2001-300517/31. WO200131042-A2 29-OCT-1999; 06-AUG-2001 03-MAY-2001. Weston B, AAD06991; AAD06991

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

by of

Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -

Agrobacterium nos Nucleotide sequenc Nopaline synthetas

3'UTR of nopaline Nos terminator nuc Nucleotide sequenc Nucleotide sequenc

AAD06367 AAF89834 AAF89833 AAZ51175 AAZ98689 AAZ51653 AAA75461 AAAD06309

21112222222

249 249 249 253 253 251 261 261

1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0

0000000000

Nucleotide sequenc Nopaline synthetas 3' nopaline syntha

PCR primer MDB355 Nucleotide sequenc

AAD06991 AAA75465 AAD06313

DB

Length

Query Match

Score

Š. Result

Description

Tue Feb 26

à g

```
AAD06313/c
                  8888888
                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35S promoter; alcohol dehydrogenase intron; nopaline synthase terminator; insecticidal Cry lAb protein toxin; transgenic plant; fungal toxin; aflatoxin; baculovirus; Lepidopteran insect; glufosinate; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a nopaline synthase terminator, which is used to create the construct of the invention. The specification describes a nucleic acid construct, comprising an expression cassette containing a cauliflower mosaic virus (CaMV) 35S promoter, a maize alcohol dehydrogenase intron, a DNA molecule encoding an insecticidal cry lAb protein toxin and a NOS (nopaline synthase) terminator in operable linkage. The nucleic acid constructs are useful for producing transgenic plants such as maize, wheat, barley, sorghum and rice. Preferably, maize plants such as field corn, sweet corn, white
                                                      The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant and harvesting the hybrid seed from the primer MDB355 used to amplify a fragment of plasmid pTCO113. The primer ls also used as a probe. The amplified fragment comprises coding region of barnase from
                                                                                                                                                                                                                                                                                                                                                    Bacillus amyloliquefaciens and promoter region of the anther-specific gone TA29 from Micotlana tabacum. This primer corresponds to position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel DNA construct comprising an expression cassette having a functional constitutive promoter, operably linked to a maize alcohol dehydrogenase intron, gene encoding Cry 1Ab protein and a terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of a nopaline synthase terminator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB Pred. No. 0.05; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sinibaldi RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Column 25-26; 24pp; English.
Claim 1; Page 26; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                             pTC0113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA75465 standard; DNA; 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0042426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0109808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mettler IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative
                                                                                                                                                                                                                                                                                                                                                                         gone TA29 from Nicoti
2667-2687 of plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-586487/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dietrich PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS6114608-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA75465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
AAA75465/c
```

```
The present invention relates to transgenic maize seed for hybrid maize plant production, comprising an expression cassette linked operably with constitutive Cauliflower mosalc virus (CaMV) 35s promoter, an alcohol dehydrogenase intron, a DNA encoding an insecticidal Bacillus thuringiaensis (B1 Crybab toxin and a nopaline synthetase (NOS) terminator. The transgenic maize seed is used in maize cultivation methods for propagating hybrid maize seeds and for growing hybrid maize plants. The maize is also used in foodstuffs preparation for animal or human consumption. The inbred maize line NP948 of the invention has creduced level of fungal toxins, hence suitable for foodstuffs preparation. Yield is high. Plant health is improved due to reduced stalk rot. Grain test weight is high and the rate of grain dry down is reduced. The present sequence is nopaline synthetase terminator of phosphinothricin acetyl transferase (PAT) gene expression cassette.
                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nopaline synthetase;
corn, silage corn or popcorn are produced. The transgenic maize is used for preparing food materials with reduced levels of fungal toxins, e.g. aflatoxins. The transgenic plants express a baculovirus crystal protein toxin, which is effective against Lepidopteran insects at relatively high levels and further provides resistance to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel transgenic maize seed for hybrid maize plant production, comprising expression cassette linked operably with CAMV 35S promoter, alcohol dehydrogenase intron, insecticidal CrylAb toxin gene or NOS terminator
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic maize; expression cassette; 358 promoter; nopaline synthet NOS terminator; alcohol dehydrogenase intron; CrylAb toxin; foodstuffs preparation; phosphinothricin acetyl transferase; PAT; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nopaline synthetase terminator of Pat gene expression cassette.
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                        100.0%; Score 21; DB 21; Length 249; 100.0%; Pred. No. 0.085;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                              ;
0
                                                                                                                                             Sequence 249 BP; 79 A; 38 C; 47 G; 85 T; 0 other;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Column 25-26; 24pp; English.
                                                                                                     non-selective herbicide glufosinate.
                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                              AAD06313 standard; DNA; 249 BP
                                                                                                                                                                                                                                                                                                              247 GTAACATAGATGACACCGCGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                á
                                                                                                                                                                                                                                                                                      1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0336627.
96US-0716836.
97US-0818573.
98US-0042426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0291238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mettler IJ, Krier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-327266/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS6222104-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1994;
22-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1998;
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD06313;
```

m

X S

à g

```
AAF89824 standard; DNA; 249 BP
                                                                                                                                            AAF89824;
                                                                                               AAF89824/c
   à
                             셤
                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to maize inbred line R412H which comprises a nucleic acid construct with two cassettes, which are transcribed in the same direction. The expression cassette comprises a Cauliflower mosaic virus (CaMV) 35S constitutive promoter operably linked to a maize alcohol dehydrogenase intron, a DNA sequence of a gene encoding a Bacillus thuringiensis (Bt) crystal 1Ab (Crylab) toxin or phosphinothricin acetyl transferase (PAT) and a nopaline synthase (NoS) terminator functional in plants. The maize inbred line R412H is useful for producing corn with reduced levels of toxins (e.g. the fungal materials for human or animal consumption, e.g. sweet corn for packaging or fresh use as human food, or grain or silage made from field corn. The present sequence is 3' NoS terminator of Pat gene expression cassette, which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                 Maize; expression cassette; 35S promoter; alcohol dehydrogenase intron; crystal 1Ab; Cry1Ab toxin; phosphinothricin acetyl transferase; PAT; nopaline synthase; NOS terminator; aflatoxin; food material; sweet corn; human food; Adhl-1S; ds.
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New maize (Zea mays) inbred line R412H (ATCC 209675), useful for producing corn with reduced levels of toxins (e.g. the fungal aflatoxin) and for preparing food materials for human or animal
                                                                                                                                                                                                                                                                                                                   3' nopaline synthase terminator of Pat gene expression cassette.
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gardiner M;
                                              Score 21; DB 22; Length 249;
Pred. No. 0.085;
                                                                               Indels
                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houghton W,
Sequence 249 BP; 79 A; 38 C; 47 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 249 BP; 79 A; 38 C; 47 G; 85 T; 0 other;
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Column 21-22; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grier SL,
                                                                             ö
                                                                                                                                                                                                                     AAD06367 standard; DNA; 249 BP
                                                                                                                            100.0%;
                                                                                                           1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0330760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0109808
98US-0042426
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mettler IJ, Plaisted DC,
                                       Query Match
Best Local Similarity 100.
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-342708/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6229075-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1999;
                                                                                                                                                                                                                                                                                    10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consumption
                                                                                                                                                                                                                                                    AAD06367;
                                                                                                                                                                                       RESULT 4
```

```
The specification describes seed and plants of maize inbred line R660H.

The seed comprises two cassettes. The first cassette comprises a cauliflower mosaic virus (cawn) 355 constitutive promoter operably linked to a maize alcohol dehydrogenase intron, a DNA sequence of a gene encoding a CrylAb protein, and a terminator functional in plants. The second cassette comprises a Cawn 355 promoter which functions in plant cells operably linked to a maize plohol dehydrogenase intron, a DNA sequence of a gene encoding for phosphinothricin acetyl transferase, and sequence of a gene encoding for phosphinothricin acetyl transferase, and the same direction and the nucleic acid construct is incorporated into the same direction and the nucleic acid construct is incorporated into the seed's genome on chromosome 8 and near position 117, between markers in the same directs since they express the protein CrylAb in high levels, and also exhibit resistance to non-selective herbicide glufosinate. The transgenic maize is suited for preparation of food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                Maize; inbred line R660H; 35S constitutive promoter; CrylAb protein; alcohol dehydrogenase; phosphinothricin acetyl transferase; chromosome 8; 21B3; UMC150a; Lepidoptera; glufosinate; sweet corn; fungal toxin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        materials for human or animal consumption e.g. sweet corn for packaging or fresh use as a human food, or grain or sliage made from field corn, containing reduced levels of fungal toxins. The present sequence represents a 3' terminator from nopaline synthetase, which is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel seed of maize inbred line R372H, useful for producing inbred maize plants which on crossing with other different maize plants produce hybrid maize seeds and plants having resistance to insects and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                      Nucleotide sequence of a 3' terminator from nopaline synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grier SL, Houghton W, Gardiner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 22; Length 2
100.0%; Pred. No. 0.085;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 249 BP; 79 A; 38 C; 47 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produce transgenic maize of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Column 19-21; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0328473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0109808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0042426
23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mettler IJ, Plaisted DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-335091/35
                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                      US6232533-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

1 gtaacatagatgacaccgcgc 21

δ

ö

Gaps

; 0

Query Match 100.0%; Score 21; DB 22; Length 249; Best Local Similarity 100.0%; Pred. No. 0.085; Matches 21; Conservative 0; Mismatches 0; Indels

AAZ51175 standard; DNA; 253 BP.

RESULT 7

(first entry)

06-JUN-2000

AAZ51175;

8

```
The specification describes seed and plants of maize inbred line R660H.
The seed comprises two cassettes. The first cassette comprises a cauliflower measile virus (CaWY) 355 constitutive promoter operably linked to a maize alcohol dehydrogenase intron, a DNA sequence of a gene encoding a CrylAb protein, and a terminator functional in plants. The second cassette comprises a CaNW 355 promoter which functions in plant second cassette comprises a CaW 355 promoter which functions in plant sequence of a gene encoding for phosphinothricin acetyl transferase, and a terminator functional in plant. The two cassettes are transferase, and the same direction and the nucleic acid construct is incorporated into the seed's genome on chromosome 8 and near position 117, between markers 1813 and UMC150a. The maize plants and seeds exhibit resistance to lepidopteran insects since they express the protein CrylAb in high levels, and also exhibit resistance to non-selective herbicide glufosinate. The transgenic maize is sulted for preparation of food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize; inbred line R660H; 35S constitutive promoter; CrylAb protein; alcohol dehydrogenase; phosphinothricin acetyl transferase; chromosome 8; 21B3; UMC150a; Lepidoptera; glufosinate; sweet corn; fungal toxin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                materials for human or animal consumption e.g. sweet corn for packaging or fresh use as a human food, or grain or sliage made from fleal corn, containing reduced levels of fungal toxins. The present sequence represents a 3 terminator from nopaline synthetase, which is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel seed of maize inbred line R660H, useful for producing inbred maize plants which on crossing with other different maize plants produce hybrid maize seeds and plants having resistance to insects and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a 3' terminator from nopaline synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gardiner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houghton W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 249 BP; 79 A; 38 C; 47 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    produce transgenic maize of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grier SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Column 23-24; 24pp; English.
                                                                                                                                                                                                                                                  AAF89833 standard; DNA; 249 BP
247 GTAACATAGATGACACCGCGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0330737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0818573,
98US-0042426,
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mettler IJ, Plaisted DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-335092/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6232534-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erbicide
                                                                                                                                                                                                                                                                                                                                AAF89833;
                                                                                                                                                                                                      AAF89833/C
```

```
combinations of introns and 5' and 3' non-translated genetic elements.

The vectors comprise a promoter sequence, a 5' non-translated leader sequence (isolated from genes of wheat fructose-1,6-bisphosphatase (bp), chlorophyll a/b binding protein, heat shock protein (hsp), peroxidase, rice beta-tubulin (btub) or amylase), an intron (isolated from genes of rice actin, sucrose synthase, phenylanine ammonia lyase, amylase or maize hsp), a DNA coding sequence and a 3' non-translated terminator sequence (isolated from genes of wheat hsp, ubiquitin, fbp, rice glutelin, lactate dehydrogenase or btub). They are used to produce transgenic plants showing resistance to microbial and fungal disease, herbicide tolerance, increased yield and nutritional enhancement. The the T-DNA in Agrobacterium tumefaciens. It is used in the construction of recombinant expression vector pMON19433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses recombinant plant expression vectors, which comprise
                                                                                                           Recombinant expression vector; intron; 5' non-translated leader; fructose-1,6-bisphosphatase; fbp; chlorophyll a/b binding protein; heat shock protein; hsp; peroxidase; beter-tubulin; btub; amylase; actin; sucrose synthase; phenylalanine ammonia lyase; ubiquitin; glutelin; 3' non-translated terminator; lactate dehydrogenase; transgenic plant; resistance; herbicide tolerance; T-DNA; nopaline synthase; 3' nos; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel plants expression vectors, containing combinations of plant introns and non-translated 5' and 3' elements, used for introducing agronomically desirable traits into plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                          3'UTR of nopaline synthase gene from Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 21; Length 253; 100.0%; Pred. No. 0.085; 1ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 253 BP; 81 A; 38 C; 48 G; 86 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 90; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ98689 standard; DNA; 254 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GTAACATAGATGACACCGCGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                         99WO-US19102
                                                                                                                                                                                                                                                                                                                                                                                                              98US-0097150
                                                                                                                                                                                                                                                       Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Santino CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-237660/20.
                                                                                                                                                                                                                                                                                            WO200011200-A2
                                                                                                                                                                                                                                                                                                                                                                       18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conner TW,
                                                                                                                                                                                                                                                                                                                                    02-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ98689/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
ð
```

ö

Gaps

ö

0; Indels

Mismatches

ö

Query Match
Best Local Similarity 100.
Matches 21; Conservative

21

247 GTAACATAGATGACACCGCGC 227

αqα

ð

gtaacatagatgacaccgcgc

100.0%; Score 21; DB 22; Length 249; 100.0%; Pred. No. 0.085;

S

us-09-698-903b-2.rng

```
Agrobacterium nos transcription termination and polyadenylation sequence.
                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis; delta-endotoxin; Cry3B; Bt toxin; insect pest; crystal protein; Coleopteran; expression cassette; transgenic plant; insecticide; nos; nopaline synthase gene; transcription termination; polyadenylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is a Agrobacterium tumefaciens nopaline synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (nos) transcription termination and polyadenylation sequence which is used in an expression cassette that provides improved expression of Bacillus thuringiensis delta-endotoxin, Cry3B or Cry3B variant proteins, in transgenic plants e.g. malze. Transgenic plants expressing higher levels of Cry3B proteins exhibit increased insecticidal activity against Coleopteran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel expression cassettes which express Bacillus thuringlensis Cry3 delta-endotoxin portion which is toxic to coleopteran insect pests, useful for producing transgenic plants with improved insecticidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 158; 171pp; English.
    AAZ51653 standard; DNA; 257 BP
                                                                                                                                                             21-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-246568/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200011185-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Romano CP;
                                                                              AA251653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA75461/
    THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the Nos terminator sequence. The terminator can be used in the production of barley endoxylanase plasmids. The invention relates to a nucleotide sequence encoding the barley endoxylanase content of relates to a nucleotide sequence encoding the barley endoxylanase is relates to a nucleotide sequence encoding the barley endoxylanase is protein. The endoxylanase has a molecular weight of 62kD. Endoxylanase is a xylan-degrading enzyme produced by plants for example during germination of cereal grain. Xylan is a constituent of plant cell walls, and its degradation is very important in commercial processes that use cereal grains, such as beer brewing. A nucleic acid construct comprising the endoxylanase nucleotide sequence, a heterologous signal peptide and a plant can be enhanced through transformation of the plant using the barley endoxylanase nucleotide sequence. The barley endoxylanase concleotide sequence. The barley endoxylanase confoxylanase in plant cells, permitting enhanced degradation of cell wall sylan is particularly important in fermentation processes that rely on fermentable sugars and nutrients provided by degradation of cereal grains. Barley malt, wheat malt, and person or cell and the plant wall are ordered grains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cereal grain malt are primary sources of required nutrients in the brewing process. When brewing beer, the amount of starch and protein degradation during malting and mashing greatly impacts the quality of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid sequence encoding barley endoxylanase, for expressing enhanced amounts of endoxylanase in plant cells, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                            Endoxylanase; barley; beer fermentation; barley malt; wheat malt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 21; Length 254; 100.0%; Pred. No. 0.085; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Den Dool RTM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 254 BP; 81 A; 38 C; 49 G; 86 T; 0 other;
                                                                                                                                                                                                                                                                             cereal grain malt; mashing; Nos terminator; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lok F, Caspers MPM, Cameron-Mills V, Va
Sinjorgo CMC, Van Zeijl-van der Valk MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Column 45-46; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CASP/) CASPERS M P M.
(VALK/) VAN ZEIJL-VAN DER VALK M J.
                                                                                                                                                             Nos terminator nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0869696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97us-0869696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAN DEN DOOL R T M. CAMERON-MILLS V.
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SINJORGO C M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fermentation of beer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-205236/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    final product.
                                                                              06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                          US6031155-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                       Synthetic.
AAZ98689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SINJ/)
(CASP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAME/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOKF/)
```

99WO-US18883 98US-0097150

```
ö
                                                                                                                                                                                                                                                                                                                                                    35S promoter; alcohol dehydrogenase intron; nopaline synthase terminator; insecticidal Cry lAb protein toxin; transgenic plant; fungal toxin; aflatoxin; baculovirus; Lepidopteran insect; glufosinate; ds.
                                                                              Gaps
                                                                              ;
                                             Length 257;
                                      100.0%; Score 21; DB 21; Length 2
100.0%; Pred. No. 0.085;
on Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of a nopaline synthase terminator.
Sequence 257 BP; 81 A; 41 C; 48 G; 87 T; 0 other;
                                                                                                                                                                                                                         AAA75461 standard; DNA; 261 BP
                                                                                                                               251 GTAACATAGATGACACCGCGC 231
                                                                                                              7
                                                                                                              1 gtaacatagatgacaccgcgc
                                                                                                                                                                                                                                                                                        15-JAN-2001 (first entry)
                                                                              21; Conservative
                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                          AAA75461;
```

247 GTAACATAGATGACACCGCGC 227

a ö

RESULT 9 AAZ51653/c

1 gtaacatagatgacaccgcgc

21

```
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                            The present sequence represents a nopaline synthase terminator, which is used to create the construct of the invention. The specification describes a nucleic acid construct, comprising an expression cassette containing a cauliflower mosalcutt, comprising an expression cassette alcohol dehydrogenase intron, a DNA molecule encoding an insecticidal operable protein toxin and a NOS (nopaline synthase) terminator in producing transgence plants such as maize, wheat, barley, sorghum and producing transgence plants such as field constructs are useful for producing transgence plants such as field corn, sweet corn, white corn, slidge corn or popocon are produced. The transgenic maize is used for preparing food materials with reduced levels of fungal toxins, e.g. aflatoxins. The transgenic plants express a baculovirus crystal protein toxin, which is a effective against lepidopteran insects at
                                                                                                                                                         Novel DNA construct comprising an expression cassette having a functional constitutive promoter, operably linked to a maize alcohol dehydrogenase intron, gene encoding Cry 1Ab protein and a terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nopaline synthetase terminator of Bt kurstaki expression cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic maize; expression cassette; 35s promoter; alcohol dehydrogenase intron; CrylAb toxin; nopaline synthetase; NOS terminator; foodstuffs preparation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                   further provides resistance to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 21; Length 261; 100.0%; Pred. No. 0.086; 1ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 261 BP; 83 A; 41 C; 50 G; 87 T; 0 other;
                                                                                                                 Mettler IJ, Sinibaldi RM;
                                                                                                                                                                                                       Claim 1; Column 21-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            non-selective herbicide glufosinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 GTAACATAGATGACACCGCGC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0336627.
96US-0716836.
97US-0818573.
                                             98US-0042426
                                                                    97US-0109808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06309 standard; DNA; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0291238
                                                                                                                                                                                                                                                                                                                                                                              relatively high levels and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
                                                                                         (NOVS ) NOVARTIS AG.
                                                                                                                                      WPI; 2000-586487/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                Metrich PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1994;
22-AUG-1996;
14-MAR-1997;
                                            13-MAR-1998;
                                                                    14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS6222104-B1
US6114608-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-APR-1999;
                       05-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD06309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1:
AAD06309/0
윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
The present invention relates to transgenic maize seed for hybrid maize blant production, comprising an expression cassette linked operably with constitutive Cauliflower mosaic virus (CaMV) 35S promoter, an alcohol dehydrogenase intro, a DNA encoding an insecticidal bacilius thuringiensis (Bt) CrylAb toxin and a nopaline synthetase (NoS) terminator. The transgenic maize seed is used in maize cultivation methods for propagating hybrid maize seeds and for growing hybrid maize human consumption. The inbred maize line NP948 of the invention has reduced level of fungal toxins, hence suitable for foodstuffs preparation. Yield is high, Plant health is improved due to reduced stalk rot. Grain test weight is high and the rate of grain dry down is reduced. The present sequence is nopaline synthetase terminator of Bt kurstaxi expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize; expression cassette; 35S promoter; alcohol dehydrogenase intron; crystal lAb; CrylAb toxin; phosphinothricin acetyl transferase; PAT; nopaline synthase; NOS terminator; aflatoxin; food material; sweet corn; human food; Adhl-15; ds.
                                                                                                                                                                                                                                                                         Novel transgenic maize seed for hybrid maize plant production, comprising expression cassette linked operably with CAMV 35S promoter, alcohol dehydrogenase intron, insecticidal CrylAb toxin gene or NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3' nopaline synthase terminator of Btk gene expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mettler IJ, Plaisted DC, Grier SL, Houghton W, Gardiner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 21; DB 22; Length 261; Best Local Similarity 100.0%; Pred. No. 0.086; Matches 21; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 261 BP; 83 A; 41 C; 50 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Column 21-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 GTAACATAGATGACACGGGG 233
                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gtaacatagatgacaccgcgc 21
                                                                                                                                        Mies
98US-0042426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD06363 standard; DNA; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0330760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0109808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-2001 (first entry)
                                                                                                                                    Mettler IJ, Krier M,
                                                                                                                                                                                                         WPI; 2001-327266/34.
                                                                    (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-342708/36.
13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6229075-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-1997;
13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                  terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD06363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD06363/c
```

```
The specification describes seed and plants of maize inbred line R660H.

The seed comprises two cassettes. The first cassette comprises a cauliflower measalc virus (CaW) 355 constitutive promoter operably linked to a maize alcohol dehydrogenase intron, a DNA sequence of a gene encoding a CrylAb protein, and a terminator functional in plants. The second cassette comprises a CaMV 355 promoter which functions in plant second cassette comprises a CaMV 355 promoter which functions in plant cappably linked to a maize alcohol dehydrogenase intron, a DNA sequence of a gene encoding for phosphinothricin acetyl transferase, and a terminator functional in plant. The two cassettes are transferibed in the same direction and the nucleic acid construct is incorporated into the seed's genome on chromosome 8 and near position 117, between markers 1813 and UNC150a. The maize plants and seeds exhibit resistance to lepidopteran insects since they express the protein CrylAb in high levels, and also exhibit resistance to non-selective herbicide capparation of food
                                                                                                                                                                                                                                                                                materials for human or animal consumption e.g. sweet corn for packaging or fresh use as a human food, or grain or sliage made from field corn, containing reduced levels of fungal toxins. The present sequence represents a 3 terminator from nopaline synthetase, which is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize; inbred line R660H; 35S constitutive promoter; CrylAb protein; alcohol dehydrogenase; phosphinothricin acetyl transferase; chromosome 21B3; UMC150a; Lepidoptera; glufosinate; sweet corn; fungal toxin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes seed and plants of maize inbred line R660H. The seed comprises two cassettes. The first cassette comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        maize plants which on crossing with other different maize plants produce hybrid maize seeds and plants having resistance to insects and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel seed of maize inbred line R660H, useful for producing inbred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a 3' terminator from nopaline synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton W,
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 261 BP; 83 A; 41 C; 50 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 22;
Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          produce transgenic maize of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grier SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Column 19-20; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF89829 standard; DNA; 261 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 GTAACATAGATGACACCGCGC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0330737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0818573
98US-0042426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gtaacatagatgacaccgcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mettler IJ, Plaisted
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-335092/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-1997;
13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6232534-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF89829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                              The present invention relates to maize inbred line R412H which comprises a nucleic acid construct with two cassettes, which are transcribed in the same direction. The expression cassette comprises a Caulillower mosaic virus (CaMV) 35S constitutive promoter operably linked to a maize alcohol dehydrogenase intron, a DNA sequence of a gene encoding a pacillus thuringiensis (H) crystal IAD (CrylAD) toxin or phosphinothricin acetyl transferase (PAT) and a nopaline synthase (NOS) terminator functional in plants. The maize inbred line R412H is useful for producing corn with reduced levels of toxins (e.g. the fungal aflatoxin). This maize line is particularly useful for preparing food materials for human or animal consumption, e.g. sweet corn for corn. The present sequence is 3' NOS terminator of Btk expression cassette, which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
chromosome 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel seed of maize inbred line R372H, useful for producing inbred maize plants which on crossing with other different maize plants produce hybrid maize seeds and plants having resistance to insects and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize; inbred line R660H; 35S constitutive promoter; CrylAb protein; alcohol dehydrogenase; phosphinothricin acetyl transferase; chromosome z1B3; UMC150a; Lepidoptera; glufosinate; sweet corn; fungal toxin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                        New maize (Zea mays) inbred line R412H (ATCC 209675), useful for producing corn with reduced levels of toxins (e.g. the fungal aflatoxin) and for preparing food materials for human or animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of a 3' terminator from nopaline synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gardiner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton W,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 261 BP; 83 A; 41 C; 50 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB Pred. No. 0.08; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grier SL,
                                                                                                                  Claim 2; Column 19-20; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Column 19-20; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 GTAACATAGATGACACCGCGC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF89820 standard; DNA; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0328473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0109808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0042426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      рС,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plaisted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-335091/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6232533-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mettler IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-1997;
                                                                                consumption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF89820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF89820/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

Gaps

ö

Length 261; 0; Indels 8

Gardiner M;

us-09-698-903b-2.rng

```
cauliflower mosalc virus (CaMV) 35S constitutive promoter operably linked to a maize alcohol dehydrogenase intron, a DNA sequence of a gene encoding a Crylab protein, and a terminator functional in plants. The second cassette comprises a CaMV 35S promoter which functions in plant cells operably linked to a maize alcohol dehydrogenase intron, a DNA sequence of a gene encoding for phosphinothricin accepty transferase, and a terminator functional in plant. The two cassettes are transcribed in the same direction and the nucleic acid construct is incorporated incompleted and a terminator functional in plant. The two cassettes are transcribed in the same direction and the nucleic acid construct is incorporated incompleted and a terminator functional in plant. The two cassettes are transcribed in the same direction and the nucleic acid construct is incorporated incompleted and a same acid and near position 17, between markers in pladopteran insects since they express the protein Crylab in high landing and also exhibit resistance to non-selective herbicide quiosant also exhibit resistance to non-selective herbicide quiosant and an animal consumption e.g. sweet corn for packaging or fresh use as a human food, or grafin or silage made from field corn, containing reduced levels of fungal toxins. The present sequence represents a 3' terminator from nopaline synthetase, which is used to produce transgenic maize of the invention.
                355555555555555555555<del>x</del>8
```

Sequence 261 BP; 83 A; 41 C; 50 G; 87 T; 0 other;

```
ö
                          Gaps
                          ö
  22; Length 261;
                         0; Indels
 100.0%; Score 21; DB 22;
100.0%; Pred. No. 0.086;
tive 0; Mismatches (
                                                           253 GTAACATAGATGACACCGCGC 233
                                               21
                                                gtaacatagatgacaccgcgc
          Local Similaricy
hes 21; Conservative
Query Match
Best Local S
Matches 21
                                               à
                                                                   q
```

Transgenic plant; selectable marker; carotenoid; pigment; nopaline synthase; phytoene synthase; plasmid pEr0203; ss Nopaline synthase 3'nontranslated region. AAT66536 standard; DNA; 263 BP (first entry) 22-JUL-1997 AAT66536; AAT66536/c ID AAT60

Agrobacterium sp. WO9714807-A1 29-MAR-1996; 24-APR-1997

(SEMI-) SEMINIS VEGATABLES Trulson AJ; Braun CJ,

95US-0543608

16-OCT-1995;

WPI; 1997-245122/22.

Visual identification of transgenic plant material - from production of carotenoid pigment encoded by cassette containing Erwinia phytoene synthase gene, useful for selecting material for The 3' nontranslated region (AAT66536) of the nopaline synthase gene can be cloned from binary vector pBI121 (Clontech). It contains sequences that in plant cells result in the termination of transcription and additional sequences that when transcribed into RNA result in the addition of a poly-A tract to the 3' end of the RNA. It is a preferred component of pETO203 (ATCC 97282), a Example; Page 37; 62pp; English. regeneration

plastid targetting signal (AAT66535), a phytoene synthase gene (AAT66535), a phytoene synthase gene (AAT66535) fused to the Erwinia herbicola Transgenic plant cells and tissues are identified by the appearance of orange colour. binary vector used in a method for the visual identification of transgenic plant material. The vector includes an expression cassette comprising the tomato E0 promoter (see also AAT66533), 88888888888

Sequence 263 BP; 83 A; 42 C; 49 G; 89 T; 0 other;

Gaps ö Query Match
100.0%; Score 21; DB 18; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 21; Conservative 0; Mismatches 0; Indels (

ö

257 GTAACATAGATGACACCGCGC 237 1 gtaacatagatgacaccgcgc 21 á

Search completed: February 25, 2002, 18:17:19 Job time: 16677 sec

Н

Appli Appli Appli Appli Appli Appli Appli Appli

Sequence 3, As Sequence 14, 2 Sequence 9, As Sequence 17, 7

Sequence

Sequence 17, Sequence 17, Sequence 17, Sequence 4,

Sequence

OM nucleic

Run on:

Sequence:

```
S-09-042-42-07.
S-09-04-07.
Patent No. 6114608
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA CONStruct Containing Bacillus
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6114608artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 21; DB 3; Length 249; 100.0%; Pred. No. 0.047; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWN APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
CLASSIFICATION: 800
ATTONNEY/AGENT INPORMATION:
NAME: HOXIE, Thomas
REGISTRATION NUMBER: 32,993
US-08-592-936B-20

US-09-111-573-20

US-08-419-075-26

US-08-485-139-3

US-08-485-139-3

US-08-750-357-3

US-08-750-357-3

US-08-750-357-3

US-08-750-357-3

US-08-750-357-3

US-08-750-357-3

US-08-750-357-3

US-08-810-720-9

US-08-811-17

US-08-811-17

US-09-025-583-17

US-09-064-121-4
                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: No. 6114608arti
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 249 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: NOS Terminator
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
S
       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07901
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-042-426-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-042-426-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
       0 0 0 0 0
                                                                                                                                                000
                                                                                                                                                                                                              O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                  ; Search time 301.6 Seconds
(without alignments)
15.769 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 8, Apsequence 18, A sequence 14, Apsequence 4, Apsequence 4, Apsequence 3, Apsequence 3, Apsequence 3, Apsequence 6, Apsequence 17, Assequence 11, Assequence 16, Apsequence 16, Apsequence 16, Apsequence 9, Apsequence 9, Apsequence 16, Apsequence 9, Apsequence 16, Apsequence 16, Apsequence 16, Apsequence 9, Appequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1
Sequence 1
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-291-238-8
US-09-310-760-8
US-09-310-760-8
US-09-310-737-8
US-09-310-737-8
US-09-291-238-4
US-09-291-238-4
US-09-310-760-4
US-09-310-760-4
US-09-310-760-4
US-09-310-75-4
US-08-064-121-3
US-08-064-121-3
US-08-064-18-015-3
US-09-084-889-3
US-09-084-889-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-592-936B-16
                                                                                                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-966-187-17
US-08-525-507-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-026-673-1
US-08-452-267-2
US-09-123-644-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-475-427-9
US-07-842-165-9
                                                                                                                                                                                                                                                                                                            351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                      GenCore version
Copyright (c) 1993 - 2000
                                                                                                                      February 25, 2002, 12:55:52
                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                           1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                                              US-09-698-903B-2
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
1287
1287
1287
1287
1859
1863
1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
```

Minimum DB Maximum DB

Database

Searched:

ö

Gaps

ö

```
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-330-760-8/C
US-09-330-760-8/C
; Sequence 8, Application US/09330760
; Patent No. 6222075
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INFORMATION:
; TITLE OF INFORMERS: 11
; CORRESPONDENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
                                                                                                                  Sequence 8, Application US/09291238
Patent No. 6222104
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DNA CONSTRUCT Containing Bacillus
NUMBER OF ESQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6222104artis Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 21; DB 4; Length 249; 100.0%; Pred. No. 0.047; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWY APPLICATION DATR:
APPLICATION NUMBER: US/09/291,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFCATION:
PRIOR APPLICATION:
PROOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: MARCH 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOXIE, Thomas
REGISTRATION NUMBER: 32,933
REFERENCE/DOOKET NUMBER: 135/1
TELEFONNICATION INFORMATION:
TELEFONNICATION INFORMATION:
TELEFONS: (919) 541-8619
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 base pairs
TYPE: nucleic acid
STRENEDNESS: double
247 GTAACATAGATGACACGCGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 GTAACATAGATGACACCGCGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 graecatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOS Terminator
                                                                                                                                                                                                                                                    ARE,
STREET: 564
STREET: Stammit
CITY: Summit
"TE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                  RESULT 2
US-09-291-238-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-291-238-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-328-473-8/C
Sequence 8, Application US/09328473
Sequence 8, Application US/09328473
Patent No. 623233
GENERAL INFORMATION:
TITLE OF INVENTION: DNA CONStruct Containing Bacillus
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 21; DB 4; Length 249; Best Local Similarity 100.0%; Pred. No. 0.047; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: No. 622253artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSTENCEATION:
CLASSTENCEATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOXA'A, THOMAS
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPRAM: (919) 541-8614
TELEPRAM: (919) 541-8614
TELEPRAM: (919) 541-8619
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (GENOMIC)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: MARCH 13, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 GTAACATAGATGACACCGCGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: NOS Terminator
New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-09-330-20-8n
```

Gaps

ö

```
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 21; DB 3; Length 254; Best Local Similarity 100.0%; Pred. No. 0.047; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                  Query Match 100.0%; Score 21; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTE: V.50.1

COMPUTER: Floppy disk
COMPOTER: Floppy disk
COMPOTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/ANS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HOXIG: Thomas
REGISTRATION NUMBER: 32,993
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INC. 00.211.2)

GENERAL INFORMATION:

APPLICANT: Cameron-Mills, Verena
APPLICANT: Lok, Finn
APPLICANT: Sinjorgo, Catharina Maria Cornelia
APPLICANT: Van Den Dool, Ronald Tako Marinus
APPLICANT: Van Zeijl-Van Der Valk, Maria Joanna
TITLE OF INVEWIION: ARABINOXYLAN DEGRADATION
FILE REFERENCE: 11225.010501
CURRENT APPLICATION NUMBER: US/08/869,696C
CURRENT FILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08869696C Patent No. 6031155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-042-426-4/c
; Sequence 4, Application US/09042426
; Setent No. 6114608
; GENERAL INFORMATION:
                                                                                                                                                                                           NOS Terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: synthetic US-08-869-696-18
                                                                                                                                                                                                                                                                                                                               US-08-869-696-18/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07901
            ; CLONE: N
US-09-330-737-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 18
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                             οy
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09330737
Patent No. 632534
CENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA CONStruct Containing Bacillus
NUMBER OF SEQUENCES: 11
CONTRESPONDENCE ADDRESS:
ADDRESSEE: No. 6232334artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 21; DB 4; Length 249; Best Local Similarity 100.0%; Pred. No. 0.047; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07901

ZIP: 07901

CMEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDER:
ILING DATE: Warch 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOXIE, Thomas
REGISTRATION NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEFONE: (919) 541-8614
TELEFAX: (919) 541-8614
TENGRATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTER:STICS:
LENGRH: 249 base pairs
TYPE: nucleic acid
                                                    135/1
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
FELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 Base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 GTAACATAGATGACACCGCGC 227
                                                                                                                                                                                                                                           STRANGE TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO NAWT-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SERNE: NO
                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: NOS Terminator
US-09-328-473-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-330-737-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ö

Gaps

Gaps

ö

```
NS-09-330-760-4/c

Sequence 4, Application US/09330760

Fatent No. 6229075

GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi

TILLE OF INVENTION: DNA CONStruct Containing Bacillus

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6229075artis Corporation

TITLE 564 Morris Avenue
                                                             Query Match 100.0%; Score 21; DB 4; Length 261; Best Local Similarity 100.0%; Pred. No. 0.047; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 4; Length 261; Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; 22
100.0%; Pred. No. 0.0
+ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: MARCH 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOxie, Thomas
REGISTRATION NUMBER: 32,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09328473
Patent No. 6232533
GENERAL INFORMATION:
                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 GTAACATAGATGACACCGCGC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ILMEDIATE SOURCE:
CLONE: NOS terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Summit
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-328-473-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-330-760-4
                                                                                                                                                                                       g
                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-291-238-4/C
US-09-291-238-4/C
Sequence 4, Application US/09291238
Fetcht No. 6222104
Fetcht No. 6222104
TITLE OF INVENTION:
MAPPLICANT: Irvin' J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DAA Construct Containing Bacillus
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6222104artis Corporation
STREET: 564 Morits Avenue
STREET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 21; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOXIE, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8614
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                        NOS terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOS terminator
                                                                                                                                                                                                                                                          ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07901
                                                                                                                                                                                                                                                                                                      ; CLONE: P
US-09-042-426-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

ö

Gaps

```
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILICATION NUMBER: US/09/042,426
FILICATION NUMBER: 1398
ATTORNEY AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 135/1
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
FELEPAX: (919) 541-864
TELEFAX: (919) 541-869
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDENNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 GTAACATAGATGACACGGGG 233
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHEAT.
ANTI-SERNE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.C
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-330-737-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA CONSTRUCT CONTAINING Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 65232533artis Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 21; DB 4; Length 261; Best Local Similarity 100.0%; Pred. No. 0.047; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                            ZIP: 07901

ZIP: 07901

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOXIG, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DCOKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHOME: (919) 541-8614
TELEFAX: (919) 541-8619
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: NOS terminator
                                                                                              STREET: 564 MOLLIS
CITY: Summit
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-328-473-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-08-064-121-3/C
US-08-064-121-3/C
Sequence 3, Application US/08064121
Patent No. 5641664
GENERAL INFORMATION:
APPLICANT: COBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STRATE: Virialia
COUNTY: United States
IPP 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIAN
COMPUTER: PATENTIN Felease #1.0, Version #1.25
SOFTWARE: PATENTIN NUMBER: US/08/04/121
FILING DATE: 24-MAY-1993
CLASSIFFCATION NUMBER: EP 90403332.1
FILING DATE: 23-MAY-1993
CRASIFFCATION NUMBER: EP 91401888.2
FILING DATE: 33-MOY-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: OB-JUL-1991
ATTORNEY ABENTE CATION: ROW-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: OB-JUL-1991
ATTORNEY ABENTE CATION: ROW-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: CTANEY. SHAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 4; Length 261; 100.0%; Pred. No. 0.047; tive 0; Mismatches 0; Indels
APPLICATION NUMBER: US/09/330,737
```

```
APPLICATION NUMBER: EP 91401888.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1251 GTAACATAGATGACACCGCGC 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: fragment of pTTM8 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -
LOCATION: 1..545
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-475-975-3/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                   /label= PTA29
/note= "Promoter from the TA29 gene of Nicotiana
tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCCATION: 882..1287

COTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene "
US-08-064-121-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: 546..881
COTHER INFORMATION: /label- barnase
OTHER INFORMATION: /note- "coding sequence of barnase gene"
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Bost Local Similarity 100.0%; Score 21; DB 1; Length 1287;
Bost Local Similarity 100.0%; Pred. No. 0.055;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-478-015-3/C

Sequence 3, Application US/08478015
Sequence 3, Application US/08478015
Sequence 3, Application US/08478015
Sequence 3, Application US/08478015
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: WONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: No. 0. box 1404
CITY: Alexandria
STREET: Virginia
STREET: United States
ZIP: 22313-1404
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILDE
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,015
FLIING DATE: 07-JUN-1995
PRIOR APPLICATION NAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DAIRS:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1287 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: fragment of pTTM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gtaacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                       NAME/KEY: - LOCATION: 1.545
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
/label- PTA29 /note= "Promoter from the TA29 gene of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: 546.881
OTHER INFORMATION: /label= barnase
OTHER INFORMATION: /note= "coding sequence of barnase gene"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 21; DB 1; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08475975

Sequence 3, Application US/08475975

Patent No. 6002070

GENERAL INFORMATION:
APPLICANT: D'HALLIN, Kathleen
APPLICANT: COBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE SISS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
FILING DATE: 08-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
FILING DATE: 23-JUN-1993
ATTORNEY AGENT INFORMATION:
NAME: MCGOWAN: MAIOCIM K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1287 base pairs
LENGTH: 1287 base pairs
TOPPLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
```

```
/label= PTA29
/note= "Promoter from the TA29 gene of Nicotiana
tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COCATION: 882..1287
CTHER INFORMATION: /label= 3'nos
CTHER INFORMATION: /note= "3' regulatory sequence containing the
CTHER INFORMATION: polyadenylation site derived from Agrobacterium
CTHER INFORMATION: T-DNA nopaline synthase gene "
US-09-084-889-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 546..881
OTHER INFORMATION: /label= barnase
OTHER INFORMATION: /note= "coding sequence of barnase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 21; DB 3; Length 1287; 100.0%; Pred. No. 0.055; tive 0; Mismatches 0; Indels (
                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/084,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPLICATION WIMBER: EP 91401888.2
FILING DATE: 08-ULL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 25, 2002, 18:05:08 Job time: 18556 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1251 GTAACATAGATGACACCGCGC 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGINAL SOURCE:
ORGANISM: fragment of pTTM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gtaacatagatgacaccgcgc 21
                                               : Virginia
RY: United States
22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: - 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: 1.545
LOCATION: 1.545
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: - 546..881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
        CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= PTA29
/note= "Promoter from the TA29 gene of Nicotiana
tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 546..881
OTHER INFORMATION: /label= barnase
OTHER INFORMATION: /note= "coding sequence of barnase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 21; DB 3; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09084889
Fatent No. 6074877
GENERAL INFORMATION:
APPLICANT: GOBEL, Elke
ITLE OF INVENTION: PROCESS FOR TRANSFORMING
ITLE OF INVENTION: MONCCTYLEDONOUS PLANTS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSER: ADDRESS:
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08 08/064,121
FILING DATE: 24-MAY-1993
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 23-NOV-1991
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-UUL-1991
ATTORNEY, AGENT INFORMATION:
REGISTRANCE, DOCKET NUMBER: 36,113
REFERRENCE, DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATIO
                                  APPLICATION NUMBER: US/08/475,975
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: fragment of pTTM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -..545
LOCATION: 1..545
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-084-889-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
```

Gaps

Perfect score:

Title:

Run on:

Scoring table: Sequence:

Searched:

Database

4 6 7 10 11 11 12

Result o S

000

```
Oryza sativa.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

Ehrhartoideae; Oryzae; Oryza.

Ehrhartoideae; Oryzae; Oryza.

Enthartoideae; Oryzae;

Enthartoideae;

Enthartoi
AW940028 GH01164.3
BGG32393 GD726676
AA3539059 EST68007
BB383808 BB383808
AA36137 EST70766
A1081942 CZ81901.x
BEL10822 UT-R-BS1-
BIO13588 CM4-ET023
N71737 Yw52911.r1
R58895 G4243 Fetal
BE710208 IL3-HT061
AV617102 AV617102
AV617102 AV617102
AV617103 AV617103
AV52895 G4243 Fetal
BE732064 G02012817
BF342064 G02012817
BF342064 G02012817
BF342064 G02012817
BG705748 G02668984
AW853029 RC1-CT024
BG705748 G02668984
BG705748 G02668984
BG705748 G02668984
BG705748 G02668984
BG705748 G02668984
BG705748 G02668984
BG70548 G026681995
BG717694 G02450930
BG717694 G024188
BG717694 G024188
BG717694 G0241188
BG711199 G02681963
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ363458 887 bp DNA GSS 16-DEC-1999
nbxb0059A08f CUGI Rice BAC Library Oryza sativa genomic clone
nbxb0059A08f, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nbxb0059A08f"
                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                             AW607872
BG705748
AW853029
                                                                                                                                                                                                                                                                                                          BE409302
BG325494
BG701119
AL546504
BG716798
                                                                                                                                                           AW652485
AV725000
                                                                                                                          AV617102
AV617103
                                                                                                                                                                                                                                                               BG702664
BG422864
BG714597
BG747014
                                                                                                                                                                                 AL121482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ363458
AQ363458.2 GI:6583332
  1. .887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa.
 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
AQ363458/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
  AQ363458 nbxb0059A
AU114795 AU114795
BE104658 G01647679
AL141149 Anopheles
BB143973 BB143973
BB244247 BB244247
AV008164 AV008164
AV684098 AY084098
AL094023 Arabidops
AI09780 GM9125.5
AZ029768 RPCI-23-3
BE038757 AB06D07 A
                                                                          February 25, 2002, 12:51:47; Search time 8261.74 Seconds (without alignments) 27.314 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                               22703874
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                       11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ363458
AU114795
BF104658
CNS01EY4
BB143973
BB244247
AV008164
AV684098
CNS00WTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1109780
A2029768
BE038757
                                                                                                                                               1 gtaacatagatgacaccgcgc 21
                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                    IDENTITY_NUC Gaport 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_gss_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_htc:*
gb_gss:*
em_gss_fun:*
em_gss_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
                                                                                                                    US-09-698-903B-2
21
                                                                                                                                                                                                                                                     length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_gss_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                    em_estin:
em_estin:
em_estom:*
em_estp1:*
em_estba:*
em_estro:*
em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                                                                                                                                                                                                                                                                                                             em_estfun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est1:*
gb_est2:*
                                                                                                                                                                                                                                                                                                                                  EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.8
82.9
82.9
82.9
882.9
880.0
880.0
880.0
                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.8
17.4
17.4
17.4
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.8
16.8
16.8
16.8
16.8
```

Length 300;

```
mRNA sequence.
BF104658
BF104658.1 GI:10887184
  82.9%;
94.7%;
                                                                                                                                   148 GTAACATAGATGCCACCGC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 TAACATAGATGACGCCGCG 582
                                                                                          1 gtaacatagatgacaccgc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 taacatagatgacaccgcg 20
    Query Match 82.9
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199
                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                        BF104658/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
CNS01EY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                 g
                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
           //Issue_type="Load Rice and Library"
//Issue_type="Load Rice and Library"
//Issue_type="Load Rice and Library"
//Index="Vector: pealoabcil; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=4) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991. The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36 864 clones with an average insert size
of 128.5 Kp providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases I to 300)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU114795 300 bp mRNA EST 19-OCT-2000 AU114795 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone yk728e10 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:6239"
/clone="yk728e10"
/clone_llb="unpublished oligo-capped cDNA llbrary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.8; DB 13; Length 887;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A complementary view of the C. elegans genome Unpublished (2000)

    300
    organism="Caenorhabditis elegans"

/clone_lib~"CUGI Rice BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex~"Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="varied"
49 c 66 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU114795
AU114795.1 GI:10928362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
AU114795/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
```

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAba:14011"
/clone=lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/tissue_type="embryonal carcinoma"
/tissue_type="embryonal carcinoma"
/tissue_type="embryonal carcinoma"
/lab_host="Dil08 (T1 phage-resistant)"
/hote="Organ: testis: Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCGAGGGGGCGCAATG-GT(30)BN-3'
(where B = A, C; or G and N = A, C, G or T). Average
insert size 1.75 kb (range 0.9-4.0 kb): 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 833)
S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.AG.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Location/Qualifiers
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSOlEY4 936 bp DNA GSS 30-MAY-2001
Anopheles gambiae GSS T7 end of clone 03E09 of NotreDamel library
from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                       BF104658 833 bp mRNA EST 19-OCT-2000 601647679R1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4041811 3',
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 833;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Score 17.4; DB 10;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.9%; Score 17.4; DB 11;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
```

m

```
Email: genome-reségsc.riken.go.jp,
URL:http://genome-reségsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.P., Nishiyama.Y., Westover.A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y.,
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
                         Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
aboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.0%; Sc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex-"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB244247.1 GI:8936993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 taacatagatgacaccg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 TAACATAGATGACACCG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.0
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB244247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. Konno, H., Alzawa, K., Akahlra, S., Akiyama, J., Arakawa, T., Carninci, P., Enbuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Kai, C., Kawal, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, J., Kai, C., Kawal, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsun, Y., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakal, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takaki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Suzuki, H., Watanabe, S., Yamamura, T., Toya, T., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Rikish Mouse ESTS (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 215)
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscoppe in collaboration with the Laboratory of Biochem. and Blol. Molec. of Insects, Institut
                                                                                                                Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Anopheles.
1 (bases 1 to 936)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB143973 215 bp mRNA EST 28-JUN-2000
BB143973 RIKEN full-length enriched, adult female vagina Mus
musculus cDNA clone 9930023C03 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                    - Web : www.genoscope.cns.fr)
2 (bases 1 to 936)
Roth.C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.4; DB 13;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="03E09"
/clone_lib="NotreDame1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 g
                                                                                              African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "end : T7
  genomic survey sequence.
                    AL141149
AL141149.1 GI:6999267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB143973.1 GI:8798910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.9%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 aacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 AACATAGAAGACACCGCGC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.7;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                          Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                         SOURCE
                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB143973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
```

```
ö
                                                                                                                                                                                                             /tissue_type="vagina"
/dev_stage="adult"
/lab_host="bullo"
/lab_host="bullo"
/lab_host="bullo"
/note="site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
GAGAGAGAAGGAICCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB244247 277 bp mRNA EST 06-JUL-2000
BB244247 RIKEN full-length enriched, 7 days neonate cerebellum Mus
musculus CDNA clone A730001C13 3', mRNA sequence.
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Location/Qualifiers
                                                                                                                         /clone_lib="RIKEN full-length enriched, adult female vagina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17; DB 10; Length 215;
Pred. No. 2.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                     /organism="Mus musculus"
                                                                                                          /db_xref="taxon:10090"
/clone="9930023C03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 g
```

Length 277;

ORGANISM

REFERENCE

JOURNAL

```
81.0%; Score 17; DB 10; I
100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="18-day embryo"
32 c 45 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gtaacatagatgacaccgcg 20
                                                                                                           2 taacatagatgacaccg 18
                                                                                                                                      65 TAACATAGATGACACCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0°
Best Local Similarity 90.0°
Matches 18; Conservative
                                                        17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                Best_Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN
          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                         RESULT
AV008164
                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV684098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                           g
                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                Manimalia, bulleta; Nobellia; Scillogiaeni; Muridae; Murinae; Mus., 10 (Dases 1 to 277)

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Etwida, S., Fikunishi, Y., Hara, A., Hayatan, N.,
Hirozane, T., Horii, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyoswa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Supahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya,
Y., Yano, K., Yasuishi, A., Yokota, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
KIKEN Mouse ESTS (Konno, H., et al.)
Lupublished (2000)
Contact: Yoshihide Hayashizaki, Y.
Contact: Yoshihide Hayashizaki
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carnindi.P., Nishiyama.Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsundi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anote-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKB. Division of Experimental Animal Research in Riken Contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAGAGGAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], CDNA WAS
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci.P. and Hayashizaki.Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 277
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A730001C13"
/clone=lib="RIKEN full-length enriched, 7 days neonate cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="cerebellum"
/dev_stage="7 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ಫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
```

source

FEATURES

BASE COUNT ORIGIN

```
Tel: 81-298-36-9145

Fax: 81-298-36-9198

Bmail: genome-resettc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S. A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S. A. 95(7):345-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acaninoi, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shabata, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Namamura, T., Yokota, T., Yoshino, M., Rike, Mouse Ests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV684098 379 bp mRNA EST 25-SEP-2000 AV684098 GKC Homo sapiens cDNA clone GKCBQG09 5', mRNA sequence. AV684098
                                                                                                                                                                                                                                                                  AV008164 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1110008H08, mRNA sequence.
AV008164 EST 25-AUG-1999
AV008164
EST 25-AUG-1999
C5008164
AV008164.1 GI:4785151
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="1110008H08"
/clone_lib="Mus musculus 18-day embryo C57BL/6J"
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 232;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 16.8; DB 10; 90.0%; Pred. No. 3.1e+02; iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
ACCESSION
```

S

ö

Gaps ö

Length 542; Indels

```
A1109780 23-APR-2001 68109.25 5prime GF Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH09125 5 similar to CG16504: Fban0016904 located on: 3R 85E13-85E13;: 04/10/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Buteryota; Neotera: Endopteryota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophila.

1 (bases 1 to 594)

1 (bases 1 to 594)

1 arvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,

Iewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project

Unpublished (2001)

On Aug 26, 1998 this sequence version replaced gi:3478104.

Other_ESTS: GH90125. 3prime
                                                                                                                                                          Score 16.8; DB 13;
Pred. No. 3.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                   139
    /db_xref="taxon:3702"
/clone_lib="TAMU"
/clone="T12G21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                   б
                                                       : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI109780
AI109780.2 GI:13757702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 TGACATAGATGACACCCCGC 292
                                                                                                                                                                                                                                                            518 GTAACATAGATTACACGGCG 537
                                                                                                                                                            80.0%;
90.0%;
                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 taacatagatgacaccgcgc 21
                                                             /note="end
                                                                                                                                                                                                                                          1 gtaacatagatgacaccgcg
                                                                                 88
C
                                                                                                                                                        Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly.
                                                                                   205 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                          AI109780
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                         Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 379)
Wu,T., Olan,D., Huang,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,
Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSOOWTL 542 bp DNA GSS 28-JUN-1999
Arabidopsis thaliana genome survey sequence T7 end of BAC T12G21 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic AL094023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 542)
Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P.,
Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: xho!"
                                                                                                                                                                                                                                              Uniputization (2007)
Contact: Zecound (2007)
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%; Score 16.8; DB 10; Length 379; 90.0%; Pred. No. 3.6e+02; 1.ve 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ىد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="GKCBQG09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="GKC
  AV684098.1 GI:10285961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 TCACATAGATGACACCGCCC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL094023.1 GI:5295177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 taacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 542)
Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 90.0
hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ø
                                          human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 18
                                      SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                               TITLE
JOURNAL
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNSOOWTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
ö
                                                                                                                                                                                                                                                                                                         /clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5" - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid CDNAs were directly ligated into
Email: http://www.fruitfly.org/EST, estéfruitfly.berkeley.edu
hit genomic AB003684: arm:3R [5513047,5732625]
estimated-cyto:85E6-85F2: 04/10/2001
Plate: GH.91 row. C column: 1
High quality sequence stop: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 16.8; DB 10; Length 594; 90.0%; Pred. No. 4e+02; 1ve 0; Mismatches 2; Indels 0
                                                                                                                                                                                                1. .594
/organism="Drosophila melanogaster"
/db_xref="taxon:727"
/clone="GH09125"
```

```
15 (Dases 1 to 710)
16 Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C., Scara, G., Wheeler, M. and Zepeda, G. R.

17 Functional Genomics of Plant Stress Tolerance
18 Inctional Genomics of Plant Stress Tolerance
19 Inchalowski, C.B.
10 Inversity of Arizona
19 Scara, G., Meest room 513, Tucson, AZ 85721, USA
19 Tel: 520-621-7982
19 Fax: 520-621-7982
19 Fax: 520-621-7982
10 Fax: 520-621-1697
11 Fax: 520-621-1697
12 Fax: 520-621-1697
13 Fax: 520-621-1697
14 Email: chm@u.arizona.edu
An open reading frame exists.
10 Location/Qualifiers
thale cress.
Arabidopsis thaliana
Bukaryots; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed.
Plate: GH.11 row: F column: 4
High quality sequence stop: 795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophila.

1 (bases 1 to 826)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Enewis,S. and Rubin,G.M.
BDGP/HIMI Drosophila EST Project
Unpublished (2001)
Other_ESTS: GH01164.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW940028 826 bp mRNA EST 19-APR-2001 GH01164.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH01164 3, mRNA sequence.
AW940028 GI:8115482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 16.8; DB 10; 90.0%; Pred. No. 4.3e+02; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
/clone_lib="AB"
/tlssue_type="leaves, seedlings"
/dev_stage="2-3 weeks"
/note="200mM NaC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ىد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 GTAACAAGATAACACCGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gtaacatagatgacaccgcg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 80.0 Best Local Similarity 90.0 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 a
                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                              REFERENCE
                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW940028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                           Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 662)
2 kao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Uppublished (1999)
Other_GSSs: RPCI-23-349G17.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Madical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI wethylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
136 c 175 g 170 t lothers
                                                                     AZ029768 662 bp DNA GSS 25-FEB-2000
RPCI-23-349G17.TV RPCI-23 Mus musculus genomic clone RPCI-23-349G17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhaottor.org

Elmail: szhaottor.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE038757 710 bp mRNA EST 07-JUN-2000 AB06507 AB Arabidopsis thaliana cDNA 5' similar to dna-binding protein, mRNA sequence.
BE038757 GI:8333878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 80.0%; Score 16.8; DB 13; Length 662; Similarity 90.0%; Pred. No. 4.2e+02; 18; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .__ccation/Qualifiers
1. .662
/organism="Mus musculus"
/strain="C57BL/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xrefe"taxon:10090"
/clone="RPCI-23-349G17"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                   , DNA sequence.
AZ029768
AZ029768.1 GI:7105152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 TAAGATAGATGACAGCGC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 taacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
BE038757
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
                  RESULT 1:
AZ029768
LOCUS
                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
```

7

```
96026280
Contact: Kerlavage, AR
                                                           487 TAACATAGATGACACTGCAC 506
                             taacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.1%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 taacatagatgacaccgc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                              RESULT 15
AA359059/c
                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                             a
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                ò
                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                 /note="Organ: head; Vector: pOT2; Site_1: EcoR1; Site_2: Arbor; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid CDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov

Tissue Procurement: ArC.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intraural Sequencing Center

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM1732 row: h column: 20

High quality sequence stop: 649.

Location/Qualifiers

1. 910

/Organism="Homo sapiens"
//Loranism="Homo sapiens"
//
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 910)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG823293 910 bp mRNA EST 22-MAY-2001
602728676F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4866115 5'
MRNA sequence.
BG823293
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                         /clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev stage==adult"
/lab_host="DH5 - alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                          Length 826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 16.8; DB 10;
ilarity 90.0%; Pred. No. 4.5e+02;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 11;
Pred. No. 4.6e+02;
0; Mismatches 2;
                                                   /clone="GH01164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG823293.1 GI:14170880
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 TGACATAGATGACACCCCGC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 taacatagatgacaccgcgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
hes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG823293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
Mannatory Continues, Catalling, Hourings, Hours, London, Landon, Landon, Landon, R. Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.W., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shirley, R., Small, R.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Benail, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Benail, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Dimke, D., Fenrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wei, Y.E., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Xhor" 74 c 61 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
AA359059 245 bp mRNA EST 21-APR-1997 EST68007 Fetal lung II Homo sapiens CDNA 5' end similar to similar to peripheral myelin protein 22, mRNA sequence. AA359059, GI:2011376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.4; DB 10; Length 245;
Pred. No. 5e+02;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="ATCC (inhost):163151"
/db_xref="taxon:9606"
/clone_lib="Fetal lung II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="fetus, 19 wks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 TCACATAGATGACACCGC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

ö

Gaps

ö

Indels

Search completed: February 25, 2002, 17:20:51 Job time: 16144 sec

A08065 Synthetic n A10061 N. tabacum (AX17241 Sequence A60108 Sequence 1 A76915 Sequence 1

```
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 21)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing same Patent: WO 0131042-A 3 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer MLD008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX127750 21 bp DNA
Sequence 3 from Patent WO0131042.
AX127750
                                                                                                                                                                                  XLU70985
AC012256
AC012254
AC013374
AC013820
AC01505
AC024941
AC024941
AC02777
AC06273
AC160273
AC160273
AF195033
AF195033
AF195033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF195038
AF195039
AF264053
DENENVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DENENVC
                                                                   A10061
AX172441
A60108
A76915
AR098307
AX172440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX127750.1 GI:14134397
             Length DB
                                                                                                                                                                                                                                                                                                                                                                       149710
179183
167409
179510
                                                                                                                                                                                                                                                                                  195516
207856
4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1485
1485
1485
1485
1485
                                                                                                                                                                                                                                                       39443
                                                                                                                                                                                                                                                                                                                                            159934
182942
                                                                                                                                                                                                                                                                                                                             123016
                                      Match
 Query
             Score
                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX127750
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
              Š
                                                                                                                                                                                                                                                                                                        υ
                                                                                                                                                                                                                                                                                                                                            000000000000000000000000
                                                                                         February 25, 2002, 17:59:54; search time 2331.3 Seconds (without alignments) 148.604 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                   2944280
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                       1472140 segs, 8248589755 residues
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 - nucleic search, using sw model
                                                                                                                                                                                  1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_vi:*
em_vico_hum:*
em_htgo_inv:*
em_htgo_inv:*
em_htg_hum:*
em_htg_hum:*
em_htg_hum:*
em_htg_tod:*
                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                                       US-09-698-903B-3
                                                                                                                                                                                                                                                                                                                                                                                                                             gb_ba:*
gb_ni:*
gb_on:*
gb_on:*
gb_on:*
gb_pl:*
gb_pl:*
gb_pl:*
gb_pl:*
gb_rr:*
gb_rr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_pat:*
em_ph:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_pl:*
em_ro:*
em_sts:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_ov:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_sy:*
                                                                                                                                                                                                                                                                                                                                                                                                                  GenEmbl:*
```

sed

Minimum DB Maximum DB

Database

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

AK17240 Sequence 1
AK17240 Sequence
AX17240 Sequence
X52283 Tobacco ant
U70985 Xenopus lae
AC022563 Homo sapi
AC013374 Homo sapi
AC013820 Homo sapi
AC013820 Homo sapi
AC013820 Homo sapi
AC07878 Homo sapi
AC07878 Homo sapi
AC078778 Homo sapi

Dengue viru

15-MAY-2001

SUMMARIES

```
artificial sequence.

1 (bases 1 to 4832)

6 Both, G. and de Beuckeleer, M.

Hybrid winter oilseed rape and methods for producing same patent; WO 0141558-A 2 14-JUN-2001;

Aventis CropScience N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                          ch 100.0%; Score 21; DB 6; Length 3266;
I Similarity 100.0%; Pred. No. 0.44;
21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 21; DB 6; Length 4832; Best Local Similarity 100.0%; Pred. No. 0.45; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT
                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="T-DNA of plasmid pTHW118"
1883. .4065
/note="Hpal restriction fragment"
a 883 c 932 g 1488 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .4832
/organism="synthetic construct"
/db_xref="taxon:32630"
 PLANT GENETIC SYSTEMS, N.V
Location/Qualifiers
1. .3266
/organism="Nicotiana tabacum"
/db_xref="taxon:4097"
1527. .2492
                                                                                                                                                      /protein_id="CAA00875.1"
/db_xref="G1:490022"
/db_xref="SWISS-PROT:P24804"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A60108 4946 bp DNA
Sequence 1 from Patent W09706267.
A60108
A60108.1 GI:3715124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX172441 4832 bp DNA
Sequence 2 from Patent W00141558.
AX172441 GI:14597553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                         1527. .2492
/gene="TA29"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 ATAGGGTGGGAGGCTATTTGG 198
                                                                   1527. .2492
/gene="TA29"
1527. .2402
                                                                                                                                                                                                                                                                                                                                                                                                                       1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct. synthetic construct
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                                                                                               1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX172441/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A60108/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MYAPKWVFISFMILLSLAICSGQPVTSDAIKAKEADHDNLKAHT
LSNIDAKGFGGGGFGIGGGWAGGGGGGGGGGGGTPNVGYNPGCSIHGCTVPGFGFL
PKPVFCVPVYSPGCGYCFADIPTGGMTESKITGISOSARLYRCKPCPNMCDSKDCNE
LLLHFVFPWDSKHDNKDEHLRYGGRRGIGLTVGGVGGFGIGFGAWGGGGGGGGGSDA
PGCSNOGCDPGFGCPRCPGCGYACPANNPSGGITEFHISGISREDGPYRCRPDWCESEDC
NELLHFVSPWQHKHENRHDHIVERSDEEEAHHQSKQHKDEDIIN"

581 c 623 g 1046 t
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana. 1 (bases 1 to 3266) Mariani.(.., Leemans, J., De Greef, W. and De Beuckeleer, M. Plants with modified stamen cells Patent: EP 0344029-A 92-NOV-1989;
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                  12-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-1994
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 6; Length 3266; 100.0%; Pred. No. 0.44;
                                                            DB 6; Length 21;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                              A08065 3266 bp DNA PAT
Synthetic nucleotide sequence of the TA29 gene.
A08065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT
                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. 3266
/organism="synthetic construct"
/db_xref="taxon:32630"
/db_xref="taxon:32630"
/gene="TA29"
1527. 2492
                                                            Score 21; DB 6,
Pred. No. 0.31;
 u
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
 9
                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 8910396-A 7 02-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/protein_id="CAA00738.1"
/db_xref="GI:413314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A10061 3266 bp DNA N.tabbacum (pTA2953) TA29 gene. A10061.1 GI:490021
   b
 10
                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1527. .2492
/gene="TA29"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                            100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 ATAGGGTGGGAGGCTATTTGG 198
                                                                                                                      1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                       synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 3266)
                                                                                                                                                                                                                                                                             A08065.1 GI:413313
   O
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana tabacum
 -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       common tobacco.
                                                                         Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
 4
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1016
                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                               LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
ORGANISM
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                       REFERENCE
```

FEATURES

RESULT A08065

ð 셤 ö

Gaps

ö

03-JUL-2001

ô

Gaps

; 0

VERSION

RESULT A10061 COCUS

ð a 06-MAR-1998

```
1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         891 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
                         891 c
                                                                           Query Match 100.0
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         1. .4946
1. .4946
                         1569 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                    RESULT 8
AX172440/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                            DEFINITION
                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX127748/c
                                                                                                                                                                                                                                                          ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                  ŏ
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                 19-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                             Query Match
100.0%; Score 21; DB 6; Length 4946;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 6; Length 4946; 100.0%; Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
891 c 963 g 1523 t
                                                                                                                                           /organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
1 891 c 963 g 1523 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENETIC TRANSFORMATION USING A PARP INHIBITOR Patent: EP 0757102-A 1 05-FEB-1997; PLANT GENETIC SYSTEMS NV (BE) LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 4946)
De Block,M.
Genetic transformation using a PARP inhibitor
Patent: US 6074876-A 1 13-JUN-2000;
Location/Qualifiers
                                                                        Genetic transformation using a PARP inhibitor
Patent: WO 9706267-A 1 20-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR098307 4946 bp DNA
Sequence 1 from patent US 6074876.
AR098307
AR098307.1 GI:12807564
                                                                                                                                                                                                                                                                                                                                                                      A/0915 4946 bp DNA
Sequence 1 from Patent EP0757102.
A76915
       Transformation vector pTHW107
Transformation vector pTHW107
artificial sequence: vectors.
1 (bases 1 to 4946)
De, B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformation vector pTHW107.
Transformation vector pTHW107
artificial sequence; vectors.
1 (bases 1 to 4946)
De, B.M.
                                                                                                                                                                                                                                                                                               Db 4716 ATAGGGTGGGAGCTATTTGG 4696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 4716 ATAGGGTGGGAGGCTATTTGG 4696
                                                                                                                                                                                                                                                                                  1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                        A76915.1 GI:6088712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
                                                                                                                                                                         1569 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
AR098307/c
LOCUS
                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                       BASE COUNT
ORIGIN
                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
FEATURES
                                                                                        JOURNAL
                                                REFERENCE
                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                   RESULT
A76915/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                         /ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
```

```
ö
                                                                                                                                       ö
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                     03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic construct
artificial sequence.
1 (bases 1 to 5865)
Weston, B. and de Beuckeleer, M.
Male-sterile brasica plants and methods for producing same
Patent: WO 0131042-A 1 03-MAY-2001;
Aventis CropScience N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                             synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 4946)
de Both,G. and de Beuckeleer,M.
Hybrid winter oilseed rape and methods for producing same Hybrid winter oilseed rape and methods for producing same Hybrid volts.
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 6; Length 4946; 100.0%; Pred. No. 0.45; 1. ive 0; Mismatches 0; Indels (
                                                                                                100.0%; Score 21; DB 6; Length 4946; 100.0%; Pred. No. 0.45;
                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct" / db_xref="taxon:32630" / note="T-DNA of plasmid pTHW107" 964. 4906 / note="Hind III fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // 15865
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="T-DNA of plasmid pc0113"
                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX127748 5865 bp DNA
Sequence 1 from Patent WO0131042.
AX127748
                                                                                                                                                                                                                                                                                                                 AX172440 4946 bp DNA
Sequence 1 from Patent W00141558.
AX172440 GI:14597552
/organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                    963 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  963 g
                                                                                                                                                                                                    Db 4716 ATAGGGTGGGAGCCTATTTGG 4696
                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 4716 ATAGGGTGGGAGGCTATTTGG 4696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX127748.1 GI:14134395
```

4

셤 ò

```
/protein_id="CAA36525.1"
/db_xref="GI:20037"
/db_xref="GI:20037"
/db_xref="GI:20037"
/db_xref="SWISP-PROT: 1.24805"
/translation="MIAVFROSIGRPPPELSIPQAGIQKKEAKTREEIAESFKTWKOD STFYHILFNGNEWAFSBGNENFICQPRSIVVMDDVFCIFSGALDNTFDLKKHYGLSRQAT COMPLEMENt(37076...4046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="stem specific, weakly expressed in other organs" complement(4288. .4472) /gene="TSJT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XLU70985 3243 bp DNA VRT 06-APR-1998
Xenopus laevis transforming growth factor-beta 5 gene, 5' flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Asnopodinae; Xenopous.

1 (bases 1 to 3243)
Vempati,U.D. and Kondaiah,P.
Characterization of the 5' flanking region of the Xenopus laevis Gene 208 (2), 323-329 (1998)
complement(join(3022. .3024,4047. .4287,4473. .4678))
/gene="TSJT1"
/note="stem specific, weakly expressed in other organs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 3243)
Vempati,U.D. and Kondaiah,P.
Vempati,U.D. and Kondaiah,P.
Submission
Submission
Submission
Submitted (17-SEP-1956) Center for Reproductive Biology and
Molecular Endocrinology, Indian Institute of Science, Bangalore,
Karnataka 560 012, India
On Jul 21, 1997 this sequence version replaced gi:1809300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps

    .2890
/note="5' flanking sequence of transforming growth
factor-beta 5"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6254;
                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(4047. .4287,4473. .4678))
/gene="TSJT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 21; DB 8; Best Local Similarity 100.0%; Pred. No. 0.46; Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .3243
/organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .>4678)
                                                                                                                                                                                                                                                                                                                                          complement(4047. .4287)
/gene="TSJT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4473.
/gene="TSJT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4778.
/note="TA29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 ATAGGGTGGGAGGCTATTTGG 198
                                                                                    /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U70985.1 GI:2267223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atagggtgggaggctatttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1082 c
                                                                                                                                                                                                                                                                                                                     /number=2
                                                                                                                                                                                                                                                                                                                                                                                                 /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
U70985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATA_signal
                                                                                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
XLU70985/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA36524.1"
/do_xref="G1:20036"
/db_xref="G1:20036"
/
                                                                                                                                                                                                                                                                                                                                                                                                                         common tobacco.

Nicotiana tabacum

Nicotiana tabacum

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                               NTA29 6254 bp DNA PLN 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TSJT1"
/note="stem specific, weakly expressed in other organs"
complement(<3022. .3075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"stem specific, weakly expressed in other organs" /gene-"TSJT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .>4678))
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ם
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-MAR-1990) Mariani T., Plant Genetic Systems, Plateaustraat 22, B 9000 Gent, Belgium
(2) (bases 1 to 6254)
Seurinck, J., Truettner, J. and Goldberg, R.B.
Nucleic Acids Res. 18 (11), 3403 (1990)
                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4287,4473.
                  Length 5865;
                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Data kindly reviewed (13-DEC-1990) by Mariani C.
Location/Qualifiers
1. 6254
/organism="Nicotiana tabacum"
/cultivar="Samsun"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .3075,4047.
          100.0%; Score 21; DB 6;
100.0%; Pred. No. 0.46;
.ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4097"
/clone_lib="lambda Charon32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1527. .2489
/gene="TA29"
/product="anther-specific"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<3022. .>4678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"anther-specific"
1527. .2492
/gene="TA29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="anther-specific"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(<3022./gene="TSJT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1477. .2714
/gene="TA29"
: 1477. .(2617.2714)
/gene="TA29"
                                                                                                                                             4717 ATAGGGTGGGAGCTATTTGG 4697
                                                                                                               1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1446. .1452
/note="TSJT1"
                                                                                                                                                                                                                                                                                                                                                                                                 tissue specific gene.
                                                                                                                                                                                                                                                                                                                                                                              GI:20035
                                                                 Conservative
        Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marian1, T.
                                                                                                                                                                                                                                                                                                                                                                           X52283.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prim_transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prim_transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                            RESULT
NTTA29
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
```

ö

```
2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5417
5517
6194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8558
8658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavity, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferrelran, P., Fizhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Merwan, P., McGurk, A., McKernan, K., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Zimmer, A. and Zody, M.
                                                                                        /product-"transforming growth factor-beta 5 (TGF-beta 5)"
/protein_id="AAC60311.1"
/d_xref="G1:2281072"
/translation="WEVLWMLLVLIVLIVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGO
ILSKLKLDKTPDVDSEKMTVPSEAIFLYNSTLEVIREKATREBEHVGHDQNIQDYYAK
OVYRFESIT"
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC022563 149710 bp DNA HTG 13-JUL-2000
Homo sapiens clone RP11-3123, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6910806. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                           Length 3243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 149710)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-3L23
                                                                                                                                                                                                                                                                                                                                                                      Score 19.4; DB 5;
Pred. No. 3.6;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                               922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project_name: L2771
Center clone name: 3_L_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- Genome Center
                                                                                                                                                                                                                                                                               ۵
                                                                                                                                                                                                                                                                               9/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1731 ATAGGGTGGGAGGCTATATGG 1711
                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC022563.2 GI:9121084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 149710)
                                                                                                                                                                                                                                                                                                                                                                        92.4%;
95.2%;
                                                                                                                                                                                                                               3225. .>3243
                                                2891. .>3224
                                                                                                                                                                                                                                                                             675 c
<1. .3224
/number=1
                                                                                                                                                                                                                                                          /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE0
                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                               Ø
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
AC022563/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
  exon
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                  ORIGIN
```

ò

```
* NOTE: This record contains 171 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low Pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0224: gap of 100 bp 10879: contig of 655 bp in length 10879: gap of 100 bp 11563: contig of 684 bp in length 1763: gap of 100 bp 12433: contig of 670 bp in length 12209: contig of 670 bp in length 13209: contig of 676 bp in length 1399: gap of 100 bp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7298: gap of 100 bp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
of 679 bp in length
100 bp
of 670 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14898: gap of 100 pp
15571: contig of 673 bp in length
215671: gap of 100 bp
16387: contig of 716 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   782: gap of 100 bp
1492: contig of 710 bp in length
1592: gap of 100 bp
2305: contig of 713 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp
f 708 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
[ 654 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00 bp -
677 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 bp
f 675 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00 bp
689 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp .
f 700 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9436: gap of 100 bp 10124: contig of 688 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 711 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151: gap of 100 bp 24267: contig of 716 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  682: contig of 682 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 686 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 673 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
f 679 bp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ap of 100 bp
contig of 709 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71: gap of 100 bp
23451: contig of 680 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 con: gap of 10879:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14089: gap of
14798: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: gap of 3867: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: gap of 6968: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7: gap of
9336: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7857: gap of
8557: cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7068: gap of 7757: co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5516: gap of
6193: co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       683 782: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4646:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5416:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17298:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21985:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10979:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23551:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10224:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12434 12533:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3210 13309:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8009 18108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18872:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9556 19655:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20420:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21212:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2405:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3967:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4746:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6293:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8657:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6388 16487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5572 1567
                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3214
3868
3968
4647
```

us-09-698-903b-3.rge

```
25967; gap of to be a control of 702 bp in length 2669; control of 702 bp in length 2744; gap of 100 bp 27445; gap of 100 bp 27445; gap of 100 bp 2824; gap of 100 bp 29002; control of 678 bp in length 29102; gap of 100 bp 29785; control of 686 bp in length 3057; gap of 100 bp 31357; control of 686 bp in length 3057; gap of 100 bp 31357; control of 686 bp in length 3156; control of 686 bp in length 3156; control of 683 bp in length 3156; control of 683 bp in length 3156; control of 683 bp in length 3156; gap of 100 bp 3155; control of 710 bp in length 3156; gap of 100 bp 315456; control of 710 bp in length 3156; gap of 100 bp 315476; gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 47243: gap of 100 bp
44 47943: gap of 100 bp
44 48043: gap of 100 bp
48 48275: contig of 684 bp in length
48 48275: contig of 684 bp in length
48 48275: gap of 100 bp
41 49640: gap of 100 bp
41 50332: contig of 692 bp in length
33 50432: gap of 100 bp
33 50432: gap of 100 bp
33 51275: contig of 692 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1755: gap of 100 bp 11 length 4244: contig of 675 bp in length 1307: contig of 673 bp in length 1307: gap of 100 bp 100 bp 143980: contig of 673 bp in length 4080: gap of 100 bp 100 bp
67: gap of 100 bp

5073: contig of 706 bp in length

73: gap of 100 bp

25867: contig of 694 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44868: gap of 100 bp 4556: contig of 688 bp in length 45656: gap of 100 bp 46448: gap of 100 bp 46448: gap of 100 bp 47143: contig of 695 bp in length 47143: contig of 695 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27: gap of 100 bp 51915: contig of 688 bp in length 52678: contig of 688 bp in length 52678: contig of 663 bp in length 78: gap of 100 bp
                                                                                                                                                     26669:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             con.
51915:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35476: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40171: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52778: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28324:
                                                                                                                                                                                                                                                                                                                                                                    27545:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29885:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31458 32169
32169 32268:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30671:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36243:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37024:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39374:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44080:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34666:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40970:
                                                                                           25173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33856:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42534:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52015
```

```
AL Uppublished

S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Adderson, S., Baldvin, J., Barna, N., Beckerly, R., Beda, F., Bodukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Porles, C., Gage, D., Galagan, J., Ferreira, P., FitzHugh, M., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Hagford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieut, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Maddrin, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Plerre, M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Stehman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Ilirell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Lammer, A. and Zody, M.

Librell, A. and Zody, M.

Librell, A. and Zody, M.

Librell, A. and Cody, M.

Librell, A. and Cody, M.

Submitted (11-DEC-1999) Whitehead Institute/MIT Center for Genome of Submitted (11-2001 this sequence version replaced gi:14029977.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A HTG 11-AUG-2001 clone RP11-424119 map 15, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                 2; Length 149710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                        Indels
               3461 53560: gap of 100 bp 53561 54251: contig of 691 bp in length 54252 54351: gap of 100 bp 54352 54921: contig of 670 bp in length 54922 55021: gap of 100 bp 55022 55702: contig of 681 bp in length 55703 55802: gap of 100 bp
53460: contig of 682 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC019254
AC019254 6 GI:15148226
HTG; HTGS_PHASE1; HTGS_RULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-424119 Unpublished
                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                           Score 19.4; DB Pred. No. 4.7;
                                                                                                                                                                                                                                                                                         Pred. No. 4.7;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 15 clone RP
IN PROGRESS ***, 4 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                    Db 47881 ACAGGTGGGAGGCTATTTGG 47861
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name:
                                                                                                                                                                                                                                                                                                                                                                        1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                           92.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179183 bp
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC019254
                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC019254/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                        ŏ
```

```
132755: gap of 100 bp
145980: contig of 13225 bp in length
146080: gap of 100 bp
                                                                                                                                                                                                                         Center project name: L10374
Center clone name: 441_0_8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ر gap of
28910: د
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cont : gap of 87095:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132756 145980; cont:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29010: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87195: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5679 15778:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7279 17378:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19465:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22946:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55276:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26500:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dipublished

S tren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barran, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barran, N., Bartlen, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Conlymore, A., Cooke, P., DeArellano, K., Dewar K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzlugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lancoque, K., Landers, T., Lehoczky, J., Levine, R., Liau, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Mellim, J., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Mardyn, T., Naylor, J., Norman, C. H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Neil, D., Olivar, T. M., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Balar, S., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vasillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M. Direct Submission
Submitted (15-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 01141, USA on Sep 23, 2000 this sequence version replaced gi:9857543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 179183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                          58790 58889; gap of 100 bp 58890 67134; contig of 8245 bp in length 67135 67234; gap of 100 bp 67235 91255; contig of 24021 bp in length 91356 91355; gap of 100 bp 91356 179183; contig of 87828 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11 Human Male BAC"
44916 c 42628 g 42401 t 340 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                           58789: contig of 58789 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 2, clone RP11-44108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19.4; DB Pred. No. 4.8; 0; Mismatches
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-424I19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                          /chromosome="15"
/map="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC073374.3 GI:10280771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.4%;
illarity 95.2%;
Conservative (
                                                       preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Thes 20; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                         48898 a
                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC073374/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
```

```
------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M3: M7815; 100% of reads Sequencing vector: M3: M7815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 154202 bases at least Q40 Consensus quality: 165990 bases at least Q30 Consensus quality: 165333 bases at least Q20 Insert size: 170000; agarose-fp Insert size: 170000; agarose-fp Quality coverage: 4.2 in Q20 bases; sum-of-contigs Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
                                Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wl.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11391: contig of 11391 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111776 111875: gap of 100 bp
111876 122023: contig of 10148 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ap of 100 bp

: contig of 2410 bp in length

ap of 100 bp

: contig of 22350 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122024 122123: gap of 100 bp
122124 132655: contig of 10532 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11392 11491: gap of 100 bp
11492 13778: contig of 2287 bp in length
13779 13878: gap of 100 bp
13879 15678: contig of 1800 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95332 95431: gap of 100 bp
95432 102696: contig of 7265 bp in length
102697 102796: gap of 100 bp
102797 111775: contig of 8979 bp in length
111776 111875: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78: gap of 100 bp 11278: contig of 1500 bp in length 78: gap of 100 bp 19365: contig of 1987 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65: gap of 100 bp 22846: contig of 3381 bp in length 464; gap of 100 bp 26400: contig of 3454 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76: gap of 100 bp
58304: contig of 3028 bp in length
04: gap of 100 bp
62806: contig of 4402 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51460: gap of 100 bp 55176: contig of 3716 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06: gap of 100 bp 69285: contig of 6379 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69385: gap of 100 bp
79212: contig of 9827 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ap of 100 bp contig of 7783 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ap of 100 bp contig of 8136 bp in length
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
```

us-09-698-903b-3.rge

source

FEATURES

```
And uppublished

E (bases 1 to 179510)

Baldwin, J., Barna, N., Backerly, R., Bougalavkiy, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Backerly, R., Bougalavkiy, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Backerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., FilzHugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, E., Karatas, A., Klein, J.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonid, P., Marquis, N.,

McEwan, P., McGurk, A., McKeran, K., McLaughiln, J., Meldrim, J.,

Peterson, K., Pollara, V., Riley, R. Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

Al Direct Submission

Al Direct Submission

All repeats were identified using RepeatMasker: html

Center Whitehead Institute/ MIT Center for Genome Research

Center Genome washington edu/RW/RepeatMasker.html

Center Whitehead Institute/ MIT Center for Genome Center

Center Sequence_submissions@genome.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Center project name: 14081
                                                                                      AC013820 179510 bp DNA HTG 01-APR-2000
Homo sapiens clone RP11-21P24, WORKING DRAFT SEQUENCE, 8 unordered
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179510)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-21P24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 6.8 in Q20 bases; agarose-fp Quality coverage: 7.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center clone name: 21-24

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175240 bases at least 040
Consensus quality: 175240 bases at least 030
Consensus quality: 17720 bases at least 020
Insert size: 183000; agarose-fp
Insert size: 178810; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 2601: contig of 2601 bp in length
2602 2701: gap of 100 bp
2702 8297: contig of 5596 bp in length
8298 8397: gap of 100 bp
8398 27253: contig of 18856 bp in length
27254 27353: gap of 100 bp
                                                                                                                                                        AC013820
AC013820.3 GI:7382157
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                            human.
                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                             ACCESSION
                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                            AC013820
                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 167409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
146081 163677: contig of 17597 bp in length 163678 163777: gap of 100 bp 163778 167409: contig of 3632 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2200 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                 /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.8%; Score 17.8; DB 90.5%; Pred. No. 39; 11ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:right"
30270 c 30508 g 52497 t
                                                                                                                                                                                                                                                                                                                                                                     11492. .13778

/note="assembly_fragment"

13879. .15678

/note="assembly_fragment"

15779. .17278

/note="assembly_fragment"

17379. .19365

/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7006- assembly_iragment.
7006- assembly_fragment.
22947. .26400
7004e- assembly_fragment.
26501. .28910
7004e- assembly_fragment.
51461. .55176
7004e- assembly_fragment.
55277. .58304
7004e- assembly_fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.00- assembly_fragment.

7.00te-"assembly_fragment.

62907 .69285

7.00te-"assembly_fragment.

63186 .79212

7.00te-"assembly_fragment.

79313 .87095

7.00te-"assembly_fragment.

7.00te-"assembly_fragment.

7.00te-"assembly_fragment.

7.00te-"assembly_fragment.

7.00te-"assembly_fragment.

7.00te-"assembly_fragment.

7.00te-"assembly_fragment.

7.00te-"assembly_fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11876. 122023

/note-"assembly_fragment"

12214. 132655

/note-"assembly_fragment"

132756. 145980

/note-"assembly_fragment"

146081. 158377

/note-"assembly_fragment"

163778. 163877
                                                                                                                        /organisme"Homo sapiens"
/db_xrefe"taxon:9606"
/chromosomee="2"

    11391
    note="assembly_fragment clone_end:8P6

                                                                                                                                                                                                                            /clone="RP11-44108"
                                                                                                                                                                                                                                                                                                                                                vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 126062 ATAGAGTTGGAGGCTATTTGG 126042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_end: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Conservative
                                                                                                                                                                                                     /map="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51934 a
                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
```

of reads

Query Match

ð

BASE COUNT

```
ö
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                      Query Match

84.8%; Score 17.8; DB 2; Length 179510;
Best Local Similarity 90.5%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 2; Indels 0;
703 others
                                                                                                                                                                                                                      vector_side:right"
131720. .179510
/note="assembly_fragment"
a 32374 c 31805 g 55501 t
                                                                                                                                                                                                                                           59127
                                                                                                                                                                                     misc_feature
                                                                                                      misc_feature
                                                                                                                  misc_feature
                                                                                                                               misc_feature
                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                              misc_feature
                                                                                                                                              misc_feature
                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                     source
                                                              FEATURES
```

Search completed: February 25, 2002, 18:00:06 Job time: 18414 sec

THIS PAGE BLANK (USPTO)

Human secreted pro Clone of recombina rodent DCMP1 C-lec SEQ ID 3 of US5914 Genomic DNA sequen

Human secreted pro Aspergillus oryzae Tomato spotted wil

Human milk kappa-c Human kappa-casein

Recombinant human

```
Plasmid pTC0113; transgenic Brassica plant; transformation event; male-sterility gene; tobacco; PCR primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                     PCR primer MLD008 to amplify a fragment of pTC0113.
                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                              AAH14886
AAH74185
                                                                                                                                                                                             AAV23920
AAV15004
                                                                                                                                                                                                             AAX23519
AAQ13998
                                                                                                                                                                                                                                             AAI33627
AAI02189
                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Bacillus amyloliquefaciens.
Chimeric - Nicotiana tabacum.
                                                                                                                                                      AAV57910
                                                                                                                                                             AAQ70890
                                                                                                                                                                              AAH16691
                                                                                                                                                                                      AAZ42247
                                                                                                                                                                                                                                                              AAF14117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0430497.
26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weston B, De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                      AAD06992 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
857
857
858
2185
13104
1418
24978
24979
394
                                                                       660
777
1026
                                                                                               1549
                                                                                                      1556
1577
1591
1602
                                                                                                                                     WO200131042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                      AAD06992;
RESULT
AAD06992
00000
                                                                                               00000
                                                                                                                                                                              υ
                                                                                                                                                                                             000000000
                                                                                                                                                                                                                                                                                                                                       Nuclectide sequenc
T-DNA of plasmid p
Nuclectide sequenc
Plasmid pTCO113 T-
Chimeric T-DNA of
Dengue-2 virus der
CDNA encoding poly
CDNA sequence enco
Human lung tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene insert i
                                                               (without alignments)
25.126 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer MLD008
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                     February 25, 2002, 18:17:19; Search time 716.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*
                                                                                                                                                              1861242
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                             930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06992
AAN92188
AAH25423
AAT55423
AAT5439339
AAD06990
AAT49304
AAT49303
AAT49303
AAT68287
                                      - nucleic search, using sw model
                                                                                                     1 atagggtgggaggctatttgg 21
                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                             length: 0
length: 2000000000
                                                                                    US-09-698-903B-3
                                                                                                                                                                                                                                      N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3265
4832
4946
4946
5864
5865
10723
10723
694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match
```

seq

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Score

Result è 21 21 21 21 21 21 21 21 21 6.8 16.8 16.8

10087654321

0 0 0 0 0 0 0 0

Human haemochromat Tomato spotted wil Soybean retroeleme Human cDNA sequenc Human normal bladd Human alpha3 integ

Receptor protein t Human kidney amino Template DNA. Syn DNA amplification

for ge used t used t oryzae thalia

Probe #2313 u Probe #2180 u Aspergillus c Arabidopsis t

Probe #2205

by of

Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -

WPI; 2001-300517/31.

Human ALD gene exo Human CDNA sequenc s1 RNA binding reg Human polynucleoti Human CDNA sequenc Human CDNA sequenc

Human sodium-depen Human ORFX ORF1666

ö

Gaps

ö

Indels

Length 3265;

```
Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene;
fertility restorer gene; barstar gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ^*tag= a
'note= "right border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "atSlA ribulose-1,5-biphosphate carboxylase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= j
/note= "Tag1 fragment from 3' UTR of nopaline
synthase gene from T-DNA of priT37 and
containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           b
"synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= f
//tag= f
/note= "synthetic polylinker derived sequences"
complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= k
/note= "synthetic polylinker derived sequences"
2941..2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= d
/note= "synthetic polylinker derived sequences"
complement (98..309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= i
/note= "synthetic polylinker derived sequences"
complement (2659.2919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "residual sequence from TL-DNA at right
border repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/note= "3' UTR from TL-DNA gene 7 of pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= g /*tag= g //note= "Streptomyces hygroscopicus bialaphos resistance (bar) gene" complement (883..2608)
        TA29 gene; tag b is the cDNA insert from pBR329 (AAN92187).
                                         Sequence 3265 BP; 1016 A; 581 C; 623 G; 1045 T; 0 other;
                                                                                          100.0%; Score 21; DB 10;
11arity 100.0%; Pred. No. 0.41;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of plasmid pTHW118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                       177 atagggtgggaggctatttgg 197
                                                                                                                                                             21
                                                                                                                                                                                                                                                             3423/c
AAH25423 standard; DNA; 4832
                                                                                                                                                          1 atagggtgggaggctatttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces hygroscopicus.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus amyloliquefaciens. Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                         22-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2609..2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310..330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..25
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
/note=
                                                                                     Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                            AAH25423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3'UTR
                                                                                                                                                                                                                                          RESULT
AAH25423/ID AAH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
            SXS
                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transformed plant cell with disrupted metabolism - from a product encoded by foreign male-sterility DNA inserted in the nuclear genome.
                             The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is PCR primer MLD008 used to amplify a fragment of plasmid pTColl3. The primer MLD008 used as a probe. The amplified plasmid pTColl3. The primer is also used as a probe. The amplified Bacillus amyloliquefaciens and promoter region of the anther-specific gene TA29 from Nicotiana tabacum. This primer corresponds to position 4697-4717 of plasmid pTColl3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pTA2983 was constructed subcloning a clai fragment contg. the TA29 gene from lambda TA29 into pLK31. The TA29 promoter is used in a vector for transforming plant cells. Tag b is the coding sequence of the
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 22; Length 21; 100.0%; Pred. No. 0.27; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Beuckeleer M;
                                                                                                                                                                                                                                                                Sequence 21 BP; 4 A; 1 C; 10 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1445..451
7.tag-a
1526..4991
/ttag-b
//tag-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Greef W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; fig. 3A; 89pp; English.
Claim 1; Page 26; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLAN-) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                 1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN92188 standard; DNA; 3265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TA29 gene insert in pTA29S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89WO-EP00495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88GB-0010120.
                                                                                                                                                                                                                                                                                                                                                                                                    1 atagggtgggaggctatttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum "Samsun".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TA29 promoter; pTA29S3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mariani C, Leemans J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1989-339961/46.
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAP93313.
```

11-APR-1990

AAN92188;

AAN92188

Query Match Best Local Matches 2

ð g

Key TATA-signal

CDS CDS 27-APR-1989; 28-APR-1988;

WO8910396-A. 02-NOV-1989

```
WPI; 1997-111050/11.
                            plasmid pTHW107; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reduces metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PLBZ ) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP757102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Block M;
                                                                                               misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                              misc_RNA
                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                                         promoter
                                                                                                                                   3'UTR
                                                                                                                                                                                                                                                                        3'UTR
                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                  CDS
   ó
                                                                                                                                                                                                                                                                                                                                                                   The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomate performance, genetic stablility and adaptability to different genetic backgrounds. The present sequence represents a fertility restorer gene. The plasmid comprises the barstar gene, which acts as plants of the invention.
                                                                                                                                                                                                                                                                                                              Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                4808..4832
/*tag= p
/note= "left border repeat from TL-DNA from pTiB6S3"
        /note= "downstream of Bacillus amyloliquefaciens
barstar coding region"
complement (2981..3253)
                                       /*teg= m
/note= "barstar gene coding region from Bacillus
amyloliquefaciens"
complement (3254..4762)
                                                                                   /note= "anther-specific gene TA29 promoter from
                                                                                                              /*tag= 0
/note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 22; Length 4832;
Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                              Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 80-82; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4602 ATAGGGTGGGAGGCTATTTGG 4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT59531 standard; DNA; 4946 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                     (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                               2000WO-EP12872.
                                                                                                                                                                                                                                                                       De Both G, De Beuckeleer M;
                                                                                                       1763..4807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-DNA of plasmid pTHW107
                                                                                                                                                                                                                                                                                          WPI; 2001-381419/40.
                                                                                                                                                                        WO200141558-A1
                                                                                                                                                                                                              06-DEC-2000;
                                                                                                       misc_feature
                                                                                                                                   misc_feature
                                                                                                                                                                                                                                  08-DEC-1999;
                                                                                                                                                                                           14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT59531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                  promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT59531/c
                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
Plasmid pTHW107 is a vector carrying T-DNA (AAT59531) comprising a barnase coding sequence under control of the tobacco TA29 gene stamen-specific promoter and a phosphinothricin acetyltransferase coding sequence under control of an Arabidopsis Rubisco small subunit gene promoter. Oilseed rape hypocotyl explants were infected with Agrobacterium tumefaciens C58ClRif carrying vector
Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP; niacinamide; Agrobacterium; T-DNA; male sterile; barnase; ribonuclease; RNase; cereal; wheat; oilseed rape; Brassica napus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= 3'97
/note= "3' untranslated region contg. the poly-A
signal of gene-7 of Agrobacterium T-DNA"
complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "promoter region of Rubisco small subunit
gene of Arabidopsis thaliana"
complement (2658..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "3'untranslated region contg, the poly-A
signal of the nopaline-synthase gene of
Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "promoter region of tobacco TA29 gene"
complement (4822..4946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product- phosphinothricin acetyltransferase complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "T-DNA left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= barnase
complement (3368..4876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 13-16; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (97..330)
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         complement (1..25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Barnase
                                                                                                                                                           Chimeric Agrobacterium sp.;
Chimeric Arabidopsis thaliana;
Chimeric Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label- PTA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= PSSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95EP-0401844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95EP-0401844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label- Bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= e
/label= 3'
                                                                                                                                                                                                                                                                                                                                                                                    /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                      ö
                                                                                                                                                                                                                                                                                   Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene; fertility restorer gene; barnase gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "3'UTR downstream of Bacillus amyloliquefaciens
barnase coding region"
complement (3032.3367)
                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "right border repeat from TL-DNA from pTiB6S3"
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "atSlA ribulose-1,5-biphosphate carboxylase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tagl fragment from 3' UTR of nopaline
synthase gene from T-DNA of prir37 and
containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= d
/note= "synthetic polylinker derived sequences"
                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag- g
/note= "synthetic polylinker derived sequences"
complement (2659..2919)
         hypocotyls were treated with the poly-(ADP-ribose) polymerases inhibitor niacinamide (250 mg/l) 4 days prior to infection. Plants regenerated from niacinamide-treated transformed calli had a low copy number and displayed less variation in the expression profile of the transgenes.
  In some treatments, the
                                                                                                Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
/note= "Streptomyces hygroscopicus bar gene"
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note "Barnase coding region from Bacillus
                                                                                                                    0; Indels
                                                                 Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "synthetic polylinker derived
complement (98..309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "tag= c
'note= "3' UTR from TL-DNA gene 7 of
                                                                                                DB 18;
                                                                                               Query Match
100.0%; Score 21; DB 18
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                 Nucleotide sequence of plasmid pTHW107
 and helper It plasmid pMP60.
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                  4716 ATAGGGTGGGAGCTATTTGG 4696
                                                                                                                                                                                           MAH23422/c
ID AAH25422 Standard; DNA; 4946 BP.
                                                                                                                                     1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                        Streptomyces hygroscopicus. Arabidopsis thaliana. Bacillus amyloliquefaciens. Nicotiana tabacum.
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2609..2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..3031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310..330
                                                                                                                                                                                                                                                                                                                                                                                                                 26..97
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                      1..25
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                            22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                          AAH25422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                             3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                     RESULT
                                                                                                                                     à
                                                                                                                                                       q
                                                                                                                                                                                                                8888888888
```

```
The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene, preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. The present sequence represents plasmid pTHW107. This plasmid comprises the barnase gene, which acts as a male-sterility gene. The plasmid is used to create transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                   /*tag= m
/note= "left border repeat from TL-DNA from pTiB6S3"
                                                           /note= "anther-specific gene TA29 promoter from Nicotiana tabacum"
                                                                                                                                         /*tag= 1
/note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pTC0113 T-DNA used to obtain male sterile oilseed rape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid prc0113; male sterile; barnase; ribonuclease; barstar; transgenic plant; oilssed rape; canole; Brassica napus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 22; Length 4946;
Pred. No. 0.42;
Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;
amyloliquefaciens'
complement (3368..4877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 78-80; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT39339 standard; DNA; 5864 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4716 ATAGGGTGGGAGGCTATTTGG 4696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2000; 2000WO-EP12872
                                                                                                             4878..4921
                                                                                                                                                                                     4922..4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 atagggtgggaggctatttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention
                                                                                                                                                                                                                                                                               WO200141558-A1
                                                                                                           misc_feature
                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-1997
                                                                                                                                                                                                                                                                                                                            14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De Both G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT39339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT39339/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Кеу
```

ö

```
Example 3; Page 33-3743-47; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
g
                                                                                                                                                                                                              ŏ
                                                                                                                                                                     /note= "region containing polyA signal of nopaline
synthase gene of Agrobacterium T-DNA"
complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                     /label= Barnase
/note= "Bacillus amyloliquefaciens barnase coding
                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                   /note= "region containing polyA signal of gene of Agrobacterium T-DNA" complement (5840..5864)
                                                       gene
                                                                                                                                                                                                                                                  /note= "promoter of stamen-specific TA29 gene
                                                                                                                                                                                                                                                                                                                             /note= "region coding for barstar of Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                        of
                                                                                                                                /note= "promoter of Arabidopsis Rubisco small
                     /note= "right border of Agrobacterium T-DNA" complement (98..330)
                                                                                                                                                                                                                                                                                                                                                                                          /*tag= k
/label= LB
/note= "left border of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                        /note= "promoter of nopaline synthase gene Agrobacterium T-DNA"
                                                                                          /note= "region coding for phosphinothricin
acetyltransferase"
complement (883..2608)
                                                   /note= "region containing polyA signal of of Agrobacterium T-DNA" complement (331.882)
                                                                                                                                                                                                                                                           Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Botterman J, Cornelissen M, Michiels F;
                                                                                                                                         subunit gene"
complement (2659..3031)
                                                                                                                                                                                                                            complement (3368..4877)
                                                                                                                                                                                                                                                                                                Agrobacterium
complement (1..25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                       /label- Barstar
                                                                                                                                                                                                                     region"
                                                                                                                                                               3'nos
                                                                                                                                                                                                                                    *tag= g
|abel= PTA29
                                                                                                                          Pssu
                                              , d2
                                                                                                                                                                                                                                                                                                                                                            /label= 3'g7
                                                                                                                                                                                                                                                                                 /label- Pnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-EP00722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95EP-0400364
               /label= RB
                                                                                                                                                                                                                                                                 924..5216
                                                                                                                                                                                                                                                                                                                                            5490..5765
                                                                                                                                                                                                                                                                                                       5217..5489
                                                                                                                   /*tag= c
/label= E
                                                                                                                                                              /label=
                                                                                    /label=
                                              /label=
                                       /*tag=
                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-402373/40.
misc_feature
                                                                                                                                                polyA_signal
                                                                                                                                                                                                                                                                                                                                              polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                        WO9626283-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-1996;
                              polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1996
                                                                                                          promoter
                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                  promoter
                                                                    SOS
                                                                                                                                                                                     SGO
                                                                                                                                                                                                                                                                                                        CDS
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= g
/note= "Promoter from the atS1A ribulose-1,5-biphosphate
carboxylase small subunit gene from Arabidopsis thaliana"
2610..2659
/*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-DNA; plasmid pTCO113; transgenic Brassica plant; transformation event; male-sterility gene; chimeric; tobacco; ds.
plasmid pTCO113 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-regulatory) gene under control of the Pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterium-mediated transformation using pTCO113 were male sterile. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Protein encoded by bialaphos resistance
gene (bar) of Streptomyces hygroscopicus"
884..2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
finete= "Residual sequence from the TL-DNA at the 98.309 /*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "Right border repeat from the TL-DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= d
/note= "The 3' untranslated end from the TL-DNA
gene 7 (3'97) of pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= b
note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/note= "Synthetic polylinker derived seguence"
                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 17; Length 5864; 100.0%; Pred. No. 0.43;
                                                                                                                                                                                                                                        Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Streptomyces hygroscopicus. Chimeric - Arabidopsis thallana. Chimeric - Bacillus amyloliquefaciens. Chimeric - Nicotiana tabacum. Chimeric - Agrobacterium tumefaciens. Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric T-DNA of plasmid pTC0113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                  4716 ATAGGGTGGGAGGCTATTTGG 4696
                                                                                                                                                                                                                                                                                                                                                                                                       1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD06990 standard; DNA; 5865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                         21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310..331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32..883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26..53
/*tag=
                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-2001
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD06990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06990/c
```

9

3'UTR

CDS

```
The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic plant with a male-fertile Brassica plant and harvesting the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is chimeric T-DNA of plasmid prCOll3. This sequence comprises right border repeat, left border repeat and 3' untranslated region (UTR) from TL-DNA of priB653, synthetic polylinker sequences, coding regions of bialaphos resistance gene from Bacillus amyloliquefaciens and promoters of atsia and barstar gene from Bacillus amyloliquefaciens and promoters of atsia rabidopsis thallana, the anther-specific gene from Arabidopsis thallana, the anther-specific gene from the T-DNA of pri137 of Agrobacterium tumefaciens.
                                                                         Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yellow fever virus; prM-E protein; flavivirus; chimeric; medicament; infection; tumor antigen; cytokine; lymphoid; reticuloendothelial; cancer; virucide; vaccine; dengue virus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 22; Length 5865; 100.0%; Pred. No. 0.43; 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guirakhoo F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dengue-2 virus derived DNA fragment.
                                                                                                                                                                                    Claim 1; Page 47-49; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..1983
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF83820 standard; DNA; 1983 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2000; 2000WO-US32821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chambers IJ, Monath TP,
                      WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-343953/36.
P-PSDB; AAB84901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ORAV-) ORAVAX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200139802-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dengue virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF83820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                      /noce= "TagI fragment from the 3' untranslated end of the nopaline synthase gene (3'nos) from the T-DNA of pT1T37 and containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-DNA of prir37 of Agrobacterium tumefaciens" 5216..5217
                                                                                                                                                                                                                                                                            /note- The 3' untranslated region downstream from the Darnase coding sequence of Bacillus amyloliquefaciens" 3033..3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= r
hotte= "Sequence from the 3' untranslated end of the
barstar gene from Bacillus amyloliquefaciens"
5531..5554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= m
/note= "Promoter region of the anther-specific gene
TA29 from Nicotiana tabacum"
4879..4924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= v
/note= "Residual sequence from the TL-DNA at the
                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Protein encoded by barnase gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= The 3' untranslated end from the TL-DNA gene 7 (3'97) of pTiB6S3"
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= x
f/note= "Left border repeat from the TL-DNA from from filess"
                                                                                                                                                                                                                   'note- "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= p
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag- u
/mote- "Synthetic polylinker derived sequence"
5774..5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= "Synthetic polylinker derived sequence" 5555..5766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **tag= w
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /"tag= q //rag= q //product- "Protein encoded by barstar gene of Bacillus amyloliquefaciens" //*rag= /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= o
/note= "Promoter of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3369..4878
/*tag= m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555..5766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..5215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..5865
                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200131042-A2
                            misc_feature
                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter
```

3'UTR

CDS

THE STATE OF THE S

ö

Gaps

ó

7

```
"C>T mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.0
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                     /*tag=
/note=
6599
                                                                                                                                           /*tag=
/note=
8571
                            /*tag=
/note=
                                                                /*tag=
/note=
    'note=
                                                                                                                                                                                  /*tag=
                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-052330/05.
                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW06591.
                                                                                                                                                                                                                                                                        06-JUN-1996;
                                                                                                                                                                                                                     WO9640933-A1
                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT49303;
                mutation
                                                                                                                                                                     mutation
                                                     mutation
                                                                                         mutation
                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
AAT49303/c
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DX SX E
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                   The invention relates to a chimeric live, infectious, attenuated virus comprising a yellow fever virus with the nucleotide sequence encoding a prive protein deleted, runcated or mutated so that functional yellow fever virus prive. Forcien is not expressed and also integrated into the genome of the yellow fever virus a nucleotide sequence encoding a prive protein of a second, different flavivirus so that the prive protein of the second flavivirus is expressed. The chimeric live, infectious, attenuated virus is used to prepare medicaments for preventing or treating flavivirus infection in a patient. The yellow fever virus vector produces its gene product (tumor antigen or cytokine) in cells of the lymphoid or reticulcendothelial system or in a precursor of these systems in patients with cancer. Plaviviruses replicate in the cytoplasm of cells on that the virus replication does not involve integration of the viral genome into the host cell. The present sequence represents a DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2B; NS2B; NS3; NS4B, NS5; PDK-53; quadravalent vaccine; immunity; serotype; chimeric DEN-2/1 virus; chimeric DEN-2/2 virus; chimeric DEN-2/2 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus; dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
Chimeric live, infectious, attenuated yellow fever viruses used for preventing and treating diseases caused by flaviviruses have prM-E nucleotide sequence from a second, different flavivirus as functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c
"A>T mutation, causes Asp to Val substitution"
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                       Length 1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_except(pos:643..645, aa:Xaa)
/transl_except(pos:1135..1137, aa:Xaa)
/transl_except(pos:1193..11395, aa:Xaa)
/transl_except(pos:2809..2811, aa:Xaa)
/transl_except(pos:3400..342, aa:Xaa)
/transl_except(pos:3208..9210, aa:Xaa)
/oote= "Xaa = unknown amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= DEN-2 attenuated polyprotein
                                                                                                                                                                                                                                                                                                Sequence 1983 BP; 645 A; 409 C; 509 G; 420 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                    80.0%; Score 16.8; DB 90.0%; Pred. No. 42; iive 0; Mismatches
                                                             Disclosure; Page 196-198; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "C>T mutation"
                                      yellow fever prM-E is not expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
97..10272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT49304 standard; cDNA; 10723 BP.
                                                                                                                                                                                                                                                                                                                                                                                                   derived from dengue-2 virus.
                                                                                                                                                                                                                                                                                                                                                                                       2 tagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dengue 2 virus, strain 16681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p
                                                                                                                                                                                                                                                                                                                                    Ouery Match 80.0 Best Local Similarity 90.0 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
/note=
2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHF; DSS; SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT49304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                               셤
 õ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the polyprotein from an attenuated derivative of Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The polyprotein comprises the capsid, prw, M. E. NSI, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the production of a quadravalent vaccine which provides immunity against all four serotypes of dengue virus. The vaccine also comprises a all four SETOTY a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to protect against infection by all four serotypes of dengue virus, DEN-1, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used to produce the recombinant protein products of the DNA constructs which are used in the vaccines.
                                                                                      f "C>T mutation, causes Leu to Phe substitution"
e "G>A mutation, causes Gly to Asp substitution"
                                                                                                                                                                                                                                                                                                       "G>C mutation, causes Gly to Ala substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 - also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a quadravalent vaccine for protecting against Dengue virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Host cells are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gubler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemorrhagic fever/dengue shock syndrome (DHF/DSS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%; Score 16.8; 90.0%; Pred. No. 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Page 122-136; 261pp; English.
                                                                                                                                                                                    g
"C>T mutation"
                                                                                                                                                                                                                                                                                                                                                                                                 "C>T mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT49303 standard; cDNA; 10723 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bhamarapravati N, Butrapet S, C
Halstead SB, Kinney R, Trent DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYMA-) UNIV MAHIDOL AT SALAYA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1104 TAGGGTGCCAGCCTGTTTGG 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 tagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US09209.
```

œ

```
Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung tumor-associated proteins and the nucleic acids that encode them, useful for preventing, diagnosing and treating lung cancer -
                         Human lung tumour protein related nucleotide sequence SEQ ID NO:205.
                                                                                                                                                                                                                30-JUN-1999; 99US-0346492.
15-OCT-1999; 99US-0419356.
30-DEC-1999; 99US-046867.
30-DEC-1999; 99US-0476300.
06-MAR-2000; 2000US-0538077.
10-APR-2000; 2000US-0538077.
10-APR-2000; 2000US-0538077.
27-APR-2000; 2000US-0546259.
                                                                                                                                                                                         30-JUN-2000; 2000WO-US18061
                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-071488/08
                                                                                                                                  WO200100828-A2.
                                                                                                           Homo sapiens.
                                                                                                                                                              04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                   Wang T,
            Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3; NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype; chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus; dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the polyprotein from Dengue 2 virus, strain 16681. The polyprotein comprises the capsid, prM, M, E, NSI, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, pK4A, NS4B and NS5 production of a quadravalent vaccine which provides immunity against all four serotypes of dengue virus. The vaccine also comprises a chimeric DEN-2/1 virus, and/or a chimeric DEN-2/4 virus, and/or a chimeric DEN-2/4 virus, and/or a chimeric DEN-2/4 virus, The new quadravalent vaccines are used to protect against infection by all four serotypes of dengue full are used to produce fever or cells are used to produce fever or cells are used to produce the recombinant protein products of the DNA constructs which are used in the vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 - also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a quadravalent vaccine for protecting against Dengue virus infection
              CDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 2 other;
                                                                                                                                                                                  /*tag= a
/produce= DBN-2 polyprotein
/transl_except(pos:9208..9210, aa:Xaa)
/note= "Xaa = unknown amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                        Gubler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 16.8; 90.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                       Chang J,
                                                                                                                                                                                                                                                                                                                                                          (UYMA-) UNIV MAHIDOL AT SALAYA.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 107-121; 261pp; English.
                                                                                                                                                       Location/Qualifiers
97..10272
                                                                                                                                                                                                                                                                                                                                                                                                    Bhamarapravati N, Butrapet S, C]
Halstead SB, Kinney R, Trent DW;
                                                                                                                          Dengue 2 virus, strain 16681.
                                                                                                                                                                                                                                                                                                        96WO-US09209.
                                                                                                                                                                                                                                                                                                                                  95US-0483292.
                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-052330/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW06590
                                                                                                 DSS; ss
                                                                                                                                                                                                                                                 WO9640933-A1
                                                                                                                                                                                                                                                                                                      06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                           19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                     Key
```

ά Carter

Vedvick TS,

Fanger GR,

Lodes MJ,

Mannion J; Bangur CS,

```
The present invention describes immunogenic portions of lung tumourassociated proteins (I) and the nucleic acids (NAs) that encode them. (I) have cytostatic activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumour-associated diagnosis of diseases associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to concers, and the protein by expressing inactive proteins and patient's genome that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (I). Additionally, the NAS may be used to produce the lung tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA conformative sequences down genes and preventing their expression by binding with the cells own genes and preventing their expression. The NA cancer. The (I) may be used as antigens in the production of smillar NA sequences in cancer. The (I) may be used as antigens in the production of antibodies and in assays to identify medulators (agonists and antagonists) of the expression and activity of the protein. ARF68083 to AAF6808 and nucleotide and protein sequences which are used in the exemplification of the need of the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 694 BP; 202 A; 111 C; 154 G; 227 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.4; Di
Pred. No. 60;
0; Mismatches
Claim 4; Page 213; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.1%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 agggtgggaggctatttg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.1
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
```

ö

Gaps

0;

Indels

5;

Pred. No. 48;); Mismatches

ö

18; Conservative

Best Local Similarity Matches 18; Conserv

1104 TAGGGTGCCAGGCTGTTTGG 1085

8 ò

2 tagggtgggaggctatttgg 21

AAF68287 standard; cDNA; 694 BP.

AAF68287 ID AAF6 XX AC AAF6 XX DT 12-P

RESULT 11

(first entry)

12-APR-2001 AAF68287;

σ

```
AAT14564 encodes human milk kappa-casein which is useful as a component of an enteral nutritional product. Kappa-casein has anti-rotaviral activity, it inhibits the attachment of human rotavirus to mammalian cells. The kappa-casein is useful in the treatment and prevention of onset of gastroenteritis and other diarrhoeal diseases caused by rotaviridae esp. in infants, children or immunodeficient patients. Kappa-casein appeared to have no side effects on the subjects treated and is unlikely to be toxic or cause an allergic reaction.
                                                                                                                                                                                                                                                                                                                                                                                           Kappa-casein used as anti-rotaviral infection agent in nutritional product - to prevent, retard or treat rotavirus infection, especially in infants, children and immuno-deficient patients
                 Milk protein; kappa-casein; rotavirus inhibition; gastroenteritis;
infant formulation; immunodeficiency; diarrhoea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 857;
                                                                                                                                                                                                                                                                                                                                   Seo AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 857 BP; 309 A; 219 C; 127 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                Mukerji P, Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.1%; Score 16.4; 1 94.4%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
107..655
/*tag= a
                                                                                            Location/Qualifiers
45..593
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 8; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ89598 standard; cDNA; 858
                                                                                                                                                                                                                     95WO-US05676
                                                                                                                                                                                                                                                    94US-0308883
94US-0308882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kappa-casein; milk protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 GGGTGGGTGGCTATTTGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 gggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                  Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human kappa-casein cDNA
                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-179724/18.
                                                                                                                                                                                                                                                                                                 (ABBO ) ABBOTT LAB.
                                                                 Homo sapiens
                                                                                                                                                                                                                      05-MAY-1995;
                                                                                                                                                                                                                                                    16-SEP-1994;
                                                                                                                                                                                                                                                                    16-SEP-1994;
                                                                                                                                                          WO9608269-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5391497-A.
                                                                                                                                                                                         21-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-1995
                                                                                                                                                                                                                                                                                                                                Baxter JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ89598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
AAQ89598/c
                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The recombinant human kappa casein is produced in high yields by means of either a eukaryotic or prokaryotic expression system. It is used as a nutrient supplement in milk based products to provide a substantial improvement of the nutritional and biological value of the formulae, making it closer in similarity to human milk. It can also be used as a pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding human kappa-casein - used for obtaining recombinant polypeptide(s) for use as nutrient supplements, partic. in infant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4; DB 14; Length 857;
Pred. No. 61;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bergstroem S, Hansson L, Hernell O, Stroemgvist M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 857 BP; 307 A; 220 C; 128 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                 'product- Human kappa casein.
                                                                                                                                                          Casein; supplement; milk; pharmaceutical; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 88-89; 110pp; English.
                                                                                                                           Recombinant human kappa casein gene.
                                                                                                                                                                                                                  Location/Qualifiers
45..593
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                              AAQ46850 standard; cDNA; 857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human milk kappa-casein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT14564 standard; cDNA; 857
                                                                                                                                                                                                                                                                                                                                                                                                                           93WO-DK000024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.18;
94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         92DK-0000088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 GGGTGGGTGCTATTTGG 342
                                                                                                                                                                                                                                                                                                /*tag= b
45..104
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 gggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.1
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                 ..593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-258675/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYMB-) SYMBICOM AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR39351
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-1992;
                                                                                            26-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                              WO9315196-A.
                                                                                                                                                                                                                                                                                                                                                                                            05-AUG-1993
                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toernell J;
                                                             AAQ46850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT14564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    formulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
RESULT 13
AAQ46850/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT14564/
                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
```

a

ö

EX PX PX PX P

ö

Gaps

```
1052 TAGGGTGGAAGGCTATTT 1035
         g
                                                                                                                                                                                                                                                                                                                                                                                      á
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                           A commercial cDNA library prepd. in lambda gtll from mRNA obtd. from human breast tissue removed during the third trimester of pregnancy was screened with rabbit anti-bovine kappa-casein cDNA. The cDNA insert of a recombinant phage was amplified by PCR. The sequence of an isolated full-length clone encoding human kappa-casein (AAR72696) is given in AAQ89598.
                                                                                                                         DNA encoding human kappa-casein - used for the prodn. of large amts. of highly purified kappa-casein milk protein for infant use.
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; biological activity; nutritional; cytokine; cell proliferation; differentiation; immune stimulating; vaccine; haematopolesis regulation; tissue growth; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides encoding secreted human proteins, derived from human fetal brain, human adult blood, human adult bladder, or human adult
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ວີ
                                                                                                                                                                                                                                                                                      DB 16; Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans
                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collins-Racie LA,
Steininger RJ;
                                                                                                                                                                                                                                                  Sequence 858 BP; 266 A; 237 C; 137 G; 218 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein clone qb401_6 encoding cDNA.
                                                                                                                                                                                                                                                                                    Score 16.4; DI
Pred. No. 61;
0; Mismatches
                                                                     Chang Y, Ham RG, Jeffers KF, Menon RS;
                                                                                                                                                       Claim 4; Column 13-16; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LaVallie ER,
Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                 AAZ21101 standard; cDNA; 2185 BP
                                                  (COLS ) UNIV COLORADO FOUND INC
                                                                                                                                                                                                                                                                                                         ö
                                92US-0962569.
                                                                                                                                                                                                                                                                                  78.18;
94.48;
            92US-0962569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0077521.
98US-0079124.
99US-0266105.
                                                                                                                                                                                                                                                                                                                                         421 GGGTGGGTGGCTATTTGG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US05243
                                                                                                                                                                                                                                                                                                                          4 gggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treacy M,
                                                                                          WPI; 1995-160470/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCCOy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551362/46
                                                                                                       P-PSDB; AAR72696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY29869
           13-OCT-1992;
                               13-0CT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAR-1998;
14-MAY-1998;
10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9946287-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ21101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                     AAZ21101/c
ð
                                                                                                                                                                                                                                                                                                                                             g
```

```
AA221093 to AA221102 encode new human secreted proteins and AAY29861 to
CC AAY29873 represent the secreted proteins encoded by the polynucleotide
CC Sequences. AA221102 to AA221112 represent probes for the secreted
CC proteins. The polynucleotides and proteins are predicted to have
CC proteins are polynucleotides and proteins are predicted to have
CC proteins are meliorating medical conditions in humans and animals,
CC although no supporting data is given. Suggested activities include
CC although no supporting activity, cytokine and cell proliferation/differentiation
CC although no supporting (e.g. as vaccines) or suppressing activity,
CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,
CC activity, chemctactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, and tumour
CC activity, cadherin/tumour invasion suppressor activity, and tumour
CC and thrombolytic activity. The polynucleotides and proteins can also be used
CC and no activity. The polynucleotides and proteins can also have utility
CC and no activity. The polynucleotides and proteins can also have utility
CC and no activity where as a carbon source, use as a nitrogen
CC and no activity as as a source of carbohydrate. They may also have utility
CC insume growth or regeneration, as well as for wound healing and tissue
CC repair and replacement, and in the treatment of burns, incisions and
CC circumstances where bone is not normally formed, have application in
CC the healing of bone fractures and cartilage damage or defects in humans
CC and other animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2185 BP; 472 A; 572 C; 548 G; 593 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.1%; Score 16.4; 94.4%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                            Claim 26; Page 109; 118pp; English.
neural tissue cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 tagggtgggaggctattt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.4
Matches 17; Conservative
```

Search completed: February 25, 2002, 18:17:21 Job time: 16679 sec

```
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Applications of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4, Appli
4, Appli
7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Appl
, Appl
Appli
                                                                                                                                                                                             (without alignments)
15.769 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2, 1
                                                                                                                                                                  ; Search time 301.6 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Seq
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptcdata/2/ina/5A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/pcTuS_COMB.seq:*
/cgn2_6/ptcdata/2/ina/pcTuS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-1136-277-23
US-08-479-403-23
US-08-835-734-23
US-08-905-118-2
US-08-724-394A-19
US-08-652-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-730-163-1
US-08-256-799-1
US-08-462-437-1
US-07-962-569A-7
US-08-462-437-30
US-08-256-799-4
US-08-462-437-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-452-872-3
PCT-US93-03985-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-111-470-7
US-08-147-777-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                               February 25, 2002, 18:05:08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                       21
                                                                                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                            IDENTITY_NUC Gaport 1.0
                                                                                                                                                                                                                                                                                                                                    1 atagggtgggaggctatttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                            US-09-698-903B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potal number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                             OM nucleic
                                                                                                                                                                                                                                                                                                                                          sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0000000000
```

```
Appl
Appli
A
      Sequence 1, Ac Sequence 18, Ac Sequence 11, Ac Sequence 1, Ac Sequence 11, Ac Sequence 12, Ac Sequence 2, Ac Sequence 1, Ac Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08817188

Patent No. 6074876

GENERAL INFORMATION:

APPLICANT: DE BLOCK, MARC

TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR

FILE REFERENCE: 2121-0127P

CURRENT APPLICATION NUMBER: US/08/817,188

CURRENT FILING DATE: 1997-05-15

EARLIER APPLICATION NUMBER: PC7/EP96/03366

BARLIER FILING DATE: 1996-07-31

EARLIER FILING DATE: 1996-07-31

EARLIER FILING DATE: 1996-07-31

SARLIER PLING DATE: 1996-07-31

EARLIER PLING DATE: 1996-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: Complement((97)..(330))
OTHER INFORMATION: 3'97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: promoter region of Rubisco small subunit gene of OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

MAME/KEY: misc_feature
LOCATION: Complement((2658)..(3031))

OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement(1311)..(882))
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: transferase
PCT - US95 - 04682 - 1

US - 08 - 676 - 279 - 38

US - 09 - 136 - 277 - 1

US - 08 - 475 - 473 - 1

US - 08 - 435 - 734 - 1

US - 08 - 835 - 734 - 1

US - 08 - 835 - 69 - 19

US - 09 - 245 - 19

US - 09 - 624 - 581 - 2

US - 08 - 624 - 581 - 1

US - 08 - 624 - 581 - 2

US - 09 - 032 - 355A - 11

US - 09 - 032 - 355A - 11

US - 08 - 744 - 354D - 3

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 - 1

US - 08 - 646 - 695 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
      9046
354
556
2750
2750
2750
2750
90050
2989
2989
13146
13146
14311
14311
14311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: Complement((5
            4.077

4.077

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00

7.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-817-188-1/c
            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
```

Appli Appli Appli

Sequence

-08-991-258A-1 -08-769-399-1

.08-991-953A-1

Sequence Seguence

US-08-231-193A-55 US-08-486-273A-55 US-08-940-086A-55 US-08-227-536-1

Sequence Sequence

Appl

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: Complement(198)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
i NAME/KEY: misc_feature

! LOCATION: Complement((3032)..(3367))

! COCATION: Complement((3032)..(3367))

! OTHER INFORMATION: Darnase: region coding for barnase

! FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((3368)..(4876))

! OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotiana

| FEATURE:

| NAME/KEY: misc_feature

| LOCATION: Complement((4922)..(4946))

| COCATION: Complement((4922)..(4946))

| OTHER INFORMATION: LB: T-DNA Left border

US-08-817-188-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTCO113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 21; DB 3; Length 4946;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-08-894-440-4/C
Sequence 4, Application US/08894440
Fatent No. 6025346
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOM
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LEASTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: Complement((1)...(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:

NAME/KEY: misc_feature

LOCATION: (4924)..(5216)

OTHER INFORMATION: promoter of nopaline synthase gene of

COTHER INFORMATION: promoter of nopaline synthase gene of

OTHER INFORMATION: Agrobacterium T-DNA (Pnos)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (5317)..(5489)

OTHER INFORMATION: region coding for barstar of Bacillus

OTHER INFORMATION: amyloliquefaciens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (5490)..(5765)

OTHER INFORMATION: region containing polyadenylation signal of gene 7

OTHER INFORMATION: of Agrobacterium T-DNA (3'97)

FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((5840)..(5864))

OTHER INFORMATION: left border of Agrobacterium T-DNA

US-08-894-440-4
NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 3; Length 5864; 100.0%; Pred. No. 0.057; arive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: NO. 5576300 applicable TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-3774
TELEFRAX: (614) 624-3074
TELEFRAX: NO. 5576300e
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ohio
COUNTY: United States
ZIP: 4315
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Lonnie R. Drayer
ADDRESSE: ROSS Products Division
ADDRESSE: Abbort Laboratories
STREET: 625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/308,883
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08308883; Patent No. 5576300; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD 4716 ATAGGGTGGGAGGCTATTTGG 4696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ClarisWorks 1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 625 Cle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-308-883-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
```

```
is the hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 45...593

LOBINITERCATION METHOD: DNA sequencing and restriction analysis
OTHER INFORMATION: The encoded product of nucleotide SEQ ID NO: 1: is the hupphilization information:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B)COMPUTER: Apple Macintosh
OPERATING SYSTEM: MacIntosh System 7.1(D)SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.1%; Score 16.4; DB 1; Length 857; 94.4%; Pred. No. 9.5; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
DESCRIPTION: Human milk kappa-casein
HYPOTHETICAL: NO
ANTI-SENSE:
FRAGMENT TYPE:
FRAGMENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM: HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANELLE:
IMMEDIATE SOURCE: Human Mammary Gland
LIBRARY:
CLONE:
POSITION IN GENOME:
                                                                                                                                                 APPLICATION NUMBER: US/08/730,163
FILING DATE:
CLASSTEICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,882
FILING DATE: 16.5EP-1994
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER: PCT/W093/15196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                TELEPHONE: (614) 624-3774
TELERA: (614) 624-3774
TELEX: NO. 5712250e
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
TYPE: Nucleic acid
STRANDEDRESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAPLOTYPE:
TISSUE TYPE: Mammary gland
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 GGGTGGGTGCTATTTGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 gggtgggaggctatttgg 21
                            United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME/SEGMENT: MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
        Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE: D
JOURNAL:
                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-730-163-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is the humar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08730163
Patent No. 5712250
GENERAL INFORMATION:
APPLICANT: MUKET]1, P.
APPLICANT: Seo, A. E.-Y.
APPLICANT: Cummaings, R.D.
TITLE OF INVENTION: Product for Inhibition of Human Rotavirus Infection.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 45...593
LOCATION: 45...593
LDENTIFICATION METHOD: DNA sequencing and restriction analysis
OTHER INFORMATION: The encoded product of nucleotide SEQ ID NO: 1:
PUBLICATION INFORMATION:
AUTHORS: L. Hansson et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.1%; Score 16.4; DB 1; Length 857; 94.4%; Pred. No. 9.5; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: Adult
HAPLOTYPE:
TISSUE TYPE: Mammary gland
CELL TYPE:
OEGL LINE:
ORGANELLE:
IMMEDIATE SOURCE: Human Mammary Gland
                                                                                 MOLECULE TYPE: CDNA
DESCRIPTION: Human milk kappa-casein
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lonnie R. Drayer
ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbort Laboratories
STREET: 625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ER: PCT/W093/15196
25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PUBLICATION DATE: 05-AUG-1993
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-308-883-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 GGGTGGGTGGCTATTTGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 gggtgggaggctatttgg 21
                                                                                                                                                 ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM: Homo sapiens
LENGTH: 857 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.1 Best Local Similarity 94.4 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
                                                                  Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Columbus
                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-730-163-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
```

```
Sequence 1, Application US/08462437

Sequence 1, Application US/08462437

Sequence 1, Application US/08462437

Sequence 1, Application US/08462437

SERBRAL INFORMATION:

APPLICANT: HANSSON, Lennart

APPLICANT: STROEMOVIST, Mats

APPLICANT: HERNELL, Ole

APPLICANT: TOERNELL, Jan

TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS

TITLE OF INVENTION: POR OBTAINING THE PROTEIN AND USE THEREOF

NUMBER OF SEQUENCES: 31

CORRESCONDENCES: 31

CORRESCONDENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURBIT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-JUN-1995
PRIOR APPLICATION NUMBER: US/08/92
FILING DATE: 23-JAN-1992
ATPORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P:
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
TELEFRAM: 202-628-5197
TELEFRAM: 202-737-3528
TELEFRAM: 202-737-3528
TELER: 248633
TELER: 248633
TELER: 248633
TELER: SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
TYPE: MOLOLIC acid
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
359 GGTGGGTGCTATTTGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
45..593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sig_peptide
45..104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
45..593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13..44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                             D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-462-437-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                    Вþ
                                    APPLICANT: HANSSON, Lennart
APPLICANT: HANSSON, Lennart
APPLICANT: BERGSTROEM, Sven
APPLICANT: BERGSTROEM, Sven
APPLICANT: BERGSTROEM, Sven
TITLE OF INVENTION: OBTAINING THE PROTEIN, PROCESS FOR
TITLE OF INVENTION: OBTAINING THE PROTEIN AND USE THEREOF
OORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Mashington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.1%; Score 16.4; DB 4; Length 857; 94.4%; Pred. No. 9.5; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 MCDUMPUTER: FLOPPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGBNT INFORMATION:
NAME: COOPER, IVET P.
REGISTRATION NUMBER: 48,005
REGISTRATION NUMBER: HANSSON-1
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
TYPE: NUCLEIC STRADED
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
45..593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
45..104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11near
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45..593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'UTR
13..44
                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
FEATURE:
                RESULT 5
JS-08-256-799-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-256-799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
```

Score 16.4; DB 4; Length 857; Pred. No. 9.5;

78.1%; 94.4%;

Query Match Best Local Similarity

ö

Gaps

0

4 gggtgggaggctatttgg 21

Best Local Similarity 94.4 Matches 17; Conservative

g

```
TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 9844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(2580..2633, 5576..5608, 6755..7216)
                                                                                                                                                                                                               OPERATING SYSTEM: PC-FDGS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-JUN-1995
PILOR APPLICATION DATA:
APPLICATION NUMBER: D8 88/92
FILING DATE: 23-JAN-1992
ATTONNEY/AGENT INPORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
                                            ADDRESSEE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.1%; Score 16.4;
                                                                                                                                                                                                                                                                                                                                                                                                                     HANSSON=1A
                                                                                CITY: WASHLED-C
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: HANG
TELECOMMUNICATION INFORMATION:
TELEFHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 246633
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 9844 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
5576..5608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
7251..9017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
2634..5575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
5609..5754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5755..7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2572..2633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426..2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362..425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-462-437-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
   ö
   Gaps
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: STROEMOVIST, MAts
APPLICANT: BERGSTROEM, Sven
APPLICANT: HERNELL, 011e
APPLICANT: TOERNELL, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 920224.01
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4; DB 1;
Pred. No. 9.5;
0; Mismatches 1;
                                                                                           RESULT 7
US-07-962-569A-7/C
US-07-962-569A-7/C
Sequence 7, Application US/07962569A
Patent No. 5391497
GENERAL INFORMATION:
APPLICANT: HONNON, RAVI S.
APPLICANT: JEFFERS, KATHLEEN F.
APPLICANT: HAM, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: REDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
STATE: AN DIEGO
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-462-437-30/c
; Sequence 30, Application US/08462437
; Patent No. 6232094
 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.18;
94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 858 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                   421 GGTGGGTGGCTATTTGG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 gggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.1 Best Local Similarity 94.4 Matches 17; Conservative
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                  92127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                              CITY: SA
STATE: C.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-962-569A-7
```

ò g ó

```
US-08462-437-4/c

Sequence 4, Application US/08462437

Patent No. 6232094

GENERAL INFORMATION:

APPLICANT: HANSSON, Lennart

APPLICANT: BERGSTROEM, Sven

APPLICANT: HERNELL, Ola

TITLE OF INVENTION: DA ENCODING KAPPA-CASEIN, PROCESS

TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF

UNDBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
                                                                                                                                           Score 16.4; DB 4; Length 13104;
Pred. No. 14;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILNG DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILNG DATE: 23-JAN-1992
ATTORNEY/AGRAT INFORMATION:
NAME: COOPER, IVET P.
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: BANSSON=1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STREET: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 13104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                           Query Match 78.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                 exon
12278..12443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: ps459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intron
8868..10014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: intron
LOCATION: 8868..1C
FEATURE:
NAME/KEY: intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intron
1..8834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
LOCATION:
                            ), NAME/KEY;

), LOCATION;

US-08-256-799-4
                              ö
                                 Gaps
                                                                                                                                                                                                                                                                                       APPLICANT: STROEMOVIST, Mats
APPLICANT: STROEMOVIST, Mats
APPLICANT: STROEMOVIST, Mats
APPLICANT: BERGSTROEM, Sven
APPLICANT: TOERNEIL, 011e
APPLICANT: TOERNEIL, 011e
APPLICANT: TOERNEIL, 018
TITLE OF INVENTION: DBA ENCODING KAPPA-CASEIN, PROCESS FOR
TITLE OF INVENTION: DBA ENCODING TITLE OF INVENTION: DATAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                              ö
                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 80/92
FILING DATE: 23-JAN 1992
ATTONNEY/AGENT INFORMATION:
Best Local Similarity 94.4%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALGORER, INCORATION:

REGISTRATION NUMBER: 28,005

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: HANSSON-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

TELEPHONE: 202-628-5197

TELEPHONE: 202-628-5197

TELEPHONE: 202-628-5197

INFORMATION FOR SED IN NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 13104 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: p9459
                                                                                                                                                                               RESULT 9
US-08-256-799-4/c
; Sequence 4, Application US/08256799
; Patent No. 6222094
; GENERAL INFORMATION:
APPLICANT: HANSSON, Lenart
                                                                                              DD 6982 GGGTGGGTGCTATTTGG 6965
                                                                       4 gggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
10015..10510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
8868..10014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
10511..12277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
8835..8867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: intron
LOCATION: 1..8834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: W
                                                                       à
```

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                  ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 24979;
                                                                                                                            Length 1418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                  Indels
      ; NAME/KEY: misc_feature
; LOCATION: 1348
; OTHER INFORMATION: /note= "poly-A addition motif"
US-09-111-470-7
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Roop, Dennis R.
APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
APPLICANT: Yuspa, Stuart H.
TITLE OF INVENTION: KERATIN KI EXPRESSION VECTORS
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/876,289
FILING DATE: APPLICATION NUMBER: 07/876,289
APPLICATION NUMBER: 07/876,1993
APPLICATION NUMBER: 0.1992
APPLICATION NUMBER: 0.1993
ATTORNEY AGENT INFORMATION:
                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC COMPATIBLE COMPATING SYSTEM: IBM MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.1%; Score 16.2; D
85.7%; Pred. No. 19;
tive 0; Mismatches
                                                                                                                                                                0; Mismatches
                                                                                                                        77.1%; Score 16.2; 85.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08147777 Patent No. 5914265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REERENCE/DOCKET NUMBER: 204/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
IELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                602 AAAGGATTGGAGCTATTTGG 622
                                                                                                                                                                                                         1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-08-147-777-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 24979 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                          Query Match 77.13
Best Local Similarity 85.77
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.15
Best Local Similarity 85.75
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                           RESULT 12
US-08-147-777-3
                                                                                                                                                                                                                                               g
                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                 78.1%; Score 16.4; DB 4; Length 13104; 94.4%; Pred. No. 14; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Walladeau, Jenny
APPLICANT: Ravel, Odile
APPLICANT: Ravel, Odile
APPLICANT: Bates, Elizabeth E.M.
APPLICANT: Saeland, Sem
APPLICANT: Saeland, Sem
APPLICANT: APPLICANT: Sebecque, Serge J.E.
TITLE OF INVENTION: Related Reagents
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/111,470 FILING DATE: 08-JUL-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,080
FILING DATE: 09-011-1997
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0695
TELECOMMUNICATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09111470 Patent No. 6277959
                                                                                                                                                                                                                                                                                                                                                                             Db 10242 GGGTGGGTGGCTATTTGG 10225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (6501496-1200 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1418 base pairs
                                                                                                                                                                                                                                                                                                                                                  4 gggtgggaggctatttgg 21
                                                                                                     exon
10015..10510
                                                                                                                                                                exon
12278..12443
                                                                                                                                                                                                                                                                 Ouery Match 78.19
Best Local Similarity 94.49
Matches 17; Conservative
      10511..12277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                             exon
8835..8867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
279..992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                 NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
FEATURE:
                                                                                                                                                                                ; LOCATION:
US-08-462-437-4
                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-111-470-7
                                                                                                                                                                                                                                                                                                                                                  ð
```

ö

a

```
DEVELOPMENT OF A VECTOR TO TARGET GENE EXPRESSION TO THE EPIDERMIS OF TRANSGENIC ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MANDEL, Jean-Louis
APPLICANT: AUBOUNG, Patrick
APPLICANT: AUBOUNG, Patrick
APPLICANT: AUBOUNG, Patrick
APPLICANT: AUBOUNG, Patrick
TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
TITLE OF INVENTION: 20 CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 23
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: COUNG & Thompson
STREET: 745 South 23rd Street
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.2; DB 5; Length 24979;
Pred. No. 19;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                    COMPUTER FEATURE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03965
FILING DATE: 19930428
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PAUL, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/POCKET UNBER: D-5478
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFRAX: 713/651-5346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                           ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
CITY: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-136-277-23
; Sequence 23, Application US/08136277
; Patent No. 5644045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3248 AAAGGGTGGGAAGCTATATGG 3268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 713/651-5246
TELEX: 762829
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24979 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atagggtgggaggctatttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                           TITLE OF INVENTION: DE
TITLE OF INVENTION: EX
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE:
PCT-US93-03985-3
      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 24979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                        Sequence 3, Application US/08452872
Patent No. 6057288
GENERAL INFORMATION:
APPLICANT: Rocby Dennis R.
APPLICANT: Rochnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
APPLICANT: Yuspa, Stuart H.
TITLE OF INVENTION: REMATIN KI EXPRESSION VECTORS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES:
CORRESPONDERS:
ADDRESSEE: LYON & LYON
STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/876,289
FILING DATE: April 30, 1992
APPLICATION NUMBER: Uncassigned (204/144)
FILING DATE: October 29, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.1%; Score 16.2; D
85.7%; Pred. No. 19;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/147,777
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204/153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9303985; GENERAL INFORMATION:
APPLICANT: Roop, Dennis R.
APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (7-3510)
INFORMATION FOR SEQ ID NO: 3:
3248 AAAGGTGGGAAGCTATATGG 3268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3248 AAAGGTGGGAAGCTATATGG 3268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . NOLECULE TYPE: DNA (genomic) US-08-452-872-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 24979 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Los Angeles
: California
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
PCT-US93-03985-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                        US-08-452-872-3
                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

ð

ó

```
| CURRENT APPLICATION DATA:
| APPLICATION NUMBER: US/08/136,277 |
| FILING DATE: 15-0cT-1993 |
| FILING DATE: 15-0cT-1993 |
| CLASSIPICATION: 424 |
| ATTORNEY/AGENT INPORMATION: 12,925 |
| REGISTRATION NUMBER: 32,925 |
| REGISTRATION NUMBER: B2272 |
| TELECOMMUNICATION INPORMATION: 1 |
| TELECOMMUNICATION INPORTATION: 1 |
| TELECOMMUNICATION: 23: 2 |
| TELECOMMUNICATION: 20: 2 |
| TOPOLOGY: 1 |
| TOPOLOGY: 1
```

Search completed: February 25, 2002, 18:05:11 Job time: 18559 sec

		•	
THIS PAGE BLANK (USPTO)			
			: •

AZ016369 RPCI-23-2 BGZ10286 RST29821 AW736851 NXNV. 063_ AW778936 PN2-CT032 BH036913 RPCI-24-3 BGZ17189 RST36890 BGZ04492 RST23896

RST14992 CM4-BN022 CM4-BN022 AV338030 mt03903.r BB252853 BB307020 BB008234

BG219740 BG205014 BE205014 BE011473 AV338030 AV338030 BB252853 BB352853 BB352853 BB36253 BB3625468 BB3625468 BB362544468 BB362544468 BB362344 BB464468 BB36234

oţ

Total number

Searched:

DB

Maximum

Database

Minimum DB

Perfect score: Sequence:

nucleic

.. 6

Run

Scoring table:

RST13406 RST19182 RST31422 RST29306 RST34712 RST39505

BG204492 BAZ188345 BG199886 BG194262 BG199887 BG211849 BG209779 BG215054 BGZ15054 BG

BB464468 EST193201 BB319109 BB319885

BB461095 HS_5092_A UI-R-BJ1-

```
Bukaryotza, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoml, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 212)

1 (bases 1 to 212)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                       BG983367 212 bp mRNA EST 12-JUN-2001
IL5-CN0067-060301-384-f12 CN0067 Homo saplens CDNA, mRNA sequence.
BG983367
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                AA850434
BB319109
BB319885
BB461095
AQ610088
BE113833
                                                                                                                                               BF328785
AV338030
                                                                                                                                                             AA178060
BB252853
BB307020
                                                                 AZ188345
BG199886
                                                                                                                                BG195797
BE011473
                                                                                                                         BG205014
                                                                                                                                                                                                                                                                                                                  BG983367.1 GI:14386102
 sequence tags
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
human.
RESULT 1
BG983367/c
LOCUS
                                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
ပ
                                                   ပပ
                                                                                                                                                                    0000
                                                                                                                                                                                                        0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF924973 IL2-NT020
AW658995 b176b06.w
AW658995 b176b06.w
AW145846 AV145846
F05593 HSC0JC091 n
W5775 Zd20c10.s1
B1188834 d3d12fs.f
BG494856 602540862
AW64184 cm38d02.w
AW69942 b187711.w
BF167952 601775688
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG983367 IL5-CN006
BF924973 IL2-NT020
                                                ; Search time 8261.74 Seconds (without alignments) 27.314 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                               22703874
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                               11351937 seqs, 5372889281 residues
                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                February 25, 2002, 17:20:51
                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF924973
AW638905
AW635936
AV145846
                                   nucleic search, using sw model
                                                                                           atagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG983367
                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                em_gss_pro: *
em_gss_rod: *
em_gss_vrt: *
em_gss_other: *
                                                                            US-09-698-903B-3
21
                                                                                                                                                             seq length: 0
seq length: 2000000000
                                                                                                                                                                                   Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                 em_gss_inv:*
                                                                                                                                                                                                                                                                                                                    em_gss_fun:*
                                                                                                                                                                                                                                                                                                                          em_gss_hum:*
                                                                                                                                                                                                                                                                                                                                         em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   110001111001
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                     em_estfun:*
                                                                                                                                                                                                                             em_esthum: *
                                                                                                                                                                                                                                          em_estom:*
em_estpl:*
em_estba:*
em_estro:*
                                                                                                                                                                                                                                                                        em_estov:*
em_htc:*
                                                                                                                                                                                                                                                                                             gb_est2:*
gb_htc:*
gb_gss:*
                                                                                                                                                                                                                                    em_estin:*
                                                                                                                                                                                                                                                                                       gb_est1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match I
                                                                                                                                                                                                               EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8882.9
881.0098
800.0098
800.00880.0098
800.00880.0098
                                                                                                                                                                                                                                                                                     2001....
2001....
```

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-CN0067-060301-384-fil2&t3=2001-03-06&t4=1)
Seq primer: puc 18 forward

BG494856 AW644184 AW639842 BF167952 BI188834

ပ

F05693 W57725

17.4 17.4 17.4 17.4 16.8 16.8 16.8 16.8 16.8 16.8

10 11 11 12

0000000

Score

Š.

Brazil

```
cdna@resgen.com
DNA Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laevis
                                                                          ø
                                                                      66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus
                                                                                                                                                                                                                                                                                                                                                   RESULT 3
AW638905/c
LOCUS
                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                      셤
                                                                                                                                            /note="Organ: colon_normal; Vector: puc18; Site_1: Smal; Ste_2: Smal; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 429)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmen, G.H., Carvahlo, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveire, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A min1-library was made by cloning products derived from CNESTEE PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0200-
281100-263-C11&t3=2000-11-28&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF924973 429 bp mRNA EST 19-JAN-2001
IL2-NT0200-281100-263-C11 NT0200 Homo sapiens CDNA, mRNA sequence.
BF924973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                     Score 17.4; DB 11; Length 212; Pred. No. 6e+02; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CN0067"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0200"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: puc 18 forward
High quality sequence stop: 351.
Location/Qualifiers
High quality sequence stop: 211.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF924973.1 GI:12320948
                                                                                                                                                                                                                                                                                                                                                                                        82.9%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 TAGGGTGGGAGGCTATGTG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 tagggtgggaggctatttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
BF924973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
```

```
D176506 W1 Blackshear/Soares normalized Xenopus egg library Xenopus laevis cDNA clone PBX0076B06 5', mRNA sequence.
AW638905
AW638905.1 G1:7396075
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions. 

2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anotes Vector: pT713-Pac; Site_1: ECORI; Site_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus Pacyts eggs. The library was constructed in the vector pT713-Pac as described in Bonaldo, M.F. Lennon, G. and Soares, M.B. 'Normalization and subtraction: two
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.

1 (bases 1 to 501)

Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G., Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soares, M.B.
The NIEMS Xenopus maternal EST project: interim analysis of the first 13,879 ESTs from unfertilized eggs
21211403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 919 541-4899
Fax: 919 541-4571
Email: black009driehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="PBX0076B06"
/clone_lib="Blackshear/Soares normalized Xenopus egg
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                         Length 429;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                Score 17.4; DB 11;
Pred. No. 6.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR PRimers
FORWARD: TGTAAACGACGCCAGT
FORWARD: TGTAAACGACGCCAGT
BACKWARD: CAGGAAACAGCTATGACC
Plate: 0076 row: B column: 06
Seq primer: T7 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female"
                                                                                                                                                                                                82.9%;
94.7%;
                                                                                                                                                                                                                                                                                                                                          392 AGCGTGGGAGGCTATTTGG 410
                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African clawed frog.
                                                                                                                                                                                          Query Match 82.9
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                            3 agggtgggaggctatttgg
```

g õ

```
185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S:
Matches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV145846/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW635936 583 bp mRNA EST 26-APR-2001 bl40d03.wl Blackshear/Soares normalized Xenopus egg library Xenopus laevis cDNA clone PBX0040D03 5', mRNA sequence.
        Genome Research
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BlackShear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G. Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soares, M.B.
The NIEHS Xenopus maternal EST project: interim analysis of the first 13, 879 ESTs from unfertilized eggs
approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNas were ligated to ECORI adapters, digested with NotI, and directionally cloned into the NotI and ECORI-digested pT773-Pac vector. The library contained approximately 7.2 x 10^5 recombinants, with average insert sizes of I-1.5 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 919 541-4899
Fax: 919 541-4571
Email: black009eniehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Hurtsville, AL 35901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pT/T3-Pac; Site_1: EcoRI; Site_2: NotI;
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Blackshear/Soares normalized Xenopus egg
                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                      Length 501;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                      DB 10; L
9.3e+02;
                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
dew_stage="unfertilized egg"
/lab_host="bH108"
                                                                                                                                                                                                                                   Score 17; DB 1; Pred. No. 9.3e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: TGTAAAACGACGCCAGT
BACKWARD: CAGGAAACACTATCACC
Plate: 0040 row: D column: 03
Seq primer:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="PBX0040D03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 267 (1), 71-87 (2001)
                                                                                                                                                                                                                                   81.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex-"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW635936
AW635936.1 GI:7393017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
1 (bases 1 to 583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              African clawed frog.
                                                                                                                                                                                                                                                                                                                                                            317 TAGGGTGGGAGGCTATT 301
                                                                                                                                                                                                                                                                                                                       2 tagggtgggaggctatt 18
                                                                                                                                                                                                                               Query Match 81.0°
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21211403
                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                             AW635936/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
```

```
lacyis eggs. The library was constructed in the vector py773-pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6.791-806, 1996. The first stranded cobnaw were ligated to NotI-dT18 primer; double stranded cDNax were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT773-pac vector. The library contained approximately 7.2 x 10°5 at 126 c 128 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 285)
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Rawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Nitisuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S. A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S. A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
PolyA-selected mRNA was prepared from unfertilized Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV145846 285 bp mRNA EST 03-JUL-1999
Y4745846 Mus musculus C57BL/6J 10-11 day embryo Mus musculus CDNA
Clone 2810449H10, mRNA sequence.
AV145846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="2810449H10"
/clone_lib="Mus musculus C57BL/6J 10-11 day embryo"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.0%; Score 17; DB 10; I
100.0%; Pred. No. 9.4e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="10-11 day embryo"
87 c 53 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@rtc.riken.go.jp

    .285
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV145846.1 GI:5349979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 TAGGGTGGGAGGCTATT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tagggtgggaggctatt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100. nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
```

RESULT 6 F05693/c LOCUS DEFINITION

ð 셤 ACCESSION VERSION

SOURCE

REFERENCE AUTHORS JOURNAL MEDLINE COMMENT

TITLE

FEATURES

```
1. .424
/organism="Homo sapiens"
/db_xref="Colone:126577"
/db_xref="Colone:126577"
/db_xref="Colone:126577"
/db_xref="Colone:126577"
/dlone="IMAGE:341202"
/clone="IMAGE:341202"
                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 424)
1 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RN
Mashington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 866 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 376.
zd20c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone MAGR:341202 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI188834 429 bp mRNA EST 10-JUL-2001 d3d12fs.fl Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone d3d12fs 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 16.8; DB 11; Length 424; 90.0%; Pred. No. 1.1e+03; 1.1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusarium sporotrichioides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
BI188834
BI188834.1 GI:14662513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 AIGGGTGGGAGGCICITIG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                        W57725.1 GI:1364441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atagggtgggaggctatttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.0
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145
                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
BI188834/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                  ACCESSION
                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="total brain"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: Not!; sex=Female; dev_stage=3 months old;
slite_2: Not!; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press*
08 a 53 c 46 g 114 t
                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Memmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)

Aufray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE: molecular_integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F05693 321 bp mRNA EST 19-FEB-1995
HSC0JC091 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-0jc09
Seq primer: (-21)M13_universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humain
Cedex, FRANCE
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                             Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.8; DB 11; Length 321;
Pred. No. 1.1e+03;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="c-0jc09"
/clone_lib="normalized infant brain cDNA"
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genexpress-Genethon
Genethon Centre de recherche sur le Genome
1,rue de l'Internationale, BP60 91002 EVRY
Tel: 33169472800
Fax: 33160778698
                Score 16.8; DB 10;
Pred. No. 1.1e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 321
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c-0jc09, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex-"Female"
                                                                                                                                                                                                                                47 TAGGGTGGGAGGCAATTAGG 28
                                                                                                                                                                         2 tagggtgggaggctatttgg 21
            Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 TGGGGTGGGAGCAATTTGG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F05693.1 GI:669509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. R. Aca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST.
human.
```

ó

Gaps

ö

BASE COUNT ORIGIN

RESULT W57725/c

δ g S

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4671903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: TGTAAAACGACGGCCAGT
BACKWARD: CAGGAAACAGCTATGACC
Plate: 0137 row: D column:
Seq primer: T7 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Perry J. Blackshear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 TGGGGTGGGAGGCAATTTGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW644184.1 GI:7401561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
1 (bases 1 to 626)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 tagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW644184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 587)

SN MIH-WGC http://mgc.nci.nih.gov/.

SN MIH-MGC http://mgc.nci.nih.gov/.

LOUDUDIShed (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
              Eukaryota; Fungl; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.

1 (bases 1 to 429)

1 (bases 1 to 429)

1 (Bases 1 to 429)

2 (Bag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: Xhoi; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript" 1 102 c 68 9 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                Email: broe@ou.edu
Contect Dr. Marian Beremand regarding clone availability Include
is the best homolog from a blastx search of Genbank nr 04-09-01
71 3.9 gil3550690|emb[CAA09 (AJ010199) variable surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG494856 587 bp mRNA EST 27-MAR-2001 602540862F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4671903 5'
                                                                                                                                                    Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1487 row: 1 column: 16 High quality sequence stop: 584. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Fusarium sporotrichioides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 11;
Pred. No. 1.1e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13-20
High quality sequence stop: 405.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Tri 10"
/db_xref="taxon:5514"
/clone="d3d12fs"
Fusarium sporotrichioides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BG494856
BG494856.1 GI:13456371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 ATTGGGAGGGAGGCTATTG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atagggtgggaggctatttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 90.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
ORGANISM
                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG494856/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                           REFERENCE
                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

```
AW644184 626 bp mRNA EST 26-APR-2001 cm38d02.wl Blackshear/Soares normalized Xenopus egg library Xenopus laevis cDNA clone PBX0137D02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blackshear, P.J., Idi, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G. Jr., Moore, D.T., Bulfard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soares, M.B.
The NIEHS Xenopus maternal EST project: interim analysis of the first 13,879 ESTs from unfertilized eggs
21211403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
Fax: 976-516-9016 att:cdna, email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, cdna4resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 16.8; DB 11; Length 587; 90.0%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
```

```
/tissue_type="unfertilized egg"
/dev_stage="unfertilized egg"
/dev_stage="unfertilized egg"
/dev_stage="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host==bloos"
/lab_host==bloos"
/lab_host==bloos"
/note="Vector: pT773-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT773-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dT18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT773-Pac vector.
The library contained approximately 7.2 x 10^5
recombinants, with average insert sizes of 1-1.5 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF167952 892 bp mRNA EST 30-OCT-2000 601775688F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017644 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E I (bases 1 to 892)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert strausberg, Ph.D.

Contact: Robert strausberg, Ph.D.

Contact: Robert strausherg, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Prayed Genomics, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM9266 row: o column: 21

High quality sequence stop: 662.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 892)
                                                                                                                                                                                      /db_xref="taxon:8355"
/clone="PBX0087H11"
/clone_lib="Blackshear/Soares normalized Xenopus egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 16.8; DB 10;
90.0%; Pred. No. 1.2e+03;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .892
/organism="Mus musculus"
/strain="c2EGH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:4017644"
                                                                                                                                                                 /organism="Xenopus laevis"
                                                          column: 11
  BACKWARD: CAUGAL...
Plate: 0087 row: H column.
Seq primer: T7 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                 library"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF167952
BF167952.1 GI:11048304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 TAGGGTGGGAGGATATTAGG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.08
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF167952/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                             /Clone=TBX013/D02"
/Clone=Ibb="BlackShear/Soares normalized Xenopus egg
Ilbrary"
/sax="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/dev_stage="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_bost="blands"
/lab_bost="blands"
/note="Vector: p7713-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector p7713-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research Soares, M.B. Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-disested p7713-pac vector. The library contained approximately 7.2 x 10.5
recombinants, with average insert sizes of 1-1.5 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bl87hl1.w1 Blackshear/Scares normalized Xenopus egg library Xenopus Aw639842 GI:7397045

AW639842 GI:7397045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibla; Batrachia; Anorous.

1 (bases 1 to 667)
Blackshear, P.J., Lal, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G., Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soares, M.B.
The NIEHS Xenopus maternal EST project: interim analysis of the first 13,879 ESTS from unfertilized eggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 919 541-4899
Email: black0099ichs.nth.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing and analyses performed by National Institutes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 16.8; DB 10; Length 626; 90.0%; Pred. No. 1.2e+03; Live 0; Mismatches 2; Indels 0

    .626
    /organism="Xenopus laevis"
/db_xref="taxon:8355"
    /clone="PBX0137D02"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: TGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 TAGGGTGGGAGGATATTAGG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 tagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW639842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21211403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
AW639842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
```

ORGANISM

REFERENCE AUTHORS JOURNAL MEDLINE

COMMENT

TITLE

ACCESSION

ð g VERSION KEYWORDS

ö

Gaps

```
/sex="Female"
//lab_nost="DHIOB"
//lab_nost="DHIOB"
//lab_nost="DHIOB"
//lab_nost="DHIOB"
//lab_nost="DHIOB"
//lab_nost="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
Broin genomic DNA was isolated and partially digested
with a compination of ECORI and ECORI Methylase.
Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies). "
36 c 49 g 59 t
                                                                                                                        AZU16369 184 bp DNA GSS 25-FEB-2000
RPCI-23-264M11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-264M11
, DNA sequence.
AZ016369
                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library BCIP-23. For BAC
Library avallability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 264 row: M column: 11
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS BG210286 284 bp mRNA EST 21-APR-2001
DEFINITION RST29821 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Other GSSs: RPCI-23-264M11.TV
Contact: Shaying Lary
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
9721 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 13;
Pred. No. 1.7e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 184
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-264M11"
/clone_llb="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                             21
                                                                                                                                                                                                                                                             AZ016369.1 GI:7091753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.1%;
94.4%;
  1 atagggtgggaggctatttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 agggtgggaggctatttg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AGGGTGGGAGGCAATTIG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
BG210286/c
                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                         AZ016369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                            SOURCE
                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 914)

Roset-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                      /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

225 c 237 g 189 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 914)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="G"
/note="Genoscope sequence ID : C0BG039BF08LP1-end : T7"
257 c 239 g 212 t 4 others
                      /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS03N93 914 bp DNA GSS 17-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 039K16 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                              80.0%; Score 16.8; DB 11; Length 892; 90.0%; Pred. No. 1.2e+03; 1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charaterization and repeat analysis of the oc
freshwater pufferfish Tetraodon nigroviridis
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="039K16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.8; DB 13;
Pred. No. 1.2e+03;
0; Mismatches 3;
/clone_lib="NCI_CGAP_Lu29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
AL251760
AL251760.1 GI:7972772
                                                                                                                                                                                                                                                                                                                                                                                                       871 TAGGGTGTGAGGCTATATGG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%;
                                                                                                                                                                                                                                                                                                                                                                              2 tagggtgggaggctatttgg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope
                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
CNS03N93/c
                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

ö

Gaps

ö

```
Location and a spiens "

1. .284

/organism="Homo sapiens"
/do_refe="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/cell_line="HT1080"
/cell_line="HT1080"
/cell_line="see 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression
Libraries using Random Activation of Gene Expression
/cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasea: 1 to 284)

Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, M., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                and Ducar, M.
Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.4; DB 11; Length 284;
Pred. No. 1.7e+03;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                               Athersys, Inc.
3201 Carnegle Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Email: scain@athersys.com
High quality sequence stop: 234.
  BG210286
BG210286.1 GI:13731973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 94.4%;
Matches 17; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 gggtgggaggctatttgg 21
                                                                                                  Homo sapiens
                                                                       human.
                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                       JOURNAL
COMMENT
                                                                                                                                                                REFERENCE
                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

Search completed: February 25, 2002, 17:20:54 Job time: 16147 sec

238 GGTGGGTGCTATTTGG 221

셤

us-09-698-903b-4.rge

```
synthetic construct.

M synthetic construct
artificial sequence.

1 (bases 1 to 15)
Paul, W.B., Scott, R.J., Hird, D.U. and Hodge, R.U.
Tapetum-specific promoters
Papetum-specific promoters
BIOGEMMA UK LIMITED (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .15
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX046662 15 bp DNA
Sequence 8 from Patent W00068403.
AX046662 GI:11876228
                                                                                                                                                                                                                                                                                                                                                                                    3 AF218866

8 PCPAL2

9 AF1913186

9 AF1913186

9 AF1913186

9 AF191318

9 AF24516

2 AF24516

2 AF24516

2 AF24516

10 BF24516

10 BF24516

2 AF24516

3 AF24516

4 AF24516

5 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVU88057
RABGLCOGEN
AC019630
                                                                                                                                                                               AF283269
GC0251757
GC029186
AF04992
AF162910
AF162910
AF162913
AF162913
AF162913
CTR242496
                                                                                                                    GMU26701
PUMPAL2A
AX127755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHTGIR
AC018291
AF325859
AF361883
AC014293
                             AX046662
AX063588
AX127751
AX167666
E08065
                                                                                                       MMU80260
                                                                                                                                                                                                                                                                                                                                                        AF052582
AF387019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX017147
AB029020
                                                                                                                                                                      HSMCRP1
 DB
                                                                                                                                                                                                                                                             1088
1092
11092
11321
11499
22115
22115
22154
22275
2384
2427
2851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4501
4953
5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5315
6201
6211
7101
9276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3246
3282
3614
3855
3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4233
 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2931
3084
 Match
                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
AX046662
LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
 8
                                                                                                                                                                                                   0000000
                                                                                                                                                                                                                                                                                                                  O
                                                                                                                                                                                                                                                                                                                                                000
                                                                                                                                                                                                                                                                                                                                                                                                                                       O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ου
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O
                                                                                     February 25, 2002, 18:00:06 ; Search time 2331.3 Seconds
(without alignments)
106.146 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                             1472140 segs, 8248589755 residues
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                               1 ntcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_htgo_hum:*
em_htgo_inv:*
em_htgo_rod:*
em_htg_hum:*
em_htg_inv:*
em_htg_rod:*
em_htg_rod:*
                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                  US-09-698-903B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_om:*
gb_pat:*
gb_ph:*
gb_p1:*
gb_pr:*
gb_rc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_sy: *
gb_un: *
gb_v1: *
em_ba: *
em_fun: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_pat:*
em_ph:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_om:*
em_or:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_sts:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_sy:*
em_un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_ba:*
gb_htg:*
gb_in:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_in:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_ov:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_pl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_ro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_v1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                      GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                               Scoring table:
```

AF19138 Home sapi M13508 Rat apolipo AF022864 Home sapi AF022864 Home sapi 272850 S.cerevisia AF025331 Drosophil AF745516 Drosophil AF005506 Mus muscu BC005506 Mus muscu AF185069 Leishmani AK11747 Sequence AE005500 Home sapi UB8057 Melao virus L10605 Oryctolagus AC019630 Drosophil AF018291 Drosophil AF018291 Drosophil AF018291 Schistcon AF561883 Schistcon AF018291 Drosophil

15-DEC-2000

PAT

ALIGNMENTS

AF162913 Replanus AX046673 Sequence U24436 Mayetiola d AJ242496 Candida t AF02258 Pusarium AF387019 Arabidops

AF218866 Caenorhab

AX127755 Sequence AF073484 Homo sapi AF283269 Anopheles AJ251757 Globodera U94186 Colletotric

Sednence:

Title:

Run on:

Searched:

Database

U80260 Mus musculu

Glycine max Petroselinu

AX127751 Sequence AX167666 Sequence E08065 Non-specifi

Description

AF049922 Petunia x AF328994 Arabidops AF162910 Hirschfel AF161333 Raphanus

SUMMARIES

Gaps

÷

03-JUL-2001

PAT

RESULT AX063588 LOCUS

g

KEYWORDS SOURCE

JOURNAL

FEATURES

```
OS None
OS Artificial sequences.
PN 19199425343-A/4
PD 13-SEP-1994
PF 03-MAR-1993 JP 1993043006
PI RIVUV YOUKOU, ROBAATO EFU UITSUTEIA, MITSUKAWA NORIHIRO PC C12N15/10,C1201/68;
CC Appothetical: No;
CC hypothetical: No;
CC hypothetical: No;
CC Appothetical: No;
FF Key
FF Source 1. .15
FT Source 1. .15
FT Source 1. .15
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E08065.1 GI:2176190

JP 194253843-A/4.

unidentified.

SM unidentified

unclassified.

E I (bases I to 15)

S RIYULY X., Robato, E.U. and Mitsukawa, N.

MYTHOD FOR AMPLIFYING DNA SEQUENCE

PATENT: JP 1994253843-A 4 13-SEP-1994;

CHTKYU KANYO SANOTO GIJUTSU KENKYU KIKO, MITSUI GIYOUSAI

SHOKUBUTSU BIO KENKYUSHO: KK
                                                                                                                                                                                                                                                                   Synthetic construct
artificial sequence.
I classes 1 to 15)
wegrich Glover, L. Budziszewski, G.J., Levin, J.Z. and Zhou, Q.
Herbicide target genes and methods
Patent: WO 0144277-A 11 21-JUN-2001;
Syngenta Participations AG (CH)
Location/Qualifiers

    .15
    /organism='Artificial sequences'.

         Score 12.4; DB 6; Length 15;
Pred. No. 2e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.7%; Score 12.4; DB 6;
100.0%; Pred. No. 2e+03;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligonucleotide"
a 1 c 3 g 5 t
                                                                                                                                                                         AX167666 15 bp DNA
Sequence 11 from Patent W00144277.
AX167666 AX167666.1 GI:14597053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
        82.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 bp
                                                                                                                                                                                                                                                        synthetic construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E08065
Non-specific primer.
E08065
        Query Match 82.7
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                   2 tcgastwtsgwgtt 15
                                                                                   2 TCGASTWTSGWGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                           LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                            RESULT A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
E08065
                                                                   ð
                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                      synthetic construct
artificial sequence.
1 (bases 1 to 15)
Habu Y., mittelsten Scheid, O., Amedeo, P. and Paszkowski, J.
Gene involved in epigenetic gene silencing
Patent: WO 0100801-A 7 04-JAN-2001;
Novartis AG (CH); Novartis-Erfindungen Verwaltungsgesellschaft
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                  24-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 15)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing same Patent: WO 0131042-A 4 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                     Query Match 82.7%; Score 12.4; DB 6; Length 15; Best Local Similarity 100.0%; Pred. No. 2e+03; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.7%; Score 12.4; DB 6; Length 15; 100.0%; Pred. No. 2e+03; tive 0; Mismatches 0; Indels
                                5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 others
                                                                                                                                                                                                                                                                  PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .15
//Organism="synthetic construct"
//db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"
a 1 c 3 g 5 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer MDB285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
t
                 ູ້ດີ
                 , 9, or c
g
                                                                                                                                                                                                                                                               AX063588 15 bp DNA
Sequence 7 from Patent WO0100801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA12/751 15 bp DNA
Sequence 4 from Patent WO0131042.
AX127751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                u,t
              /note="n is a,
                                                                                                                                                                                                                                                                                                          AX063588.1 GI:12541312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX127751.1 GI:14134398
                                                                                                                                                                                                                                                                                                                                         synthetic construct
                                r
U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                  Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                m.b.H. (AT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ø
                                                                                                                                                                                                                                                             AX063588
misc_feature
                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
```

ö

Gaps

ö

Length 15; Indels 29-SEP-1997

PAT

TITLE

FEATURES

REFERENCE AUTHORS

KEYWORDS

RESULT AX127751

à

```
82.78;
71.48;
                                                                                                                                                                                                                                                                                           82.78;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L37355.1 GI:567856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ၁
66
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                   ||||:|:|:|||
| 132 TCGAGTTTGGAGTT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1111:1:1:111
363 TCGAGTTTCGAGTT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                     2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                     Ø
                                                                                                                                                                                                                                   81
 9364938
                                                                                                                                                                                               repeat_unit
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
TATA_signal
                                                                                                                                                                             repeat_unit
satellite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
               REFERENCE
AUTHORS
                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
   PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                        PUMPAL2A
                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                      Woodcock, D.M. and Linsenmeyer, M.E. Direct Submission Submitted (29-NOV-1996) Research, Peter MacCallum Cancer institute, St. Andrew's Place, East melbourne, Vic 3000, Australia
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morgante, M., Jurman, I., Shi, L., Zhu, T., Keim, P. and Rafalski, J.A. The STR120 satellite DNA of soybean: organization, evolution and chromosomal specificity
Chromosome Res. 5 (6), 363-373 (1997)
98030220
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                  MMU80260 206 bp DNA ROD 19-DEC-1996
Mus musculus clone ma9 L1 retrotransposon LINE1 repeat region
U80260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 206;
                                                                                                                82.7%; Score 12.4; DB 6; Length 15; 100.0%; Pred. No. 2e+03; 1ve 0; Mismatches 0; Indels
                                                           5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.4; DB 10;
Pred. No. 2e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transposon="L1 retrotransposon"
/db_xref="taxon:10090"
/clone="ma9"
                                                         5
t
             1. .15
/organism="unidentified"
/db_xrefe"taxon:32644"
a 1 c 3 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .206 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMU26701 240 bp DNA
Glycine max satellite STR120-B.1.
U26701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family-"LINE1"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.78;
71.48;
                                                                                                                                                                                                                                                                                                                     U80260.1 GI:1737239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U26701.1 GI:1142703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 71.4 Matches 10; Conservative
                                                                                                                 Query Match 82.7
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                         2 tcgastwtsgwgtt 15
                                                                                                                                                                                                  2 TCGASTWTSGWGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 TCGAGTTTCGAGTT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
GMU26701/c
                                                         BASE COUNT
                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                               RESULT
MMU80260
                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
Logemann, E., Parniske, M. and Hahlbrock, K.
Modes of expression and common structural features of the complete
Modes of expression and common structural features of the complete
Modes of expression and common attractural
Modes of supplementation and supplementation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phenylalanine ammonia-lyase.
Petroselinum crispum DNA.
Petroselinum crispum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.

1 (bases 1 to 411)
2 (bases 1 to 240)
Morgante,M. and Rafalski,J.A.
Morgante,M. and Rafalski,J.A.
Direct Submission
Submitted (09-MAY-1995) Michele Morgante, Dip. di Produzione
Vegetale, Universita di Udine I-33100, Via delle Scienze, 208,
Udine I-33100, Italy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUMPAL2A 411 bp DNA PLN 21-JUL-1995 Petroselinum crispum phenylalanine ammonia-lyase (PAL-2) gene, promoter region and 5' end of cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Petroselinum crispum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.4; DB 8;
Pred. No. 2e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.4; DB 8
Pred. No. 2e+03;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4043"
/note="(vector lambda EMBL4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                            1. .240

/organism="Clycine max"

/cultivar="Ripley"

/db_xxef="taxon:3847"

1. .120

1. .240

/note="STR120-B.1"

121. .240

a 49 c 60 g 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1, .260
230, .235
409, .411
/gene="PAL-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX127755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AX127755
LOCUS
```

ö

ó

Gaps

```
Anopheles gambles controlled to the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-JUN-2000) Department of Medical and Molecular Parasitology, New York University School of Medicine, 341 East 25th Street, New York, NY 10010, USA
Location/Qualifiers
1. 676
/organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"ribosomal protein S26"
/protein_dd-"AAG15374 1"
/db_xref="G1:1024304"
/translation-"MLERRNGGRCKHNRGHVKAVRCTNCARCVPKDKAIKKEVIRNIV
EAAANRDISDASYYSSYVLPKILYAKLHYCVSCAIHSKVVRNRSKETRRIRTPPQRSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRO251757 733 bp mRNA INV 12-JAN-2001
Globodera rostochiensis mRNA for for hypothetical protein (clone
A18).
                                                                                                                                                                                                                       AF283269 676 bp mRNA INV 16-OCT-2000
Anopheles gambiae ribosomal protein S26 (IrpS26) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 676)
Oduol, F.O., Xu, J., Niare, O., Natarajan, R. and Vernick, K.D.
Direct Submission
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.4; DB 3; Length 676;
Pred. No. 2e+03;
4; Mismatches 0; Indels
                           Indels
                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 t
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="immune-responsive"/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
1. .676
                                                                                                                                                                                                                                                                                                                                                       African malaria mosquito.
                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="IrpS26"
30. .374
/gene="IrpS26"
                                                                                                                                                                                                                                                                                    AF283269
AF283269.1 GI:10242303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORF.
Globodera rostochiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ251757
AJ251757.1 GI:12227170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDMNRQQNAQRK*
179 c 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.7%;
ilarity 71.4%;
Conservative 4
                       Conservative
                                                            2 tcgastwtsgwgtt 15
                                                                                   582 TCGAGTTTCGTGTT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160
                    10;
                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GR0251757/c
                                                                                                                                                                           1
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                          88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                AF283269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                              ŏ
                                                                                                      QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens MHC class I-related protein MRI precursor (MRI) gene, AF073484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo. (base) 1 to 636)

Yamaguchi, H., Kurosawa, Y. and Hashimoto, K.
Expanded genomic organization of conserved mammalian MHC class Blochem. Biophys. Res. Commun. 250 (3), 558-564 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUN-1998) Institute for Comprehensive Medical Science, Fujita Health University, Toyoake, Aichi 470-1192, Japan Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  /organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' border flanking region of elite event MS-B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                   synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 415)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing same Patent: WO 0131042-A 8 03-MAY-2001;
Aventis Cropscience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.4; DB 9;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.4; DB 6
Pred. No. 2e+03;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .636
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
/chromosome="lacanta"
Sequence 8 from Patent WO0131042. AX127755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                     1. .234
/note="plant DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138
                                                AX127755.1 GI:14134402
                                                                                                                                                                                                                                                                                                                                                                                                                             235. .415
/note="T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF073484.1 GI:3859892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="1q25.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 82.7%;
1 Similarity 71.4%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene-"MR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TCGAGTTTGGTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hashimoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ಪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 of 2
                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                            VERSION
KEYWORDS
SOURCE
ORGANISM
  DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                  Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSMCRP1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
```

à 셤 ö

Gaps

```
10859200
                                                                                                                                                                                                                                                                                               233
 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
AF049922/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                 Direct Submission
Submitted (03-DEC-1999) Qin L., Laboratory of Nematology, Wagenigen
University, Binnenhaven 10, 6709 PD Wageningen, NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="CAC21848.1"
/db_xref="G1:12227171"
/translation="hypereferoavcoluvabaspppktnytklekgpasagnaesypglp
PQNRWDTDAHHKDLTLTDG1.VQNNGKDKEWRYVFAKQSIPKDGIFYYEVKILEKGTR
VQIGTATKONPLDKPVGWSGTYAYASAGYFWGHKDSKCTIGTANGRPYIKGPWFGNG
VDIGTATKONPLINTELHVDSAAKLYPCVSMFMPGTKIEANFGPF"
168 c 171 g 184 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-MAR-1997) CRCTPP, University of Queensland, St.Lucia,
                 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
1 (bases 1 to 733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stephenson, S.-A., Maclean, D.J. and Manners, J.M.
Disruption of a novel pathogenicity gene of Colletotrichum
gloeosporioides results in a hypersensitive response in the host
                                                                 Qin,L., Overmars,H., Helder,J., Popeijus,H., van der Voort,J.R., Groenink,W., van Koert,P., Schots,A., Bakker,J. and Smant,G. An efficient cDNA-AFLP-based strategy for the identification of putative pathogenicity factors from the potato cyst nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colletotrichum gloeosporioides nitrogen starvation-induced glutamine rich protein mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="dorsal gland"
/dev_stage="infective second stage juvenile"
23. 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.4; DB 3; Length 733; Pred. No. 2e+03;
                                                                                                                                                                 Mol. Plant Microbe Interact. 13 (8), 830-836 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephenson, S.-A., Maclean, D.J. and Manners, J.M. Direct Submission
                                                                                                                                                                                                                                                                                                                               /organism~"Globodera rostochiensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brisbane, Queensland 4072, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                 /isolate="Rol-Mierenbos"
/db_xref="taxon:31243"
/clone="A18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                            Globodera rostochiensis
Globodera rostochiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stylosanthes guianensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glomerella cingulata.
Glomerella cingulata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U94186.1 GI:2707190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ORF"
                                                                                                                                                                                                  (bases 1 to 733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 905)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 905)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 TCGAGTTTGGTGTT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glomerella.
                                                                                                                                                                               20393248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCU94186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210
                                                                                                                                                                                                                     Qin, L
                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
GCU94186/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                          JOURNAL
                                                    REFERENCE
                                                                       AUTHORS
                                                                                                                                                               JOURNAL
                                                                                                                                                                                 MEDLINE
                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           윱
```

FEATURES

```
2 (bases 1 to 927)
Guyon,V., Astwood,J.D. and Taylor,L.P.
Direct Submission State Submitted (23-FEB-1998) Genetics and Cell Biology, Washington State University, Science Hall, Pullman, WA 99164-4234, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /processi_d="Add02548.1"
/db_xref="G1:4105782"
/db_xref="G1:4105782"
/translation="MNTFRLAcDMTHLASVLVLLLKIHTIKSCAGVSLKTQELYALVF
/translation="MNTFRLACDMTHLASVLVLLLKIHTIKSCAGVSLKTQELYALVF
/translation="MNTFRLACDMTHLASVLVLLKIHTIKSYDKDQDTFRHLFLVL
PCLLLALVINDRFTFREWMFPSIYLEAVALLPQLVLLLQRTRNIDNLTGQYIFLLGAY
RSFYILNWVYRYFTEPHFVHWITWIAGLIQTLLYADFFYYYFQSWKNNTKLELPA"
                                                                                                                                                                                                                                                /protein_id="AAB92223.1"
/db_xref="G1:2707191"
/translation="MSSNDYYGNSGHGQQGYNQGYQQQGYGQQGGYPQQPSYASQQQ
                                                                                                                                                                                                                                                                                                                                      PGGYPOQSHSPYQOGGGYNAPQOHGYGGPQQPTYAQGGQQNQGYSSGHDNRGHSSYPQ
QQQYGGQHQQQQQQGYGQQGQGQGQQCQYDPNGPVGPDGERGLGATLVGGGTAGWAAH
KGGGLLGTLGGAIAGANAMLEHAGKKHKKEKKHKKDKHHKRGLSGSSSSSD"
273 c 273 c 156 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Core eudicots; Asteridae; euasterida; Eustaridae; euasterida; Solanales; Solanaceae; Petunia.

1 (bases 1 to 927)
Guyon, V.N., Astwood, J.D., Garner, E.C., Dunker, A.K. and Taylor, L.P. Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia plant Physiol. 123 (2), 699-710 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Petunia x hybrida"
/db_xref="taxon:4102"
/tissue_type="germinating petunia pollen treated with
kaempferol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF049922 927 bp mRNA PLN 05-JUL-2000
Petunia x hybrida PGPS/D6 (PGPS/D6) mRNA, complete cds.
AF049922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                   /note="glutamine rich protein similar to glutenins;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ER lumen protein retaining receptor homolog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
/organism="Glomerella cingulata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.4; DB 8;
Pred. No. 2e+03;
1; Mismatches 0;
                                                                                                                                                                                                 nitrogen starvation-induced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        putative HDEL receptor
                       /isolate="UQ62"
/db_xref="taxon:5457"
/note="biotype B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="PGPS/D6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dene="PGPS/D6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dene="PGPS/D6"
                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF049922.1 GI:4105781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.7%;
71.4%;
                                                                                                             biotype: B" 74. .721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.4*
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petunia x hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Petunia x hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 TCGAGTATCGAGTT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
```

305

176

O

ø 273

```
Search completed: February 25, 2002, 18:00:08 Job time: 18416 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis lyrata.
Arabidopsis lyrata
Arabidopsis lyrata
Arabidopsis lyrata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 942)
Schlerup, M.H., Mable, B.K., Awadalla, P. and Charlesworth, D. Identification and Characterization of a Polymorphic Receptor
Kinase Gene Linked to the Self-Incompatibility Locus of Arabidopsis
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF328994 942 bp DNA PLN 17-MAY-2001
Arabidopsis lyrata putative S-glycoprotein (S) gene, S-13-4 allele,
partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 942)
Schierup, M.H., Mable, B.K., Awadalla, P. and Charlesworth, D.
Direct Submission
Burder Submission
Ny Munkegade, Building 540, Aarhus 8000, Denmark
Location/Qualifiers
1.942
| 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.942 | 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                  ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
                                                                                                                                        Length 927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.4; DB 8; Length 942;
Pred. No. 2e+03;
4; Mismatches 0; Indels
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <1. .>942
/gene="S"
/product="putative S-glycoprotein"
<1. .>942
                                                                                                                                                                                           ö
                                                                                                                                 .
8
                                                                                                                           Score 12.4; DB 8
Pred. No. 2e+03;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics 158 (1), 387-399 (2001) 21231627 11333247
            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="S"
/allele="S-13-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĀF328994
AF328994.1 GI:13345390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.7%;
71.4%;
                                                                                                                       Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                694 TCGAGTTTCGTGTT 681
                                                                                                                                                                                                                                               2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 TCGAGTTTCGAGTT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 togastwisgwgit 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
AF328994/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sonrce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

g



pro pro seg

Human secreted Polynucleotide

Right (5') border Parallel detection Human protein enco Human pollinosis-a

AAD06997

border

Arabidopsis thalia Candida tropicalis Human pollinosis-a Human protein enco E. coll MG1655 rrn Mycobacteriophage

AAC48642 AAX87946 AAC64160 AAH99730 AAX24984 AAX35000

Oligonucleotide fo Probe #24516 used DNA sequence that Arabidopsis thalia

AAZ24665 AAI55830 AAV03550 AAC52235 **AAH52999**

 S. epidermidis ope zea mays DNA fragm Eucalyptus grandis Arabidopsis thalia Human secreted exp Fusarium venenatum

AAC38143 AAA79427 AAC37052 AAA45066 AAF09195

Drosophila melanog Probe #11456 used Human cDNA clone (

Arabidopsis thalia

ALIGNMENTS

BP

AAC48567

Fusarium venenatum

AAQ83845 AAT16559 AAF10353 AAH29686 AAI42770 AAH07816

Hepatitis C virus Hepatitis C virus

Pyrolobus fumarius Maize Mac2T-3 codi Human cDNA sequenc

AAV03315 AAC86489

DNA sequence upstr

```
New DNA amplification method - without cyclisation of the DNA or ligation of oligonucleotide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymerase chain reaction; PCR; amplify; primer; specific; non-specific; DNA polymerase; deoxyribonucleotide; cyclisation; ligation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-specific primer #1, for amplification of T-DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 10; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-0043006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0043006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ79175 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1995 (first entry)
335
336
388
415
633
679
802
836
                                                                                                                                                                                                         4345
5098
49272
                                                                                            951
1321
2914
3198
                                                                                                                                            4233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-328991/41.
JP06253843-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
AAQ79175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAQ79175
 O
                                                                                                                                                                                  υo
                                                                                                                                                                                                                   υ
                                                                                                                                                                                                                                                                                               000
                                                                                                                                                                                                                                                                                                                                                                                  υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-specific prime
PCR primer CA54 us
PCR primer MDB285
PCR primer ARB1 fo
Degenerate primer
PCR primer MDB285
Degenerate TAIL-PC
Arabidopsis DNA pr
Malze Mac2 gene de
Human pollinosis-a
Parallel detection
                                                                             February 25, 2002, 18:17:21; Search time 716.55 Seconds (without alignments) 17:947 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                               | Single-Signatury | Single-Sign
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ79175
AAA88455
AAAA48993
AAZ49933
AAF86681
AAR86681
AAA89358
AAA89358
AAA89358
                                                         nucleic search, using sw model
                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                        1 ntcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ü
                                                                                                                                                                                                                                                                   length: 0
length: 2000000000
                                                                                                                              US-09-698-903B-4
15
                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5155555112
555555112
575555112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
15
15
15
15
15
15
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112.4
112.4
112.4
112.4
112.4
112.4
113.4
                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                         OM nucleic
                                                                                                                                                        Sequence:
                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                Run on:
```

O

Result . 8 The 16713 gene encodes a protein (see AAB19528) that is essential for normal plant development. Chemicals that inhibit the function of the 16713-encoded protein are likely to have detrimental effects on plants and are potentially good herbicide candidates.

00000x8

Sequence 15 BP; 1 A; 1 C; 3 G; 5 T; 5 other;

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel genes isolated from Arabidopsis coding for proteins essential for normal plant development, are useful to discover new herbicides and to identify inhibitors that are potential herbicides
            used in conjunction with the non-specific primers given in AAQ79175-77 in the DNA amplification method of the invention. The method comprises mixing a DNA sequence and a primer. DNA polymerase and deoxyrthonuclectides. The DNA is denatured allowing annealing of the primers. The amplification cycle consists of one cycle at a temperature to allow non-specific annealing of non-specific primers, numerous cycles at a temp. to allow specific annealing of specific to hybridise specifically to complementary sequences. This method allows amplification of neighbouring sequences with known sequences, efficiently without cyclisation of the DNA or ligation of
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This degenerate oligonucleotide, termed CA54, is a primer used in the border rescue of the 16713 gene (see AAA88448) from Arabidopsis thallana embryo-lethal line #16713. DNA flanking the borders of line #16713 was isolated using TAIL PCR. CA54 is 10 of 6 primers (see AAA88451-56) used in combination with 2 sets of nested, T-DNA specific primers for the right border (see AAA88457-59) as well as for the left border (see AAA88460-62) of the T-DNA region of pCSA104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16713 gene; essential gene; herbicide; screening; transgenic plant; Arabidopsis thaliana; PCR primer; ss.
sequences given in AAQ79172-74 are specific primers which were
                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                       Length 15;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levin JZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer CA54 used to identify Arabidopsis 16713 gene.
                                                                                                                                                                                                                                                                                  Score 12.4; DB 15;
Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcelver JA,
                                                                                                                                                                                                                                Sequence 15 BP; 1 A; 1 C; 3 G; 5 T; 5 other;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4c; Page 53; 92pp; English.
                                                                                                                                                                                                                                                                    82.7%; Scur
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA88455 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0263385.
99US-0309036.
99US-0327662.
99US-0408196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-2000; 2000WO-EP01884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                  2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patton DA, Ashby CS,
Budziszewski GJ;
                                                                                                                                                                                                                                                                                                                                                                               2 tcgastwtsgwgtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPI; 2000-594330/56.
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                  oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agrobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO200053782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-1999;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA88455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8888888888888888
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                 8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a transgenic glufosinate tolerant rice plant. The tolerant rice plants are generated by transformation with the Streptomyces hygroscopicus bar gene. This gene encodes the enzyme phosphinothricin acetyl transferase (PAT), which confers resistance to the herbicidal compounds phosphinothricin (also called glufosinate) and blalaphons. The 3' insertion site of the transgene was determined by thermal asymmetric interlaced (TAIL) PCR. The present sequence is the arbitrary degenerate PCR primer, WDB285, used for the TAIL PCR. Glufosinate Locarant rice plants are useful as they give better yields and growth, compared to untransformed plants, after application of a
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New glufosinate tolerant rice plants with genomic DNA capable of yielding at least 3 restriction fragments and having bar gene under control of CaMV 35S promoter at specific location
                                                                                                                                                                                                                                                        PCR primer MDB285 used to locate bar gene insertion in rice plant.
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
 Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                                                       bialaphos; bar;
PCR primer; TAIL;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Score 12.4; DB 21;
Pred. No. 3.1e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.7%; Score 12.4; DB 21;
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 1 A; 1 C; 3 G; 5 T; 5 other;
                                                                                                                                                                                                                                                                                    Herbicide, phosphinothricin, glufosinate, phosphinothricin acetyl transferase; PAT; thermal asymmetric interlaced; rice; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 25; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PLBZ ) PLANT GENETIC SYSTEMS NV.
                             ö
                                                                                                                                                                 DNA; 15 BP.
82.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0185244.
                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25667
                                                                                                                                                                                                                            (first entry)
Query Match 82.7
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson K;
                                                           15
                                                                         tcgastwtsgwgtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-365598/31.
                                                                                                                                                                AAA48993 standard;
                                                                                                                                                                                                                                                                                                                                                                            WO200026345-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-1998;
                                                                                                                                                                                                                            28-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michiels F,
                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                              AAA48993;
                                                                                                                                     m
                                                          a
                                                                                                                                                AAA48993
                                                                                                                                                                                              ð
                                                                                      셤
```

2 tcgastwtsgwgtt 15

ŏ

m

```
PCR primer MDB285 to generate the flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New herbicide target genes encoding proteins having ET1158, GT6839 or ET5262 activity, for identifying an inhibitor of protein activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis seedling growth and development. The essentiality of the genes provides a means of discovering new herbicides. Screening assays for identifying inhibitors that are potential herbicides are provided. The invention is also applied to the development of herbicide tolerant plants, and plant tissues, seeds and cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of degenerate primer CA54. Arbitrary degenerate primers LWAD1, CA51, CA52, CA53, CA54 and CA55 (see AAF9051-56) were used to prime Arabidopsis thaliana genomic DNA flanking a Ds transposon insertion. The degenerate primers were used in combination with 2 sets of 3, nested, transposon-specific primers (see AAF90557-62) that were homologous to regions of the Ds elements which lie at the outermost ends of the transposons. A series of low- and high-stringency PCR amplifications were performed using the TAIL-PCR protocol. DNA fragments were produced which corresponded to the genomic DNA that was directly adjacent to
                                                                                                                                                                                           ET1158 gene; GT6839 gene; ET5262 gene; herbicide; screening;
herbicide tolerance; transgenic plant; crop protection; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the transposon insertion. Sequence analysis of PCR products from tagged seedling lethal lines ET1158, GT6839 and ET5262 identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   novel genes (see AAF90548-50) each of which was essential for
                                                                                                                                           Degenerate primer CA54 used to prime Arabidopsis genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.7%; Score 12.4; DB 22;
100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levin JZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 1 A; 1 C; 3 G; 5 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Budziszewski GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 39; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
AAF90555 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       14-DEC-2000; 2000WO-EP12748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0465040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06993 standard; DNA; 15
                                                                                             22-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-398122/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wegrich Glover L,
                                                                                                                                                                                                                                                                                                                                         WO200144277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-2001.
                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD06993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD06993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EX PX PX B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is used to control seed germination and seedling growth especially to regulate gene products of glbberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are glbberellin deficient, and have shortened hypocotyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primers AA299438-42 were used to amplify the soybean AX5 promoter. The amplified sequence is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Glabberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a least abeta-hydroxylase polynucleotides to achieve this. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                  Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; AX5 promoter; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heck GR, Kishore GM, Logusch EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and/or epicotyl phenotypes compared to normal plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.7%; Score 12.4; DB 21;
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                      PCR primer ARB1 for the soybean AX5 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 1 A; 1 C; 3 G; 5 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 98; 267pp; English.
                                                                                                                                           AA299438 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown SM, Elich TD, Heck G
Piller KJ, Rao S, Ream JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0137977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US18066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0096111
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.7
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 tegastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-224351/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200009722-A2.
```

Zhou Q;

10-AUG-1999;

24-FEB-2000.

Glycine max.

07-JUN-1999; 10-AUG-1998;

03-JUL-2000

AAZ99438

g

ö

Gaps

ö

AAF90555 RESULT

ò qq

Length 15; Indels nucleic

Mayer J;

Keese PK,

Kilian A, Nottenburg C,

99US-0155036

```
The invention relates to a method of generating transgenic plants
that have modified gene activity or nucleic acid structure. The method
involves the cross-fertilisation of two transgenic plant lines to produce
seed, which is then grown to produce a plant. One of the parental plant
lines contains a gene encoding a non-native site-specific nucleic acid
effector molecule under the control of a minimal promoter and operably
linked to an endogenous enhance relement, and the other contains a
recognition sequence to which the nucleic acid effector molecule can
crecognition activator, methylation enzyme, repressor, gyrase,
crecognitional activator, methylation enzyme, or single or double
transcriptional activator, methylation enzyme, or single or double
creasing the nucleic acid effector molecule accordinate
creasing plant lines are crossed, in which a transgenic plant lines are crossed, in which a transgenic plant lines are crossed, in which a transgenic cross-breed plant,
creasing of the nucleic acid effector molecule to the recognition sequence
specificity of gene expression, the timing of gene expression, the tissue
creasing a desired phenotype can then be selected. The method of the
invention can be used to generate transgenic plants, including Gramineae
creasing maize, rice, barley, rye, oats, sugarcane), solanaceae
creasing maize, rice, barley, rye, oats, sugarcane), solanaceae
creasing mapping of T-DNA and Ds element insertion elements in
creasing mapping of T-DNA and bs element insertion elements in
                                                                                                                                                                                                                                                                                       Generating transgenic plants with modified genetic activity or nucle acid structure comprises crossing transgenomic plant with gene for nucleic acid effector with transgenomic plant with binding site for
                                                                                                     (MOLE-) CENT APPL MOLECULAR BIOLOGY INT AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 27; 42pp; English.
20-SEP-2000; 2000WO-US25778.
                                                                                                                                                                                                                                     WPI; 2001-335475/35.
                                                                                                                                                      RA,
                                                   20-SEP-1999;
                                                                                                                                                                                    Stachel SE;
                                                                                                                                                      Jefferson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic plant; cross-fertilisation; cross-breeding; modified gene activity; expression; timing; tissue specificity; modified nucleic acid structure; nucleic acid effector molecule; activator; methylation nezyme; repressor; gyrase; kinkase; topoisomerase; class I restriction enzyme; recognition sequence; phenotype selection; Gramineae; Solanaceae; Leguminosae; insertion site mapping; T-DNA, Ds element; rice; TAIL PCR primer; thermal asymmetric interlaced PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility ene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is degenerate PCR primer MDB285 used to generate right (5') and left (3') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
        MS-B2 elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Degenerate TAIL-PCR primer AD1, used for mapping insertion sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.4; DB 22;
Pred. No. 3.1e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 1 A; 1 C; 3 G; 5 T; 5 other;
                                         male-sterility gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 28; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                      (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF86681 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.7%; ;
100.0%;
                                                                                                                                                                                                                                                   2000WO-EP10680.
                                                                                                                                                                                                                                                                                                       99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                          De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-300517/31.
                                                                                                                                           WO200131042-A2
                                                                                          Unidentified
                                                                                                                                                                                                                                                26-OCT-2000;
                                                                                                                                                                                                                                                                                                    29-OCT-1999;
                                                                                                                                                                                            03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                          Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF86681;
```

```
Gaps
                                                          ö
                                      Length 15;
                                                          Indels
                                 82.7%; Score 12.4; DB 22;
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0;
Sequence 15 BP; 1 A; 1 C; 3 G; 5 T; 5 other;
                                                                                                                                                                                                                                                        Gene silencing; PCR primer; ss.
                                                                                                                                                               BP.
                                                                                                                                                                                                                                Arabidopsis DNA primer AD1.
                                                                                                                                                             AAA89358 standard; DNA; 15
                                                                                                                                                                                                           (first entry)
                               Query Match 82.7
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                    2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                               Arapidopsis thaliana.
                                                                              2 tcgastwtsgwgtt
                                                                                                                                                                                                                                                                                                    WO200100801-A2.
                                                                                                                                                                                                          23-APR-2001
                                                                                                                                                                                    AAA89358;
                                                                                                                                       RESULT
AAA89358
```

40200121781-A2.

Synthet1c

RESULT AAF86681

à

29-MAR-2001

ó

S

```
Example 2; Page 16; 45pp; English.
                                                                                                                                                                                                                                               AAC64167;
                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                 AAC64167,
 X \times C C C C C C \times S
                                                                                                                                                        ò
                                                                                                                                                                          g
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid sequences encoding tapetum specific promoters, pMAC2 and pMAC20, or promoter sequences that control the expression of coding sequence homologous to the promoters, for artificial male sterility -
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                  primers (see AAA89358-64) expected to bind to Arabidopsis thaliana DNA flanking the site of a T-DNA insert. These primers were used with 3 specific, nested primers (see AAA89355-57), located close to the right border of T-DNA, in the cloning of the silencing gene (see AAA89353) of Arabidopsis thaliana. Genomic DNA from the plant containing only T-DNA co-segregating with a hygromycin resistant mutant phenotype was isolated. Gene silencing is useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tapetum-specific promoter; artificial male sterility; agriculture; crop yield; disease resistance; AMS; maize; MAC2; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                           ţu
                                                                                                                                                                          sequence of primer AD1, which is 1 of 7 degenerate
                                                                                                                                                                                                                                                                                                       Length 15;
                                                                                                                           Novel gene encoding a protein that controls gene silencing,
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                    Amedeo P, Paszkowski
                                                                                                                                                                                                                                                                                                      Score 12.4; DB 22;
Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                       molecular tool for regulating gene expression.
                                                                                                                                                                                                                                                                                              82.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                          Sequence 15 BP; 1 A; 1 C; 3 G; 5 T; 5 other;
                                                        (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize Mac2 gene degenerate PCR primer AD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hodge R;
                                                                                                                                    particular silencing of plant genes
                                                                                                                                                     Example 4; Page 11; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               AAC86474 standard; DNA; 15 BP
                                                                                   Mittelsten Scheid O,
                  2000WO-EP05761
                                    99GB-0014623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2000; 2000WO-GB01789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99GB-0010796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paul W, Scott RJ, Hird D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOG-) BIOGEMMA UK LTD.
                                                                                                                                                                                                                                                                                                                                             2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-137952/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-016099/02.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200068403-A2
                  21-JUN-2000;
                                    23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1999;
                                                                                                                                                                          This is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-2000
04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC86474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays.
                                                                                   Habu Y,
                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                       AAC86474
ò
                                                                                                                                                                                                                                                                                                                                                              g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the human pollinosis-associated gene 581 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates also relates to the protein encoded by pollinosis-associated gene 581; to expression constructs and host cells comprising pollinosis-associated gene 581 nucleic acids; pollinosis-associated gene 581 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 581 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 581 nucleic acids; The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 581 in pollen
The present invention provides tapetum-specific promoters which can be used to create artificial male sterility (AMS) systems in plants. These are useful in agriculture as they enable the production of plants with increased yield and greater disease resistance. They also result in uniform offspring, which have the same germination time, height of growth, susceptibility to disease, flowering time etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gunji S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human pollinosis-associated gene 581 hybridisation probe, SEQ ID NO:8
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; pollinosis-associated gene 581; IgE; immunoglobulin E; cedar polline allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; expression analysis; hybridisation probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pollenosis-associated gene 581 undergoing significantly low exp
in subjects with high cedar pollen-specific IgE levels, useful
diagnosis of allergic diseases and screening drug candidates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obayashi M,
                                                                                                                                                                                                                                                                                                                                            Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kashiwabara T, Oshida T, Obay.
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                         Score 12.4; DB 22;
Pred. No. 3.1e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                      BP; 1 A; 1 C; 3 G; 5 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; Page 24; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                82.7%; Scor.
100.0%; Pre
0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-2000; 2000WO-JP02732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0120492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC64167 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity luv...
Act 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOX RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-687341/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200065048-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1999;
                                                                                                                                                                                                                                         Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Obayashi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagasu T,
```

9

ö

Gaps

ö

Indels

Score 12.4; DB 22; Pred. No. 3.6e+02; 1; Mismatches 0;

82.7%; 71.4%;

Conservative

Similarity

Query Match Best Local Simi Matches 10;

2 tcgastwtsgwgtt 15

ò

Length 304;

```
antigen-stimulated T-cells in the presence of a test compound relative to a control Pollinosis-associated gene 581 is useful in the diagnosis of allergic diseases and in the screening of Grug candidates for the treatment of such diseases. The present sequence represents a hybridisation probe used in human pollinosis-associated gene 581
                                                                                                                                       expression analysis.
     8888888888
```

Sequence 30 BP; 9 A; 9 C; 4 G; 8 T; 0 other;

```
ó
                                    Gaps
                                    ö
Score 12.4; DB 21; Length 30;
Pred. No. 3.2e+02;
4; Mismatches 0; Indels (
Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
```

2 tcgastwtsgwgtt 15 30 TCGAGTATGGTGTT 17 g ð

RESULT 11 AAH21085

AAH21085 standard; DNA; 304 BP. (first entry) 03-SEP-2001 AAH21085;

Parallel detection of methylated genomic DNA associated DNA SEQ ID 31. DNA methylation; parallel detection; 5-unmethylated cytosine; CpG; CpNpG; amplification; transcription regulation; genetic imprinting;

tumorigenesis; primer; ss.

Unidentified

WO200142493-A2.

14-JUN-2001.

06-DEC-2000; 2000WO-DE04381

06-DEC-1999;

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C;

WPI; 2001-381705/40.

Parallel detection of the methylation pattern of many genomic DNA regions, useful for detecting aberrant methylation, includes multiple amplification of chemically modified DNA.

Disclosure; Page 63; 63pp; German.

This invention describes a novel method for the parallel detection of the methylation status of genomic DNA (I) which involves a (I) sample being treated chemically to convert 5-unmethylated cytosine to uracil, thymidine or some other base having hybridization behavior different from that of C, then amplifying simultaneously at least 10 different fragments of fewer than 2 kb) using synthetic oligonucleotide (ON) primers. These primers are based on regulatory, transcribed and/or translated segments primers are based on regulatory, transcribed and/or translated segments present in the sample after chemical treatment. The sequence context of all, or some, of the CpG and CDNG motifs in the amplified products is then determined. The method is used to detect aberrant methylation parterns in the genome, these are implicated in regulation of transcription, genetic imprinting and tumorigenesis. Many target regions in the genome can be analyzed simultaneously and it is not essential to the application of particular segments of analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and it is not essential to the analyzed simultaneously and its essential to the analyzed simultaneously and i (e.g. promoters and exons).

Sequence 304 BP; 37 A; 35 C; 131 G; 101 T; 0 other;

ö

Gaps

ó

Indels

Score 12.4; DB 21; Length 335; Pred. No. 3.6e+02; 4; Mismatches 0; Indels 0;

4;

Conservative

Query Match Best Local Similarity Matches 10; Conserv

||||:|:||:|| 194 tcgagtttggagtt 207 2 tcgastwtsgwgtt 15

ò ద

82.78; 71.48;

```
The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length
                                                                                                                                                                                                                                                 expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 335 BP; 71 A; 75 C; 89 G; 89 T; 11 other;
                                                                                                                                                                                                             Human secreted protein 5' EST, SEQ ID NO: 2396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 2396; 71pp + CD-ROM; English.
                                                                                                    AAC02398 standard; cDNA; 335 BP
                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0122487.
                                                                                                                                                                             (first entry)
|||||:|:|:|||
112 tcgagtttggagtt 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAG02392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET.
                                                                                                                                                                                                                                                 Human; 5' EST;
gene therapy;
                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                          EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                           06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
                                                                                                                                        AAC02398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vectors.
                                                                    12
```

```
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                   24-JUN-1997;
                                                                                                                                            WO9859034-A2
                                                                                                                                                                                           23-JUN-1998;
                                                                                                                                                                    30-DEC-1998.
                                                                                                                                                                                                                                                                   Fraser CM;
           AAX20974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD06997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human secreted proteins, and encode the proteins given in AAY12681 to human secreted proteins, and encode the proteins given in AAY12681 to AAY12913, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for products for diagnosis and therapy. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, reproductive hormone activity, tissue growth regulating activity, reproductive hormone activity, tissue growth regulating activity, anti-inflammatory activity, tumour inhibition activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activity and chromosome mapping products can be used in forensic, gene therapy and chromosome mapping promoter sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                         forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemotantic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from testis, ovary, uterus and spleen tissue
                                                                                                                                 EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 336 BP; 72 A; 75 C; 89 G; 89 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.4; DB 20;
Pred. No. 3.6e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  Lacroix B;
                                                                                                      Human secreted protein 5' EST SEQ ID NO:65.
                                                                                                                                                                                                                                                                                                                                                                  Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 192; 522pp; English.
                                  AAX51486 standard; cDNA; 336 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX20974/c
ID AAX20974 standard; DNA; 388 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.7%;
71.4%;
                                                                                                                                                                                                                                                                                          98WO-IB01231
                                                                                                                                                                                                                                                                                                                  97US-0905279
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                 secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 tcgagtttggagtt 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-153779/13.
                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY12708
                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                           W09906549-A2
                                                                                                                                                                                                                                                                                          31-JUL-1998;
                                                                                                                                                                                                                                                                                                                  01-AUG-1997;
                                                                               21-JUN-1999
                                                                                                                                                                                                                                                                   11-FEB-1999
                                                        AAX51486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                     AAX51486
          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                             ð
```

```
AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                             Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MS-B2 elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.7%; Score 12.4; DB 20; Length 388; 71.4%; Pred. No. 3.6e+02; ative 4; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 388 BP; 121 A; 68 C; 77 G; 117 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "Corresponds to plant DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 998-999; 1150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD06997 standard; DNA; 415 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0050667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Agrobacterium sp.
Chimeric - Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235..415
/*tag= b
05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 TCGAGTTTGGTGTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               male-sterility gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 10; Conserv
                                                                                                                                                               enzyme production;
                                                                                                                                                                                                                           Treponema pallidum
```

```
The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                            Transgentc Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
 /note= "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 51; 53pp; English.
                                                                                                                                                                          (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                   26-OCT-2000; 2000WO-EP10680.
                                                                                                                                        99US-0430497.
                                                                                                                                                                                                           Weston B, De Beuckeleer M;
                                                                                                                                                                                                                                           WPI; 2001-300517/31.
                                    WO200131042-A2
                                                                                                                                        29-OCT-1999;
                                                                   03-MAY-2001
```

Search completed: February 25, 2002, 18:17:22 Job time: 16680 sec

ö

Gaps ; 0

Score 12.4; DB 22; Length 415; Pred. No. 3.6e+02; 1ndels 0; Indels 0

4

Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative

2 tcgastwtsgwgtt 15
||||:|:|:|:||
2 tcgagtttggtgtt 15

ò 合

```
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-08-614-770A-1/c
                                                                                                                                                                                                                         US-09-503-391-13
                        SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
0000
                                                                                 0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 100, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
Appli
Appli
Appli
Appli
App
), App
), App
), App
), App
), App
                                                                     (without alignments)
11.264 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, App]
                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000,,000
                                                            ; Search time 301.6 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-614-770A-1

US-08-08-428B-1

US-08-290-665A-1

US-08-290-665A-1

US-09-046-894-30

US-09-187-049-11

US-08-187-049-11

US-08-187-049-11

US-08-187-049-11

US-08-187-049-11

US-08-187-049-11

US-08-187-049-11

US-08-181-11

US-08-181-11

US-08-181-100

US-08-181-1100

US-08-181-100

US-08-181-100

US-08-444-803-100

US-08-444-803-100

US-08-445-043-100

US-08-456-2658-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-455-244-100
US-08-454-876-100
US-08-457-364-100
US-08-456-262-100
                                                                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                                                                351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                           February 25, 2002, 18:05:11
                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          - nucleic search, using sw model
                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                  ntcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                       Issued_Patents_NA:*
                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                 US-09-698-903B-4
15
                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                    576
576
576
576
1268
22341
2493
2493
2493
3139
3139
3139
1567
1567
1567
1567
1567
                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match I
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of
                                                                                                           Perfect score:
                                                                                                                                     Scoring table:
                                           OM nucleic
                                                                                                                    Sednence:
                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                       Database
                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                  0000000000
```

```
ö
                                                                                                                                                                    Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appli
Appl
Sequence 100, A Sequence 1, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                Sequence 1, p. Sequence 1, p. Sequence 1, p. Sequence 1, p. Sequence 3, p. Sequence 6, p. Sequence 6, p. Sequence 1, p. Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08614770A
Patent No. 5773267
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
TITLE OF INVENTION: D29 SHUTTLE PHASMIDS AND USES THEREOF NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PAICON, David A.
APPLICANT: Ashby, Carl S.
APPLICANT: Thomas, Carla R.
APPLICANT: Thomas, Carla R.
APPLICANT: Molas, Carla R.
APPLICANT: Molas, Carla R.
APPLICANT: Molase, Carla R.
APPLICANT: Levin, Joshua Z.
TILLO F. INVENTION: Herbicide Target Genes and Methods
FILE REFERENCE: PB/5-30852A
CURRENT APPLICATION NUMBER: US/09/503,391
CURRENT FILING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence:; OTHER INFORMATION: oligonucleotide
US-09-503-391-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
   US-08-456-240-100
US-08-455-736-100
US-08-350-600-100
US-08-309-341-1
US-08-608-267-1
US-08-608-224-1
US-08-608-224-1
US-08-608-224-1
US-08-608-224-1
US-08-608-224-1
US-08-608-224-1
US-08-608-267-149-1
US-08-759-767-6
US-08-729-767-6
US-08-729-767-6
US-08-73-185-1
US-08-473-185-1
US-08-473-185-1
US-08-473-185-1
US-08-473-185-1
US-08-848-7608-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 69;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.7%; Score 12.4;
100.0%; Pred. No. 69
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09503391
Patent No. 6300091
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
          11567
11567
11567
2068
2068
2068
3117
3117
7400
7400
7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 14; Conserv
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11.4; DB 1; Length 576; Pred. No. 3.4e+02; 4; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: AMINO ACID SEQUENCES
TITLE OF INVENTION: OF 51 ISOLATES OF HE
TITLE OF INVENTION: OF REGENTS DELIVED
TITLE OF INVENTION: DIAGNOSTIC METHODS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2026-4070US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION WUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION NUMBER: 36,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 30,459
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                              NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08468570 Patent No. 5871962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.0%;
69.2%;
                                                                                                                                                                                                                              TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: DK7
US-08-086-428B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.0
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGINE 576 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: I. CORRESPONDENCE ADDRESSE: ADDRESSEE: MORGAN & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 tcgastwtsgwgt 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 TCGAGTATCGTGT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-468-570-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEATITIES C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.4; DB 1; Length 49272;
Pred. No. 1e+02;
4; Mismatches 0; Indels 0;
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,770A
FILING DATE: MACH 7, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 95/901
REGISTRATION NUMBER: 95/901
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TO STORE THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08086428B Patent No. 5514539 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: MYCOBACTERIOPHAGE INDIVIDUAL ISOLATE: D29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.78;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 29087 TCGAGTTTCGTGTT 29074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MUCITILE OF INVENTION: OF STITLE OF INVENTION: OF STITLE OF INVENTION: OF TITLE OF INVENTION: DIAGNORARY OF SEQUENCES: 159 CORRESPONDENCE ADDRESSE ADDRESSEE: MORGAN & FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-614-770A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-08-086-428B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
```

```
NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.4; DB 5;
Pred. No. 3.4e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: FLOPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/200/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INPORMATION:
NAME: RICHARD W. BORK
                                                                                                                 Sequence 1, Application PC/TUS9510398
GENERAL INPORMATION:
PAPPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09046894 Patent No. 6190857 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.0%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ralph, David
APPLICANT: An, Gang
APPLICANT: O'Hara, Mark S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.0
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: homosapiens INDIVIDUAL ISOLATE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                        TITLE OF INVENTION: NO TITLE OF INVENTION: AN TITLE OF INVENTION: AN TITLE OF INVENTION: AN TITLE OF INVENTION: SI NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 tcgastwtsgwgt 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEW YORK
: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-046-894-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEGIENCES IN DIAGNOSTIC METHODS AND VACCINES 263
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                              Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 576;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                           Score 11.4; DB 2;
Pred. No. 3.4e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11.4; DB 2;
Pred. No. 3.4e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKHL, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
APPLICANT: FUNCELL, R.H.
APPLICANT: SEQUENCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/290,665A FILING DATE: 15-AUG-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEOTIDE AN TITLE OF INVENTION: AMINO ACID SE TITLE OF INVENTION: CORE GENES OF TITLE OF INVENTION: SEQUENCES IN NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: ADDRESSE: AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08290665A
Patent No. 5882852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                           76.0%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%;
ilarity 69.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 421792
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
CORGINAL SOURCE:
CORGANISM: homosapiens
INDIVIDUAL ISOLATE: DK7
US-08-468-570-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDIVIDUAL ISOLATE: DK7
                                                                                                                                                                                                                           Ouery Match 76.0
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homosapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10154
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 tcgastwtsgwgt 14
||||:||:||:||
55 TCGAGTATCGTGT 67
                                                                                                                                                                                                                                                                                                                                                                 2 tcgastwtsgwgt 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
'-hag 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-290-665A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

Gaps

ö

Length 576; Indels

Gaps

ö

```
.
0
                                                                                                                                                                                                                                                                                 Length 2220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.0%; Score 11.4; DB 3; Length 2341; ilarity 69.2%; Pred. No. 3.6e+02; Conservative 4; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GERERAL INFORMATION:
APPLICANT: Lamppa, Gayle K.
TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME
TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME
TITLE OF INVENTION: THAT CLEAVES PRECURSOR POLYPEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSE: PLO. BOX 10395
                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/187,049
                                                                                                                                                                                                                                                                               Score 11.4; DB 5;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09187049
Patent No. 6117666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION
PRICA APPLICATION
APPLICATION NUMBER: 08/695,177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFRENCE/DOCKET NUMBER: 7814
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 321-4299
TELEFAX: 312 321-4299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 234 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                           76.0%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis CPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                        TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        CDS
536..1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                |||||:|:|:||
975 TCGAGTTTGGAGT 963
                                                                                                                                                                                                                                                                                                                                                          2 tcgastwtsgwgt 14
                                                                                            TOPOLOGY: unknown MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE: NO
; ORIGINAL SOURCE
; ORGANISM: Aru
US-09-187-049-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-09-187-049-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60610
                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                         ;
LOCATION:
PCT-US95-13749-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9513749
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS FOR INCREASED
TITLE OF INVENTION: BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.4; DB 4; Length 1268;
Pred. No. 3.5e+02;
4; Mismatches 0; Indels 0
APPLICANT: Veltri, Robert
TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING MENA
TITLE OF INVENTION: PROFILES IN PERIPHERAL LEUKOCYTES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,894
FILING DATE: CONCULTENTLY HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US95/13749
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,576
FILING DATE: 24-MAR-1997
ATTONNEY/AGENT INFORMATION:
NAME: NAKASHIMA, Richard A.
REGISTRATION NUMBER: P-42,023
REFENCE/DOCKET NUMBER: UROC:014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1268 base pairs
TYPE: nucled: acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              850 CGAGTTTCGTGTT 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 cgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                               STATE: Teac.
COUNTRY: USA
                                                                                                                                                                                    Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
PCT-US95-13749-2/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-046-894-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

ó

Gaps

S

```
Length 2493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: PIPEPPY DISK
COMPUTER: PATENTY
COMPUTER: PATENTY
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION UNMER: US/08/720,229
FILING DATE: 26-SEP-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 11.4; DB 3;
Pred. No. 3.6e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPTRY: USA
ZIP: 19406-0939
COMPUTER: 19406-0939
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: PASTESCO FOR WINGOWS VERSION 2.0
SOFTWARE: 10005
SOFTWARE: 10005
SOFTWARE: 10005
FILING DATE: 10007
FILING DATE: 10007
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,064
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9607991.8
FILING DATE: 18-APR-1996
FILING DATE: 18-APR-1996
FILING DATE: 18-APR-1996
FILING DATE: NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Brown, James
APPLICANT: Jaworski, Deborah
APPLICANT: Jaworski, Deborah
APPLICANT: Jawlor, Blizabeth
APPLICANT: Wang, Min
TITLE OF INVENTION: NOVEL valS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                     ATCHARY AGENT INFORMATION:
NAME: Schiff, J. Michael
REGIESTRATION NUMBER: 2938-20002.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 813-5600
TELEFAX: (415) 494-0792
TELER: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2493 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-953-492-1; Sequence 1, Application US/08953492; Patent No. 5849555; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.0%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.0
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1369 TCGAGTATCGTGT 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 tcgastwtsgwgt 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-720-229-11
Palo Alto
                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: PA
                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.0%; Score 11.4; DB 3; Length 2493; 69.2%; Pred. No. 3.6e+02; tive 4; Mismatches 0; Indels 0
                                                                   KESULT 10
US-08-804-4394-11
Sequence 11, Application US/08804439A
Fatent No. 6015565
GENERAL INFORMATION:
APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Ste 1400
CITY: La Jolla
STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/0872029
Fatent No. 6022542
GENERAL INFORMATION:
APPLICANT: Rose, Timothy M.
APPLICANT: Strand, Rutr
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
NUMBER OF SEQUENCES: 100
CORRESPONDENCE-ADDRESS:
ADDRESSEE: MOTTISON & FOEFSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FEATURE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,439A
FILING DATE: February 21, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 39,347
REFERENCE/DOCKET NUMBER: 09176/004001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2493 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||:|:|:||
| 1369 TCGAGTATCGTGT 1381
                2 tcgastwtsgwgt 14
|||||||||||||||||
599 TCGACTATGGAGT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 tcgastwtsgwgt 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-804-439A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
ZIP: 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-720-229-11
                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                   ð
```

ö

Gaps

ö

ò

Gaps

```
;
0
                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08377228

Patent No. 5545546

GENERAL INFORMATION:
APPLICANT: ALLEN, Rebecca L.
APPLICANT: LONSDALE, David M.
ITLE OF INVENTION: A POllen-Specific Promoter From Maize NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington Street, N.W., Suite 500
STATE: D.C.
COUNTY: USA
LIP: 20007-5109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC Compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/377,228
FILING DATE: 09-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,695
FILING DATE: 09-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/911,532
FILING DATE: 09-UUL-1992
ATTORNEY/ASTRATION NUMBER: US 07/911,532
FILING DATE: NOWENT: STEPHEN A.
REGISTRATION NUMBER: US 97/911,532
REGISTRATION NUMBER: 29,768
REFERENCE ADDRESSET INFORMATION:
NAME: BENT, STEPHEN A.
REFERENCE ADDRESSET NUMBER: 29,768
REFERENCE ADDRESSET NUMBER: 29,768
                                                                                                   Score 11.4; DB 1; Length 2873;
Pred. No. 3.6e+02;
4; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.4; DB 1; Length 2873;
Pred. No. 3.6e+02;
4; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33229/290/PIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-693-457-1
; Sequence 1, Application US/08693457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202,
TELEFAX: (202,
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 base pairs
"VPE: nucleic acid
"VPE: nucleic acid
                                                                                                   76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.0%;
69.2%;
                                                                                               Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.2
Matches 9; Conservative
               ; TISSUE TYPE: Pollen
US-08-149-695-1
                                                                                                                                                                                                           111 CGAGTTTGGAGTT 123
                                                                                                                                                                                   3 cgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 CGAGTTTGGAGTT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 cgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-377-228-1
                                                                                                                                                                                                                                                                                                        US-08-377-228-1
                                                                                                                                                                                                                        g
                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08149695

Patent No. 5412085

GENERAL INFORMATION.

APPLICANT: Allen, Rebecca L.

APPLICANT: Lonsdale, David M.

ITILE OF INVENTIONS: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held and Malloy

STREET: 500 W. Madison, 34th Floor

STATE: Illinois

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                             Score 11.4; DB 2; Length 2652;
Pred. No. 3.6e+02;
4; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,695
NAME: Glmmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31458-4/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: US/US/149,093
FILING DATE: US/US/149,093
FILING DATE: 09.0UL-1992
ATORNEY/AGENT INFORMATION:
NAME: POCHOPIEN: 32167
REGISTRATION NUMBER: 32167
REFERENCE/DOCKET NUMBER: 92 P139
TELEPHONE: (312,707-889)
TELEPHONE: (312,707-889)
TELEFAX: (312)707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 base pairs
TYRE: nucleic acid
                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2652 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                   TOPOLOGY: linear / MOLECULE TYPE: Genomic DNA US-08-953-492-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 1892 TCGAGTTTGGTGT 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 tegastwisgwgt 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Zea mays
STRAIN: Line W22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-149-695-1
                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

ö

Gaps

```
GREARL NO. 5880330
GREARL LIFORMATION: SHOOT WRISTEN SPECIFIC PROMOTER
TITLE OF INVENTION: SHOOT WRISTEN SHOOT STREET: 425 Executive Square, Suite 1400
COMPANY STATES STATES SHOOT SHOOT STREET: 42 JOIN STATES SHOOT STATES SHOOT STATES SHOOT STATES SHOOT STATES SHOOT STATES SHOOT SHOOT STATES SHOOT S
```

THIS PAGE BLANK (USPTO,

```
BB191477 BB191477
AV066958B AV06958B
BF460492 UI-M-CGOP
AJ28424 4A3B-AAU-
F14485 ATT55207 Or
AV558749 AV558749
BB255970 BB255970
AV411222 AV421222
BB2550639 BB250639
BB250639 BB250639
BF098143 EST428664
AV302544 AV20264
AV302544 AV392544
AV302544 AV392544
AV302544 AV392544
AV534046 AV334046
AV23054 AV334046
AV41349 AV441349
BF778123 NXS1_O77_
AA742965 AV42965
AV202387 AV409979
AV42965 AV42965
AV42965 AV42965
AV42965 AV42965
AV42965 AV42965
BE192723 EST331452
BF31781 BR231452
BF31781 BF3184005
BF778123 AV409979
AV42965 AV42965
AV42965 AV42965
BF4176 RE38940.5
BE192723 EST331452
BF31874 BRE3165
BF31876 AV42965
AV42965 AV42965
AV42965 AV42965
BF4176 RE38940.5
BF13176 RE38940.5
BF13176 RE38940.5
                                                                                                                                                                                                                                                                                                                                                                                               GSS; genome survey sequence.
Tetracdon nigroviridis.
Tetracdon nigroviridis.
Eukaryotus, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontidae, Tetracdontiformes;
1 (bases 1 to 101)
                                                                                                                                                                                                                                                                                                                                              CNSO4Q4L 101 bp DNA GSS 24-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 128H18 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 101)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                      AV441349
BF590524
AV410421
                                                                                                                                                                     BE321781
BE778123
AA754245
AV202387
AV202461
AV422965
                                                                                                                                                                                                                                 AW796228
BI241776
BE192723
BF483146
BG630990
AW859801
          AV069588
BF460492
AJ284234
                                                                           BF098143
AV209024
AV392544
AW693454
                                                                                                                     AV534046
AJ284258
                                                                                                                                                                                                                                                                                                                                                                                 AL302142
AL302142.1 GI:8179769
  (bases 1 to 101)
 377
382
382
386
394
397
405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
 CNS04Q4L
                                                                                                                                                                                                                                                                                                                                                                          sednence
 RESULT 1
CNSO4Q4L/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
   000000
                                                                                                                                                                            0000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL302142 Tetraodon
BG199530 RST18821
BB258732 BB258732
BB411504 BB411504
AL367282 MtBA13H05
AV427766 AV427766
BG057582 mAB92d01.
AV122451 AV129451
BB074324 BB074324
AV331577 AV331577
BE53468 M77022STM
AZ921129 1006024200
                                                          // Search time 8261.74 Seconds
(without alignments)
19.510 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                        22703874
           version 4.5
- 2000 Compugen Ltd
                                                                                                                                                     11351937 seqs, 5372889281 residues
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                           February 25, 2002, 17:20:54
                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSO404L
BG199530
BB2530
BB411504
AL367282
AV427766
BG074324
BB074324
BB074324
BE53058
AX31577
                                           OM nucleic - nucleic search, using sw model
                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                              1 ntcgastwtsgwgtt 15
           GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ü
                                                                                                                                                                                                                                                                                                                                                                                                                                   em_gss_other:*
                                                                                                                                                                                                                                                                                                                                                                                                          em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                          US-09-698-903B-4
15
                                                                                                                                                                                                                                                                                                                                                                                 em_gss_hum:*
em_gss_inv:*
                                                                                                                                                                                                                                                                                                                                                                          em_gss_fun:*
                                                                                                                                                                                                                                                                                                                                                                                                  em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3000110011
                                                                                                                                                                                                                                                           em_estfun:*
em_esthum:*
em_estin:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                    em_estom: *
em_estpl: *
em_estba: *
em_estba: *
                                                                                                                                                                                                                                                                                                                                      gb_est1:*
gb_est2:*
gb_htc:*
gb_9ss:*
                                                                                                                                                                                                                                                                                                                      em_estov:*
em_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
203
203
204
221
221
224
247
247
252
257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST:
```

sed

Minimum DB Maximum DB

Database

Perfect score:

Title:

Run on:

Sequence:

Scoring table:

Searched:

Direct Submission Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis

Genoscope.

AUTHORS TITLE JOURNAL COMMENT

Score

ę U

Result

112.4 112.4 112.4 112.4 112.4 113.4 113.4 113.4 113.4 113.4 114.4 115.4

000

5 6 7 10 11 12 12

υo

O

```
Mus musculus
                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-44 (1999)
                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                            VERSION
KEYWORDS
                                                              BB258732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 203)

Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J., Lefner, L., Krashoc, D., McBiligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Libraries using Random Activation of Gene Expression, Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Creation of Genome-wide Protein Expression Libraries using Random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG199530 203 bp mRNA EST 21-APR-2001
RST18B21 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG199530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 203
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                             /clone_lib="G"
/note="Genoscope sequence ID : COBG128DD09SPl~end :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                  Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.7%; Score 12.4; DB 11; Length 203; llarity 71.4%; Pred. No. 3e+03; Conservative 4; Mismatches 0; Indels 0
       at
                                                                                                                                                                                           1 others
                                                                                                                                                                                                                                                                                                       Indels
For more information, please take a look
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
                                                    1. .101
/ Organism="Tetraodon nigroviridis"
/ db_xref="taxon:99883"
/ clone="128H18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Exax: 216 361 9596 Email: scain@athersys.com
                                                                                                                                                                                                                                                              Score 12.4; DB 13;
Pred. No. 2.5e+03;
4; Mismatches 0;
                   http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                         ų
                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 153.
Location/Qualifiers
                                                                                                                                                                                         δ
                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG199530.1 GI:13721217
                                                                                                                                                                                                                                                                82.7%;
71.4%;
                                                                                                                                                                                         31 c
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                      PUC-Or1"
                                                                                                                                                                                                                                                                                                                                      2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                        26 rcGAGTTTGGTGTT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 tcgastwtsgwgtt 15
||||:|:|:|||
38 TCGACTTTGGAGTT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                         Ø
                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 10
                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
BG199530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
```

```
### BR258732 TO 40 Up mRNA EST 06-JUL-2000

### BR258732 COA Up mRNA ENTITION CONTROLL CONTROL C
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carhinci.p-, Nishilyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y., Abibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS Konno, H., Atabatra, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Tehkuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hivozane, T., Hivozane, T., Hara, T., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Suzuki, H., Taqawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Yokta, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokta, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Shibata, K., Yoshino, H., Watanabe, S., Xamamura, T., Yasanaka, I., Yano, R., Yasanishi, A., Yokhida, Y., Oshida, K., Yoshino, H., et al.)
cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTACATTAAATTAAATACCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 16-JUL-2000 CDN4 RIKEN full-length enriched, 7 days embryo Mus musculus CDNA clone C430023B01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                   Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                            Score 12.4; DB 10;
Pred. No. 3e+03;
4; Mismatches 0;
                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                               36 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB411504.1 GI:9232859
                                                                                                                                                                                                                                                                                                                                                            82.78;
71.48;
                                                                                                                                                                                                                            40 c
                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 71.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 TCGACTTTGGTGTT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
BB411504/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

source

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
                                                                                                                                                                                                                                    AL367282 216 bp mRNA EST ' 03-AUG-2000 MEBAl3H05F1 MtBA Medicago truncatula cDNA clone MtBAl3H05 T3, mRNA
                                                         /clone_lib="RIKEN full-length enriched, 7 days embryo" /dev_stage="7 days embryo" /lab_host="Nullub" /lab_host="Nullub" /note="Site=1: SalI; Site=2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
BP 191 91006 EWRX cedex - France
Bmail: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie woleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-estétoulouse.inra.fr Website
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Glaninazzi-Pearson, V. and Gamas, P. Medicago truncatula ESTs from nitrogen-starved roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="MtBA"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.4; DB 10; Length 210;
Pred. No. 3e+03;
4; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://sequence.toulouse.inra.fr/Mtruncatula.html).
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA13H05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
/organism="Mus musculus"
                  /db_xref="taxon:10090"
/clone="C430023B01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:9667035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.78;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago.
1 (bases 1 to 216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 TCGAGTATCGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       barrel medic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL367282
AL367282.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
AL367282/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
```

```
ESM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Mus.

E 1 (bases 1 to 247)

RS Garninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Alzawa,K.,

Akahira,S., Akiyama,J., Fukuda,S., Fukuduishi,Y., Funayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Owa,C.,

Sato,K., Shibata,Y., Shigemoto,Y., Shizawa,H., Oda,H., Owa,C.,

Sato,K., Shibata,Y., Shigemoto,Y., Shizawa,H., Owa,C.,

Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,

RIKEN Mouse ESTS

Contact: Chie Owa

Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .226
/organism="Homo sapiens"
/db_xref="Homo sapiens"
/db_xref="Laxon:9606"
/clone=lib="wcl_CGAP_HN17"
/clone=lib="wcl_CGAP_HN17"
/tasue=_vpe="normal epithelium"
/lab_host="normal nasopharyns; Vector: pAMP10; mRNA made from normal nasopharyngeal epithelium, cDNA made by oligo-dr priming. Non-directionally cloned into UDG sites.
Size-selected on agazose gel, average insert size 50 pp. Primary library. cDNA Library Preparation: David B. Krimary library. PREPERENCE: Krizman et al. (1996) Cancer Research 553 a 59 c 43 g 61 t
                        BG057582 226 bp mRNA EST 25-JAN-2001
nah92d01.x1 NCI_CGAP_HN17 Homo sapiens cDNA clone IMAGE:4258200 3',
                                                                                                                                                                                               Homo saplens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 226)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
unknown library type
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV129451 247 bp mRNA EST 01-JUL-1999
AV129451 Mus musculus C57BL/6J 11-day embryo Mus musculus CDNA
clone 2700068H03, mRNA sequence.
AV129451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.4; DB 11;
Pred. No. 3.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Chie Owa
Genome Science Laboratory
RIKEN
                                                                                                                           BG057582.1 GI:12523216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV129451.1 GI:5315686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.7%;
illarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 rcGACTTTGGTGTT 15
                                                                          mRNA sequence.
BG057582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV129451/c
LOCUS
DEFINITION
                                              DEFINITION
                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
xhoi; Plants were grown in an aeroponic chamber for 14 days on ntrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zapXR vector from Strategene and packaged using Glapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France).*
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; sslate=Miyakojima MG-20"
60 c 25 g 63 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 221)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV427766 221 bp mRNA EST 23-MAY-2000 AV427766 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM086e02_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.7%; Score 12.4; DB 10; Length 216; Best Local Similarity 71.4%; Pred. No. 3e+03; Matches 10; Conservative 4; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.4; DB 10; Length 221;
Pred. No. 3.1e+03;
4; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM086e02_r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV427766.1 GI:7788042
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 71.4 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lotus japonicus.
Lotus japonicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tegastwisgwett 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 tegastwisgwett 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||:|:|:|||
TCGACTTTCGAGTT 36
```

RESULT 6 AV427766/c LOCUS

g

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

MEDLINE COMMENT

FEATURES

JOURNAL

Query Match

49

g ð

RESULT BG057582

BASE COUNT ORIGIN

ö

Gaps ö S

```
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV331577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
AV331577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 248)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horl, F., Ishikawa, T., Itch, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kaya, J., Ishikawa, T., Itch, M., Matsuno, Y., Kaya, J., Kikuchi, N., Matuno, Y., Kayan, J., Kai, C., Kaya, J., Kikuchi, N., Matuno, Y., Shigemoto, Y., Shigemoto, Y., Shigemoto, Y., Shinayawa, A., Fakahashi, F., Tominaga, N., Toya, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Yokta, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokta, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Gontact: Yoshihide Hayashizaki, Y. Contact: Yoshihide Hayashizaki, Y. The Institute of Physical and Chemical Research (RIKEN)

The Institute of Physical and Chemical Research (RIKEN)

Tel: 81-45-503-9216

Fax: 81-45-503-9216
                                                               Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB074324 27-JUN-2000 BB074324 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330013E13 3' similar to S78234 nuc2 homolog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mus musculus C57BL/6J 11-day embryo"
/sex~"mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.4; DB 10; Length 247;
Pred. No. 3.1e+03;
4; Mismatches 0; Indels 0
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="11-day embryo"
41 c 34 g 95 t
                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .247
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="2700068H03"
                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BB074324
BB074324.1 GI:8584322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.78;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TCGAGTTTGGTGTT 108
                                                                                                                                                                                                                                             further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB074324
                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
```

ð g

```
trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Ritsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, High-efficiency full-length cDNA cloning. Methods Enzymol. 303, plass visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 252) (bases 1 to 252) (bases 1 to 252). Ritheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kaqawa, I., Kai, C., Kawai, J., Kikuchi, M., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] GAGAGAGAGGAGGCTCTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV331577 252 bp mRNA EST 11-NOV-1999
AV331577 RIKEN full-length enriched, adult male medulla oblongata
Mus musculus cDNA clone 6330524M18 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_fype="diencephalon"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/note="site_l: Sall: Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
Location/Qualifiers
1. 248
/organia="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone_1330013B13"
/clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.4; DB 10; Length 248;
Pred. No. 3.1e+03;
4; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diencephalon"/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV331577.1 GI:6371629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 c
```

```
Owa,C., Ozawa,Y., Salto,H., Sano,M., Sato,K., Shibata,K., Shibata, Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watahabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Konno,H., et al. 1999)

Contect: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fex: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) ICDh.M., Kitsunal, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="6330524M18"
/clone_lib="RIKEN full-length enriched, adult male medulla
oblongata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"

/lab_host="HH10B"

/note="Site_1: Sail; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Sclence Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGGAGGAGGAGGCTTTTTTTTTTTTTTTVN] 3'), CDNA was GAGGAGGAGGAGGAGGCTTTTTTTTTTTTTTVN] 3'), CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Saski,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.4; DB 10;
Pred. No. 3.2e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
/tissue_type="medulla oblongata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .252
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.78;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                      COMMENT
```

```
Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                         rel: 517 355 1609

Email: benningensu.edu
Clones were originally prepared at Michigan State University.

Arabidopsis Biological Resource Center. The Ohio State University.
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 IEL: 61429293371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 288) Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MESSO468 257 bp mRNA EST 19-MAR-2001
M77D22STM Arabidopsis developing seed Arabidopsis thallana CDNA
Clone 600039982R1 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A2921129 288 bp DNA GSS 20-MAR-20
1006024D02.y1 1006 - RescueMu Grid G Zea mays genomic, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.4; DB 10;
Pred. No. 3.2e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                BE530468.1 GI:9788458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:13392455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 82.7%;
1 Similarity 71.4%;
10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 tcgastwtsgwgtt 15
                                                                                                           thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ921129
AZ921129.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
RESULT 11
BE530468/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                       DEFINITION
                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ921129/c
                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

Gaps

;

Indels

10; Conservative

Best Local Similarity Matches 10; Conser

129 TCGACTTTGGTGTT 142

2 togastwisgwgtt 15

ð

```
82.7%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moc.
FLC I.
76 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 TCGACTTTGGTGTT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
AV069588/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                          TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon: survey.com" ris/riso/pi);
/db_xref="taxon: survey.com" riso/riso/pi);
/clone_lib="l006 - RescueMu Grid G"
/tisowe.yppe="leaf"
/dev_stage="adult"
/lab_host="adult"
/lab_host="adult" Vector: RescueMu (engineered from pBlueScript backbone); Site_l: BamHi; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.lastate.edu' and follow the links for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Locates Locate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'RescueMu.' Grid G was grown at Stanford in 2000. DNA was setracted from leaf punches, double digested using BamHI and Balli, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
   Malze genomic sequences found using engineered RescueMu transposon oppublished (2001)
Contact: Walbot v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB191477 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNa lone A330067M09 3' similar to AK001545 Homo sapiens CDNA FLJ10683 fis, clone NYZPR3000142, highly similar to Homo sapiens sapiens mRNA for KIAA0592 protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 291)
                                                                                                                                                                                                                                                                                       Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006024 row: D column: 02
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dackground W23/A188/B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.4; DB 13;
Pred. No. 3.3e+03;
                                                                                                   Department of Biological Sciences
Stanford University
SES California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/cultivar="mixed bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB191477.1 GI:8852096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ampicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 TCGACTATCGAGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB191477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
BB191477
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
```

g ô

```
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
V., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, adult male spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV069588 297 bp mRNA EST 24-JUN-1999 AV069588 Mus musculus small intestine C57BL/6J adult Mus musculus cDNA clone 2010310L11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.4; DB 10; Length 291;
Pred. No. 3.3e+03;
4; Mismatches 0; Indels 0;
,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="spinal cord"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A330067M09"
                                                                        Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host-"DH10B"
```

œ

```
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Lo 297; Lo 297; Lo 207; Lo 200; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF460492 298 bp mRNA EST 04-DEC-2000 UI-M-CG0p-bmd-c-02-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CG0p-bmd-c-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukammalia; Eutherla; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5 and Soares, M.B.
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mus musculus small intestine C57BL/6J adult."
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.7%; Score 12.4; DB 10; Length 297; 71.4%; Pred. No. 3.3e+03; Live 4; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-1-1 Koyadal, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     issue_type="small intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
/db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="2010310L11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chie Owa
Genome Science Laboratory
                                 AV069588.1 GI:5189416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF460492.1 GI:11529649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 tcgastwtsgwgtt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 TCGAGTTTGGTGTT 61
                                                                                                                                            Mus musculus
                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF460492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 3
                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF460492/C
                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
```

```
Email: mEST@mail.nih.gov

The sequence contained an oligo-dr track that was present in the oligo-drougleotide that was used to prime the synthesis of first oligo-ucloctide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Notl site and the oligo-dr track served to identify it as a clone from the retina tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and Seg primer: MIS Forward
POLNA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Grain="C57BL/G"
/ Carain="C57BL/G"
/ Carain="C57BL/G"
/ Carain="C57BL/G"
/ Carain="C57BL/G"
/ Clone="U1-W-CCOp-DM-C-0_C-0_U"
/ Clone="U1-W-CCOp-DM-C-0_C-0_U"
/ Clone="Lib="NIH_BMAP_Red4_S2"
/ Tab_host="DH10B (Life Technologies)"
/ Note="Vector: pT773D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_Red4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
rad_LIB=NH=BMAP_Red4_S2
TAG_IIS=NH=BMAP_Red4_S2
TAG_IIS=NH=BMAP_Red4_S2
TAG_SEG-GTCAGCGGGGCAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12.4; DB 11;
Pred. No. 3.3e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .298
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 25, 2002, 17:20:57 Job time: 16150 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.7%;
71.4%;
                                                                                                                                   Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.7
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||:|:|:||
| 121 TCGAGTTTGGAGTT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tcgastwtsgwgtt 15
```

X05579 Soybean bet A10942 Nucleotide A10939 Nucleotide A10943 Nucleotide AJZ51013 Transform AJZ51014 Transform

AX172441 Sequence A60108 Sequence 1 A76915 Sequence 1

TBI251013 TBI251014

A10939 A10943

6 6 12

BB

AX172441

A60108 A76915

AR098307 AX172440

4946 4946

A71437 A60112

AR098311 AX127748 AX127748

E31991

5349 5560 5560 5865 5865 6539 6548 6548

AX127752 Sequence AX172446 Sequence

```
AX127752 25 bp DNA
Sequence 5 from Patent WO0131042.
AX127752
                                                                                                                                                                                                                                                                                                                                         AX127752.1 GI:14134399
                                                                                                                                                                                                                                                                                                                                                    synthetic construct. synthetic construct
     Length
                                                                                                                                                                                                                                        188272
298616
                                                                                                                                                                                                                                                         93489
149172
                                                                                                                                                                                                                  152883
Query
                                                 19.2
18.8
18.6
17.8
17.8
17.6
17.6
17.6
17.6
     Score
                                                                                                                                                                                                                                                                                                            RESULT 1
AX127752
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                  TITLE
Result
                                                                               Š.
                                                   0000000000
                                                                                                                                                                                                                                   0000
                                                                                                                                                                                                                                                               000
                                           (without alignments)
176.910 Million cell updates/sec
                                     February 25, 2002, 18:00:08; Search time 2331.3 Seconds
                                                                                                                2944280
    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                     1472140 segs, 8248589755 residues
                                                                                                              Total number of hits satisfying chosen parameters:
                                                                        ggatcccccgatgagctaagctagc 25
                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                          - nucleic search, using sw model
                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                               em_htg_hum:*
em_htg_inv:*
em_htg_rod:*
em_htg_other:*
                                                                                                                                                                                                                                                                                                                                                          em_htgo_rod:*
                                                                                                                                                                                                                                                                                                                                         em_vi:*
em_htgo_hum:*
                                                                                                                                                                                                                                                                                                                                                     em_htgo_inv:*
                                                                                                                           length: 0
length: 2000000000
                                                            US-09-698-903B-5
25
                                                                                                                                                                                   gb_nn:*
gb_om:*
gb_om:*
gb_pat:*
gb_ph:*
gb_pr:*
gb_ro:*
gb_ro:*
                                                                                                                                                                                                                                                   gb_vi:*
em_ba:*
em_fun:*
                                                                                                                                                                                                                                                                                                 em_pat:*
em_ph:*
                                                                                                                                                                                                                                                                    em_hum:*
                                                                                                                                                                          gb_ba:*
gb_htg:*
                                                                                                                                                                                                                                                                                                                        em_sts:*
em_sy:*
                                                                                                                                                                                                                                                                          em_in:*
                                                                                                                                                                                                                                                                                            em_ov:*
                                                                                                                                                                                                                                                                                                                  em_ro:*
                                                                                                                                                                                                                                                                                                                                    em_un:*
                                                                                                                                                                                                                                                                                 em_om: *
                                                                                                                                                                                                                                                                                     em_or:*
                                                                                                                                                                                                                                                                                                             em_p1:*
                                                                                                                                                                   GenEmbl:*
                                                                                                                                                                                                                                  sed 1
                                                            Title:
Perfect score:
                                                                                    Scoring table:
                                                                                                                           Minimum DB
Maximum DB
                          OM nucleic
                                                                        Sequence:
                                                                                                     Searched:
                                                                                                                                                                    Database
                                     Run on:
```

AR098307 Sequence AX172440 Sequence A71437 Sequence 7 A60112 Sequence 5 AR098311 Sequence AX127748 Sequence E31991 Mutated bar A60109 Sequence A76916 Sequence 2 AR098308 Sequence E31990 Mutated bar AX063413 Sequence E31990 Mutated bar AX063413 Requence E31590 Mutated bar AX063413 Requence

144104 Sequence 23 144103 Sequence 22 A24783 plasmid pPS AR07438 Sequence A24782 plasmid pJD AR074387 Sequence AR074875 Sequence AR074875 Sequence AR074875 Sequence AR074819 Oryza sat

AR078675 AP004068 AC084319 AC021890

AR074388

144104 144103 A10941

AC020475 AC010842 AC005639 AE003461

A10941 I44104

AX063413 BINHYGDNA

12

6548 7599 12095

A60109 A76916 AR098308 E31990

Homo sapi Drosophil Drosophil Drosophil

AC021890 AC020475 AC010842 AC005639 AE003461 AF072897 AC005359 AC005359

Arabidops

REVERSE-

Human DNA Homo sapi

15-MAY-2001

PAT

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

artificial sequence.

1 (bases 1 to 25)
Weston, B. and de Beuckeleer, M.
Wale-sterile brasica plants and methods for producing same Patent: WO 0131042-A 5 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
1. .25
//organism="synthetic construct"
//db xref="taxon:32630"
//note="primer MDB251" source FEATURES

ð

```
/note="theroretical fusion junction (24) with gene 7 of Ti
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1993
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                           ; Score 25; DB 12; Length 249;
; Pred. No. 0.043;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                A10942 1037 bp DNA PAT 2
Nucleotide sequence 4 from patent number DE3920034.
A10942 A10942 GI:492369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence 1 from patent number DE3920034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                1. .13
/note="beta-1-tubulin sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 25; DB 6; Best Local Similarity 100.0%; Pred. No. 0.039; Matches 25; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                    ı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: DE 3920034-A 4 31-MAY-1990;
                              14. .28
/mote="pUC 13 polylinker" 29. .35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: DE 3920034-A 1 31-MAY-1990;
Location/Qualifiers
1. .1085
                                                                                                                                                                                   /note="polyA site"
220. .225
/note="put.polyA signal"
47 c 38 g 86
                                                                                                                                             173. .178
/note="put.polyA signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unidentified"
/db_xref="taxon:32644"
174 c 166 g 359
                                                                                     /note="Sal I linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .1037
                                                                                                                                                                                                                                                                                                                                                1 ggatccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       767 GGATCCCCCGATGAGCTAAGCTAGC 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                36 GGATCCCCCGATGAGCTAAGCTAGC
                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 25; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1085 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unclassified.
1 (bases 1 to 1085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A10939.1 GI:492367
                                                                                                                                plasmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified.
unidentified
                                                                                                                                                                                                                                 9/
             misc_feature
                                                                      misc_feature
                                                                                                misc_feature
                                          misc_feature
                                                                                                                                            misc_feature
                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A10939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
A10942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A10939
                                                                                                                                                                                                                                                                                                                                                  ă
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOSKET,D.E.
The expression of a chimeric soybean beta-tubulin gene in tobacco Mol. Gen. Genet. 207, 328-334 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUSJATA GINGOUS,
beta-tubulin; fusion gene; plasmid.
Synthetic construct.
synthetic construct
attificial sequence.
1 (bases 1 to 249)
Guiltinan,M.J., Velten,J., Bustos,M.M., Cyr,R.J., Schell,J. and
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARGMTUB 249 bp DNA SYN 02-APR-1988 SOybean beta-1-tubulin gene fused to Ti plasmid unit 7 3UTR. X05579
                                                                                                                                                                                                                             03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="fusion product (17AA); Protein sequence is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                        synthetic construct.

synthetic construct
artificial sequence.

1 (bases 1 to 25)
de Both, 6, and de Beuckeleer, M.

Hybrid winter oilseed rape and methods for producing same Patent: WO 0141558-A 7 14-JUN-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 25;
                                                        Query Match 100.0%; Score 25; DB 6; Length 25
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 100.0%; Score 25; DB 6; Length 25. I Similarity 100.0%; Pred. No. 0.05; 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                             PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
/protein_1d="70As29084.1"
/box.ref="G1.437641"
/translation="AMAMASSNWSTDPPMS"
                                                                                                                                                                                                                                                                                                                                                                                                                           1. .25
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer 251"
a 8 c 7 g 4 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 249
/organism-"synthetic construct"
/db_xref="taxon:32630"
1. 51
       4
                                                                                                                                                                                                                     AX172446 25 bp DNA
Sequence 7 from Patent W00141558.
AX172446 AX172446.1 GI:14597558
    7 9
                                                                                                                  1 ggatcccccgatgagctaagctagc 25
                                                                                                                                   1 GGATCCCCCGATGAGCTAAGCTAGC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X05579.1 GI:58087
    æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 25; Conserva
      ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e
S
    و
                                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                              Source
                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                      AX172446
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
ARGMTUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                         RESULT
```

q ò

ö

ö

```
/translation-"NHHQTGFSPAGANQRGPLAATLSGPGGEGQSAVARLTGEKKNHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-DNA sequence of the plant transformation binary vector pBAR-A Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cardon,G.H.
Direct Submission
Submitted (12-NOV-1999) Cardon G.H., Molecular Plant Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TBI251014 3236 bp DNA SYN 26.
Transformation binary vector pBAR-35S, T-DNA region.
AJ251014 AJ251014.1 GI:6453667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to transposable element Tn5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synthetic multiple cloning site"
2192. .2314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ar to T-DNA right border"
699 g 600 t
derived from plasmid pGPTV-BAR"

1. .148
/note="similar to T-DNA left border"
/complement(149. .279)
/gene="lac1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 12; 100.0%; Pred. No. 0.037; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t-dna; transformation binary vector.
Transformation binary vector pBAR-35S.
Transformation binary vector pBAR-35S
artificial sequence; vectors.
1 (bases 1 to 3236)
Cardon, G. H. and Huijser, P.
                                                                                                                      /transl_table=11
/protein_id="CAC42834.1"
/db_xref="G1:14572627"
                                                                                                                                                                                                                                                                                                                                                            complement(<956. .>1544)
/gene="bar"
                                                                                                                                                                                                                                           complement(<577, .>732)
/gene="lac2"
                                                                             complement(<149. .>279)
                                                                                                                                                                                                                                                                                                                                                                                                  complement(956. .1544)
                                                                                                                                                                                                                                                                            complement(577. .732)
                                                                                                                                                                                                                                                                                                                      transcript 7"
                                                                                                                                                                                                                                                                                                                                      733. .955
/gene="transcript 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961 GGATCCCCCGATGAGCTAAGCTAGC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                              /note="M13 ori"
/direction=RIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /388..2157
/gene="NOS"
/note="similar t
2158..2191
/gene="NOS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2192. .2314
/gene="NOS"
2315. .2476
/note="similar t
                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="NOS"
1838.
                                                                                                                                                                                                                                                                                             /gene="lac2"
                                                                                                                                                                                                                                                                                                                                                                                                                               1545. .1837
/gene="NOS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 3236)
                                                                                                                                                                                                                                                                                                                                                                                                               /gene="bar"
1545. .1837
                                                                                                                                                                                                                                                                                                614 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                   280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563
                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                  rep_origin
                                                                                                                                                                                                                                                                                                          terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
TBI251014/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                              mRNA
                                                  gene
                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Related sequences: U09365, J01825, J01636, X02513, V00090, X05822, X01077, J01826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Transformation binary vector pBAR-A"
/db_xref="taxon:108140"
/note="Can be cultured in Escherichia coli or
Agrobacterium tumefaciens-T-DNA region of a binary vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (12-NOV-1999) Cardon G.H., Molecular Plant Genetics,
Max-Planck- Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg
10, 50829 Cologne, GENMANY 201825 20183, V00090, X0582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   artificial sequence; vectors.

1 (bases 1 to 2476)
Cardon, G.H. and Huijser, P.
T-DNA sequence of the plant transformation binary vector pBAR-A
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                            27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1160;
                                                                                        Length 1085;
                                                                                                                                                                                                                                                                          Nucleotide sequence 5 from patent number DE3920034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TBI251013 2476 bp DNA SYN :
Transformation binary vector pBAR-A, T-DNA region.
AJ251013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                      0; Indels
                                                                                         Score 25; DB 6;
Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 6;
Pred. No. 0.039;
Mismatches 0
                                 343 t
                                                                                      ch 100.0%; Score 25; DB 1 Similarity 100.0%; Pred. No. 0.0 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t-dna; transformation binary vector. Transformation binary vector pBAR-A. Transformation binary vector pBAR-A
                                                                                                                                                                                                                                                                                                                                                                                                         Patent: DE 3920034-A 5 31-MAY-1990;
Location/Qualifiers
1. 1160
/organism="unidentified"
/db_xref="taxon:32644"
367 a 194 c 188 g 411
 /organism="unidentified"
/db_xref="taxon:32644"
218 c 155 g 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                    1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 25; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ251013.1 GI:6453666
                                                                                                                                                                                                                                                            1160 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 2476)
                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1160)
                                                                                                                                                                                                                                                                                                     A10943.1 GI:492370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1, .2476
                                                                                                                                                                                                                                                                                                                                   unidentified.
unidentified
unclassified.
                                                                                      Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardon, G.H.
                                 ø
                                                                                                                                                                                                                                                            A10943
                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
TB1251013/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                             RESULT
A10943
                                                                                                                                                                                                                                                            LOCUS
                                                                                                                                                    õ
                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
```

03-JUL-2001

PAT

```
synthetic construct.

SM synthetic construct
artificial sequence.

If (Dases 1 to 4832)
S de Both,G. and de Beuckeleer,M.
Hybrid winter oilseed rape and methods for producing same
Hybrid winter oilsed rape and methods for producing same
Aventis CropScience N.V. (BE)
S Location/Qualifiers
I. 4832
/organism="synthetic construct"
/db_xxef="taxon:32630"
/db_xxef="taxon:32630"
/db_xxef="taxon:32630"
/note="TroNA of plasmid pTHW118"
Sc_feature 1883: 4065
/note="Hpai restriction fragment"
                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels
                              AX172441 4832 bp DNA
Sequence 2 from Patent W00141558.
AX172441 GI:14597553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 GGATCCCCGATGAGCTAGC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1569 a
                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A60108
                                       DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
A60108/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
              4X172441/C
                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A76915/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                        á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                        /transl_table=11
/protein_id="Cac42835.1"
/db_xref="G1:14572628"
/translation="NHHQTGFSPAGANQRGPLAATLSGPGGEGGSAVARLTGEKKNHP
                                                                         1. 3236
/organism="Transformation binary vector pBAR-35s"
/db_xref="taxon:108141"
/note="can be cultured in Escherichia coli or Agrobacterium tumefaciens-T-DNA region of a binary vector derived from plasmid pGPTV-BAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
Max-Planck- Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg
10, 50829 Cologne, GERMANY
Related sequences: U09365, J01825, J01636, X02513, V00090, X05822
X01077, J01826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1545. 1837

/gene="NOS"

1838. 2157

/note="similar to transposable element Tn5"

2167. 2707

/gene="caMV 35s"

2168. 2730

/gene="caMV 35s"

2708. 2730

/gene="caMV 35s"

2708. 2730

/gene="caMV 35s"

2731. 2956

/gene="caMV 35s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 25; DB 12; Length 3236;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 25; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                     1. .148
/note="similar to T-DNA left border"
complement(149. .279)
complement(<149. .>279)
/gene="laci"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2957. .3074
/genew.mos gene promoter"
2957. .3074
/genew.mos gene promoter"
3075. .3136
/notew.similar to T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="M13 or1"
complement(<577. .>732)
/gene="lac2"
complement(577. .732)
/gene="lac2"
733. .955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(956. .1544)
                                                                                                                                                                                                                                                                                                                                                                                                                                733. .955
/gene="transcript 7"
733. .955
                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ggatccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="NOS"
1545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene-"bar
545. 183
                                                                                                                                                                                                                                                                                                                                                  280. .576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           804
                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                             CDS
                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

ö

Gaps

;

```
ö
       06-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                   Length 4946;
                                                                                                                                                                                                                                                                /organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
a 891 c 963 g 1523 t
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                          Genetic transformation using a PARP inhibitor
Patent: WO 9706267-A 1 20-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
       PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 25; DB 6; Best Local Similarity 100.0%; Pred. No. 0.035; Matches 25; Conservative 0; Mismatches 0;
A60108 4946 bp DNA
Sequence 1 from Patent WO9706267.
A60108 A60108.1 GI:3715124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A76915 4946 bp DNA
Sequence 1 from Patent EP0757102.
A76915 A76915.1 GI:6088712
                                                                                  Transformation vector pTHW107.
Transformation vector pTHW107
artificial sequence; vectors.
1 (bases 1 to 4946)
De,B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 GGATCCCCGATGAGCTAGC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A76915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
```

RESULT

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAR-1998
                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 25; DB 6; Length 5349; Best Local Similarity 100.0%; Pred. No. 0.035; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 6; Length 5560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pTHW142"
                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic transformation using a PARP inhibitor Patent: WO 9706267-8 5 20-FEB-1997; PLANT GENETIC SYSTEMS NV (BE) LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Transformation vector
/db_xref="taxon:126817"
1199 c 1244 q 1576 +
      /db_xref="taxon:32630"
/note="T-DNA of plasmid pTHW107"
964. .4906
                                                                                                                                                                            Score 25; DB 6;
Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1487 t
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases I to 5349)
Michiels,F. and Williams,M.
IMPROVED BARSTAR GENE
Patent: WO 9810081-A 7 12-MAR-1998;
MICHIELS FRANK (BE)
                                                                     /note="Hind III fragment"
891 c 963 g 1523
                                                                                                                                                                                                                                                                                                                                                                                                     A/1437 5349 bp DNA
Sequence 7 from Patent WO9810081.
A71437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A60112 5560 bp DNA
Sequence 5 from Patent W09706267.
A60112.1 GI:3715128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:32644"
1233 c 1290 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transformation vector pTHW142.
Transformation vector pTHW142 artificial sequence; vectors.
1 (bases 1 to 5560)
De, B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .5349
                                                                                       963 g
                                                                                                                                                                                                                                                              100.0%; Scu.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A71437.1 GI:4775050
                                                                                                                                                                     Query Match
Best Local Similarity 100.'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unidentified
                                                                                         1569 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1339 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1533 a
                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
A71437/c
                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A60112/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct.
synthetic construct
synthetic construct
synthetic construct
synthetic squence.
1 (bases 1 to 4946)
de Both, G. and de Beuckeleer, M.
Hybrid winter oliseed rape and methods for producing same
Hybrid winter oliseed rape and methods for producing same
Hybrid winter oliseed rape and methods for producing same
Hybrid winter oliseed rape and methods for producing same
Hybrid winter oliseed rape and methods for producing same
Hybrid winter oliseed rape and methods for producing same
Hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same
hybrid winter oliseed rape and methods for producing same and 
                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 6; Length 4946; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25, DB 6; Length 4946; 100.0%; Pred. No. 0.035; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                               /organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
a 891 c 963 g 1523 t
                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
Transformation vector pTHW107.

M Transformation vector pTHW107
artificial sequence; vectors.

1 (bases 1 to 4946)
De,B.M.
GENETIC TRANSFORWATION USING A PARP INHIBITOR PACHT: EP 0757102-A 1 05-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown.
Unclassified.
1 (bases 1 to 4946)
10 Block.
Genetic transformation using a PARP inhibitor Patent: US 6074876-A 1 13-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR098307 4946 bp DNA
Sequence 1 from patent US 6074876.
AR098307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AXI72440 4946 bp DNA Sequence 1 from Patent W00141558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
891 c 963 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 GGATCCCCCGATGAGCTAAGC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ggatccccgatgagctaagctagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX172440.1 GI:14597552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:12807564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                              1. .4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR098307.1
                                                                                                                                                                                                                                                              1569 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1569 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX172440/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
AR098307/c
                      ORGANISM
                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                   REFERENCE
                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
```

à q

ò a ó

; 0; Gaps Best Local Similarity 100.0%; Pred. No. 0.035; Matches 25; Conservative 0; Mismatches 0; Indels

Search completed: February 25, 2002, 18:00:10 Job time: 18418 sec

us-09-698-903b-5.rng

Н

Page

```
PCR primer for fla
PCR primer MDB251
USP-Promoter-casse
                                                                                                                                    Search time 716.55 Seconds (without alignments)
29.912 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     **Side State State
                                                                                                                                                                                                                                                                                                                                                                                                                                      1861242
4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                     930621 seqs, 428662619 residues
                                                                                                                                        ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
    GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                      February 25, 2002, 18:17:22
                                                                                                                                                                                                                                                                      ggatcccccgatgagctaagctagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH25426
AAD06994
AAQ04705
AAQ04703
AAT39337
AAT59531
AAT59531
AAF86422
AAF25423
                                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ū
                                                                                                                                                                                                                     US-09-698-903B-5
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %
Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1100.00
11000.00
11000.00
11000.00
11000.00
11000.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                        ..
oo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š.
```

υ	13	25	100.0	5864	17	AAT39339 AAT39339	PT
Ü	15	25		∞	N 6	AAD06990 AAD06990	Chimeric T-DNA of Chimeric T-DNA of
	16	25		ഗധ	-1	AAZ91097	plasmi
	18	25		חור	∽ ∞	AAT61394	prs1/2.
	19 20	25		R 4	-c	AAZ91096 AAF86441	E. coli plasmid pr Plasmid pr3346. U
	21	25		יער	10	AAF25320	Nucleotide sequenc
	22	24			40	AAQ04704	USP-Promoter-casse
	24	24		10	10	AAQ15144	pvE36 Bt ICP codin
	25	24		S (4 .	AAQ42160	Plasmid pPS0212 co
	27	4 6		۰	40	AAQ42159 AAH43929	Plasmid pJD884 con Agrobacterium tume
	28	-			10.6	AAH25165	PCR primer used to
υ	50	17.2		2562	9	AAI59154	Human polynucleoti
	31			າຕ	4 N	AAI59608	Human polynucleoti Human polynucleoti
υ	32	_			4	AAQ42148	Bt884 oligonucleot
	33	17			п,	AAZ29122	Plasmid DV131 comp
	ع د 4 م	17	-			AA229121	Plasmid DV130 comp
	36	17			-	AAZ29123	Plasmid DV132 used
υ	37	17				AAN50226	Sequence of opine
ပ	æ c	٦,			- 0	AAN50182	tid
c	ر ا ا	ė u			סת	AAZ9630/	S. pneumoniae deri
ני	41			347	ש ש	AAV30458	Streptococcus phen Rhizobium species
	42	ė			σ	AAV30459	Rhizobium species
	43	٠,		457	~ :	AAC53867	sis thali
	4 4 4 7	16.2		521		AAC54447 AAC52318	Arabidopsis thalla Arabidopsis thalla
						ALIGNMENTS	
RESI	RESULT 1	П					
ID	AAH2542	9	standard	i; DNA;	25 I	BP.	
X X	AAH25	5426;					
XX							
DŢ	22-AUG	JG-2001	(fir	st entry	(X)		
DE	PCR F	primer	for fl	flanking	regions	lons in transgenic	enic plant MS-BN1.
X X X	Trans	sqenic	plant;	winter	O	rape;	orid seed; male-sterility gene;
KW	fertil	ility r	estor	H	11	ene;	er; ss.
SO	Syntheti	hetic.					
XX	TA10050W	7141558	- A 1				
XX		}					
D.	14-JUN	JN-2001	_;				
XX PF	06-DEC	EC-2000		2000WO-EP1287	2872.		•
XX PR	08 - DEC	EC-1999	σ.	9US-0457	7037		
XX				Ç		į	
A X	(AVET	^	AVENTIS C	CROPSCIE	ENCE	NV.	
PI	De Bc	Both G,	De Be	Beuckelee	er M;		
DR N	WPI;	2001-3	381419/40	.40.			
PT P	Trans	Transgenic wi		iter oilseed qualities,		l rape plants suited comprises a male-st	ted for producing hybrid seed:
E A	resto	torer ge	•	tegrated		депоше	
4 0	E V D	7 0 0	A oned	12. QBpr	;	glich	

Example 4; Page 42; 98pp; English.

ьS

Legumin-signalpept USP-signalpeptide Plasmid pTS88 (Eco Nucleotide sequenc T-DNA of plasmid p Nucleotide sequenc Plasmid pTS172delt T-DNA of pTTS24.

1085 11160 11303 4832 4946 55228 5349

ပပပ υ a

```
ö
            The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene (e.g. barnase gene), and the other plant has an expression cassette comprising a fertility restorer gene (e.g. barstar gene), integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. PCR primers AAH25425-26 were used to amplify the flanking region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic plant is useful for producing a hybrid seed by crossing the hybrid seed from the transgenic Brassica plant and harvesting the hybrid seed trom the transgenic Brassica plant.

The present sequence is primary thermal interlaced (TAIL)-PCR primer MDB251 used to right (5') and left (3') border flanking region of elite event MS-B2. This primer corresponds to position 293-317 of plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer MDB251 to generate the flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MS-B2 elite event; transgenic Brassica plant; transformation event; male-sterility gene; PCR primer; thermal asymmetric interlaced;
                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                            Score 25; DB 22;
Pred. No. 0.0053;
                                                                                                                                                                                                                                     Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                            25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 28; 53pp; English.
                                                                                                                                                                                                                                                                                          100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                          1 ggatcccccgatgagctaagctagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0430497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD06994 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-2001
                                                                                                                                                                                                         cransgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD06994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pTC0113
                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD06994
ID AAD0
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
×888888888888888
                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA and the
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The unique BglII-Ort (720-725) site is for ligating foreign DN: HindIII-Ort in the 3' polylinker (1032-1037) for cloning the cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is transfected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 11; Length 1037;
Pred. No. 0.007;
Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Incorporation of DNA into higher plant genome - by specified
                                              Length 25;
                                                                  Indels
                                                                                                                                                                                                                                                    Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; legumin; USP-Pr.T7-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1037 BP; 338 A; 174 C; 166 G; 359 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Wobus
                                          100.0%; Score 25; DB 22;
100.0%; Pred. No. 0.0053;
iive 0; Mismatches 0;
          Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Legumin-signalpeptide cassette Le-Sig.T7.
                                                                                                                                                                                                                                                                                                                                                                                                  Hai
                                                                                                                                                                                                                                                                                                                                                                                                 Α,
                                                                                    1 ggatcccccgatgagctaagctagc 25
                                                                                                           25
                                                                                                                                                                                                                                USP-Promoter-cassette USP-Pr.T7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ggatccccgatgagctaagctage 25
                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                               Baumlein H, Muntz
                                                                                                  1 ggatccccgatgagctaagctagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                                                                                               AAQ04705 standard; DNA; 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ04703 standard; DNA; 1085
                                                                                                                                                                                                                                                                                                                                89DE-3920034.
                                                                                                                                                                                                                                                                                                                                                     88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                         (PFLA-) VE KOMB PFLANZENZUC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant DNA techniques.
                                                                                                                                                                                                           (first entry)
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also AAQ04703-Q04706.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-172459/23.
                                                     Best_Local Similarity
Matches 25; Conser
                                                                                                                                                                                                                                                                                                                               20-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                    19-SEP-1988;
                                                                                                                                                                                                          12-OCT-1990
                                                                                                                                                                                                                                                                                   DE3920034-A.
                                                                                                                                                                                                                                                                                                           31-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                                Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-1990
                                                                                                                                                                                     AAQ04705;
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ04703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                    AAQ04705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ04703
                                                                                                                                         RESULT
XX OS
                                                                                     ð
                                                                                                         q
                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XEXEXEX
```

 \sim

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region containing polyadenylation signal of gene 7 og Agrobacterium \mathtt{T}\text{-}\mathtt{DNA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= p35S
/function= 35S promoter of cauliflower mosaic virus
strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds.
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                         The unique BglII-Ort (890-895) site is for ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1155-1160) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected. See also AAQ04703-Q04706.
                                                                                                                                                                                                                                                                                                                                             Length 1160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
transgenic plant; rice; Oryza sativa; maize; corn; Zea mays;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/label= barstar
/product= Bacillus amyloliquefaciens barstar
968..1287
                                                                                                                   Incorporation of DNA into higher plant genome - by specified
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                Sequence 1160 BP; 369 A; 192 C; 188 G; 411 T; 0 other;
                                            Wobus U;
                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 25; DB 11; Best Local Similarity 100.0%; Pred. No. 0.007; Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= e
/label= pGEM2
/note= "polylinker of pGEM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= pGEM2
/note= "polylinker of pGEM2"
                                            Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                            Baumlein H, Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT39337 standard; DNA; 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= 3'g7
             (PFLA-) VE KOMB PFLANZENZUC.
                                                                                                                                 recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1288..1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      695..967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..35
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36..694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                        WPI; 1990-172459/23
P-PSDB; AAR05199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9626283-A1
                                            Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT39337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT39337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                 The Legumin gene B4 is used. The unique BglII-Ort (815-820) site is for ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1080-1085) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
            higher plant genome; legumin; B4 gene; signalpeptide; Le-Sig.T7.; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 11; Length 1085;
Pred. No. 0.007;
Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                          Incorporation of DNA into higher plant genome - by specified recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; signalpeptide; USP-Sig.T7.; ss.
Foreign DNA incorporation; recombinant DNA techniques;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1085 BP; 368 A; 219 C; 155 G; 343 T; 0 other;
                                                                                                                                                                                                                                                                    Wobus U;
                                                                                       /product=Legumin-signalpeptide
                                                                                                                                                                                                                                                                    Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-signalpeptide 747..817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USP-signalpeptide cassette USP-Sig.T7
                                         Location/Qualiflers 747..814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA004706 standard; DNA; 1160 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; P
Matches 25; Conservative 0;
                                                                                                                                                                            89DE-3920034
                                                                                                                                                                                                                                     (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89DE-3920034
                                                                                                                                                                                                        88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                   Baumlein H,
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAQ04703-004706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               708..817
                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                             WPI; 1990-172459/23.
P-PSDB; AAR05198.
                                                                                                                                                                            20-JUN-1989;
                                                                                                                                                                                                          19-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1988;
                                                                                                                  DE3920034-A.
                                                                                                                                                                                                                                                                   Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE3920034-A.
                                                                                                                                               31-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ04706;
```

intron

RESULT AAQ04706

à 윱

ö

```
WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200141558-A1
                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Both G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                          3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3'UTR
                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....sycuic plant; winter ollseed rape; hybrid seed; male-sterility gene;
fertility restorer gene; barstar gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "right border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The HindIII-ECORI fragment (AAT39337) of plasmid pTS88 contains barstar DNA under control of a 35S promoter. The plasmid was used with prg134 (see also AAT39336) contg. barnase DNA under control of the stamen-specific promoter El to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pVE136 (see also AAT39338) contg. barnase DNA under control of the stamenspecific PCA55 promoter to produce male sterile malze plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible low level expression of barnase DNA in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                               Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note = "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "residual sequence from TL-DNA at right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 17; Length 1303; 100.0%; Pred. No. 0.0071; 1ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
                                                                                                                                                                                                                       Cornelissen M, Michiels F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of plasmid pTHW118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                border repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 38; 56pp; English.
                                                                                                                                                                         È
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                (PLBZ ) PLANT GENETIC SYSTEMS
                                                            96WO-EP00722.
                                                                                                             95EP-0400364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH25423/c
ID AAH25423 standard; DNA; 4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces hygroscopicus.
Arabidopsis thaliana.
Bacillus amyloliquefaciens.
Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..25
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54..90
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91..97
                                                                                                                                                                                                                                                                           WPI; 1996-402373/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 25; Conserv
                                                                                                                                                                                                                       Botterman J,
                                                                                                             21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
  29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH25423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
NAME OF COLOR OF COLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME OF THE PERMINENT O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid
                                                                                                                                                                                                                                                                                                                                                                     /note- "atS1A ribulose-1,5-biphosphate carboxylase small subunit gene from Arabidopsis thallana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= p
/note= "left border repeat from TL-DNA from pT1B6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Taq1 fragment from 3' UTR of nopaline
synthase gene from T-DNA of pT1f37 and
containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "downstream of Bacillus amyloliquefaciens
barstar coding region"
complement (2981..3253)
                                                                                                                                                        /*tag= f
/note= "synthetic polylinker derived seguences"
complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= i
/note= "synthetic polylinker derived sequences"
complement (2659..2919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= k
/note= "synthetic polylinker derived sequences"
2941..2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= n
/note= "anther-specific gene TA29 promoter from
Nicotiana tabacum"
/*tag= d
/note= "synthetic polylinker derived sequences"
complement (98..309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "tag= o
'note= "synthetic polylinker derived sequences"
                                                                                                              of pTiB6S3'
                                                                                                                                                                                                                                        /*tag= g
/note= "Streptomyces hygroscopicus bialaphos
resistance (bar) gene"
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= m
/note= "Barstar gene coding region from I
amyloliquefaciens"
complement (3254..4762)
                                                                                                              7
                                                                                                         UTR from TL-DNA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 80-82; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2000; 2000WO-EP12872.
                                                                                   /*tag= e
/note= "3'
                                                                                                                                                                                                                                                                                                                                                                                                                            ..2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2920..2940
                                                                                                                                    330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                            2609.
```

us-09-698-903b-5.rng

S

```
/note= "T-DNA left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
misc_feature
                                                                                                                                                                                       (PLBZ ) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                               04-AUG-1995;
                                        EP757102-A1
                                                                            05-FEB-1997.
                                                                                                                                                                                                                            De Block M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH25422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                           ö
seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. The present sequence represents plasmid prHWHIB. This plasmid comprises the barstar gene, which acts as a fertility restorer gene. The plasmid is used to create transgenic plants of the invention.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               niacinamide, Agrobacterium, T-DNA, male sterile, barnase, ribonuclease, RNase, cereal, wheat, ollseed rape, Brassica napus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/label= 3/97
/note= "3' untranslated region contg. the poly-A
signal of gene-7 of Agrobacterium T-DNA
complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter region of Rubisco small subunit
gene of Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "3'untranslated region contg. the poly-A signal of the nopaline-synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP;
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "promoter region of tobacco TA29 gene"
complement (4822..4946)
                                                                                                                                                                   Length 4832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= phosphinothricin acetyltransferase complement (883..2608)
                                                                                                                                                                                                         Indels
                                                                                                             Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
                                                                                                                                                                                                         ö
                                                                                                                                                                  Score 25; DB 22;
Pred. No. 0.0078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "T-DNA right border"
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= barnase
complement (3368..4876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (2658..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (97..330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                               317 GGATCCCCCGATGAGCTAAGCTAGC 293
                                                                                                                                                                                                                                            1 ggatcccccgatgagctaagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (1..25)
                                                                                                                                                                  Query Match 100.0%; Some Sest Local Similarity 100.0%; P. Matches 25; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                           AAT59531 standard; DNA; 4946 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- Barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Agrobacterium sp.;
Chimeric Arabidopsis thaliana;
Chimeric Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- PTA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- PSSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/label= RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- LB
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-DNA of plasmid pTHW107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pTHW107; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                AAT59531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cos
                                                                                                                                                                                                                                                                                                                                       RESULT
 8588888
                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                               HANDER TO THE TOTAL TO THE TOTA
```

```
Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene; fertility restorer gene; barnase gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
"right border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 barnase coding sequence under control of the tobacco TA29 gene stamen-specific promoter and a phosphinothricin acetyltransferase coding sequence under control of an Arabidopsis Rubisco small subunit gene promoter. Oilseed rape hypocotyl explants were infected with Agrobacterium tummefaciens C58ClRif carrying vector pyrWUOT and helper Ti plasmid pwRGO. In some treatments, the hypocotyls were treated with the poly (ADP-ribose) polymerase inhibitor niacinamide (250 mg/l) 4 days prior to infection. Blants regenerated from niacinamide-treated transformed calli had a low copy number and displayed less variation in the expression profile of the transgenes.
                                                                                                                                                                                                                                                                                             Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and reduces metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pTHW107 is a vector carrying T-DNA (AAT59531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 25; DB 18; Similarity 100.0%; Pred. No. 0.0078; 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 13-16; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..25
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ggatcccccgatgagctaagctagc 25
                                                                                                                  GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
AAH25422/C
ID AAH25422 standard; DNA; 4946 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 GGATCCCCGATGAGCTAAGCTAGC
                                                       95EP-0401844.
95EP-0401844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces hygroscopicus. Arabidopsis thaliana. Bacillus amyloliquefaciens. Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
26..97
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                        WPI; 1997-111050/11.
```

ö

Tue Feb

Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;

S

```
The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid different genetic backgrounds. The present sequence represents plasmid pfHWN107. This plasmid comprises the barnase gene, which acts as a male-sterility gene. The plasmid is used to create transgenic plants
                                                                                                                                                                                                                                                                                                                               /note- "3'UTR downstream of Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                          /note= "atSlA ribulose-1,5-biphosphate carboxylase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "left border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                            "Taql fragment from 3' UTR of nopaline synthase gene from T-DNA of prit37 and containing plant polyadenylation signals"
                                                            /*tag= d
/note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                      /*tag= g
/note= "synthetic polylinker derived sequences"
complement (2659..2919)
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "anther-specific gene TA29 promoter from Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= 1
note= "synthetic polylinker derived sequences"
1922..4946
                   /*tag= c
/note= "3' UTR from TL-DNA gene 7 of pT1B6S3"
                                                                                                    /*tag= e
/note= "Streptomyces hygroscopicus bar gene"
                                                                                                                                                                                                                                                                                                                                                                                   /note= "Barnase coding region from Bacillus amyloliquefaciens" complement (3368.4877)
                                                                                                                                                                                                                                                                                                                                                barnase coding region"
complement (3032..3367)
                                                                                                                                  complement (883..2608)
     complement (98..309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 78-80; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Both G, De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-2000; 2000WO-EP12872
                                                                                                                                                                                        2609..2658
                                                                                                                                                                                                                                                                                                     2920..3031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1878..4921
                                               310..330
                                                                                         331..882
                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200141558-A1
                                            misc_feature
                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2001
                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                  3'UTR
  3'UTR
                                                                                                                                                                                                                                3'UTR
                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                           CDS
```

the invention

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for producing male sterile plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapesed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                  Male sterile plant; RNAase inhibitor; plasmid pTS172delta; ds.
    Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5228 BP; 1384 A; 1307 C; 1263 G; 1274 T; 0 other;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 25; DB 22; I Best Local Similarity 100.0%; Pred. No. 0.0079; Matches 25; Conservative 0; Mismatches 0;
                             ö
Score 25; DB 22;
Pred. No. 0.0078;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 14-17; 29pp; Japanese.
                                                                 11 GGATCCCCCGATGAGCTAGC 293
                                                 1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4957 ggatccccgatgagctagc 4981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ggatcccccgatgagctaagctagc 25
                                                                                                                                          AAF86439 standard; DNA; 5228 BP.
                          ö
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV23239 standard; DNA; 5349
                                                                                                                                                                                                                                                                                                                                                           12-SEP-2000; 2000WO-JP06222.
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               (NISB ) JAPAN TOBACCO INC.
                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hamada K, Nakakido F;
                                                                                                                                                                                                                          Plasmid pTS172delta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-266212/27.
           Local Similarity
                                                                                                                                                                                                                                                                                                       WO200124616-A1.
                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1999;
                                                                                                                                                                                                 25-JUN-2001
                                                                                                                                                                                                                                                                                                                                2-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1998
Query Match
                                                                                                                                                                      AAF86439
           Best Loca
Matches
                                                                                                                               AAF86439
                                                  ŏ
                                                                          qq
                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

^

ö

Gaps

ö

Indels

```
/note= "region containing polyA signal of nopaline
synthase gene of Agrobacterium T-DNA"
complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= j
/label= 3'g7
/note= "region containing polyA signal of gene 7
of Agrobacterium T-DNA"
complement (5840..5864)
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "region containing polyA signal of gene 7 of Agrobacterium T-DNA" complement (331..882)
                                                                                                                                                                                                                     Plasmid pTC0113 T-DNA used to obtain male sterile oilseed rape.
                                                                                                                                                                                                                                                Plasmid pTCO113; male sterile; barnase; ribonuclease; barstar; transgenic plant; oilssed rape; canole; Brassica napus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "promoter of stamen-specific TA29 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= i
/label= Barstar
/note= "region coding for barstar of Bacillus
amyloliquefaciens"
5490..5765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= d
/label= Pssu
/note= "promoter of Arabidopsis Rubisco small
                                                                                                                                                                                                                                                                                                                                                                                 /note= "right border of Agrobacterium T-DNA" complement (98..330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= f
/label= Barnase
/note= "Bacillus amyloliquefaciens barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "promoter of nopaline synthase gene
Agrobacterium T-DNA"
5217..5489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "region coding for phosphinothricin
acetyltransferase"
complement (883..2608)
 ö
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit gene"
complement (2659..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (3368.4877)
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                          317 GGATCCCCCGATGAGCTAAGCTAGC 293
                                                                                                                                                                                                                                                                                                                                       complement (1..25)
                             1 ggatcccccgatgagctaagctagc 25
                                                                                                                                BP.
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= e
/label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= g
|abel= PTA29
                                                                                                                               AAT39339 standard; DNA; 5864
                                                                                                                                                                                                                                                                                                                                                                                                                               /label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= h
/label= Pnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/label= bar
                                                                                                                                                                                                                                                                                                                                                                     /label- RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1924..5216
                                                                                                                                                                                       22-JAN-1997 (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                   polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyA_signal
 25;
                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                             AAT39339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                   RESULT 12
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                  AAT39339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                              δλ
                                                       g
                                                                                                                                                             DNA encoding an improved barstar protein – used to restore fertility
in male-sterile plant lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence was used in the preparation of an improved Bacillus amyloliquefaciens barstar, i.e. barnase inhibitor, which can be used to restore fartility to male-sterile lines. The DNA sequence encoding the improved barstar, leads to increased barstar production in tapetum cells, due to improved translation, and possibly protein stability.
                                                                                                                                                                                                                                                                                        /note= "region coding for phosphinothricin acetyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= g
/label= 3'_chs
/note= "region containing 3' untranslated end of
chalcone synthase gene"
complement (5325..5349)
                                                                                                                                                                                                    /label= 3'_g7
/note= "region containing 3' untranslated end of
Agrobacterium T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                Anote= "355 promoter of Cauliflower Mosaic Virus' 2281..3969
                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "promoter of El gene of rice (WO9213956)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5349 BP; 1339 A; 1233 C; 1290 G; 1487 T; 0 other;
                           Barstar; barnase inhibitor; fertility restoration; male-sterile line; plasmid pTTS24; T-DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 19;
Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= h
/note= "T-DNA left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product improved_barstar
                                                                                                                                                          /note= "right boarder"
complement (98..331)
                                                                                                                                                                                                                                                                                                                        complement (884..2258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Pages 41-43; 54pp; English.
                                                                                                  Location/Qualifiers
                                                                                                                  complement (1..25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                         /*tag= d
/label= P35S
                                                                                                                                                                                                                                                               /*tag= c
/label= bar
                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/label= PE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-EP04739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96EP-0202446
                                                                                                                                            /label- RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1246..4577
                                                                                                                                                                                                                                                                                                                                                                                                                                           3970..4245
                                                                                                                                                                                                                                                332..883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-193630/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
T-DNA of pTTS24.
                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9810081-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michiels F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1998
                                                                    Synthetic
```

promoter

CDS

CDS

promoter

3'UTR

CDS

coding

of

ō

```
WPI; 1996-402373/40.
                                                                                               polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9626283-A1
                                                                                                                                                                                                                                                                                                                                     polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-1996
                                               promoter
                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                          promoter
                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                        CDS
         ö
                                                                                                                                                                                                                                      Plasmid pTCOll3 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-regulatory) gene under control of the pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterium-mediated transformation using pTCOll3 were male sterile. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of barstar counteracted any low level expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                       Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "region containing polyA signal of gene 7 of Agrobacterium T-DNA" complement (331.882)
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid prcoll3 r-DNA used to obtain male sterile oilseed rape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pTCO113; male sterile; barnase; ribonuclease; barstar; transgenic plant; oilssed rape; canole; Brassica napus; ds.
                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 25; DB 17; Length 5864;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 25; Conservative 0; Mismatches 0; Indels 0
 /*tag~ k
//abel~ LB
/note= "left border of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- RB
/note- "right border of Agrobacterium T-DNA"
complement (98..330)
                                                                                                                                                                                                                                                                                                                                    Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;
                                                                                                                                                                                                                     Example 3; Page 33-3743-47; 56pp; English.
                                                                                                                                      Michiels F;
                                                                                                                                                                                                                                                                                                                                                                                                                         5546 ggatcccccgatgagctaagctage 5570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
complement (1..25)
                                                                                                                                                                                                                                                                                                                                                                                                       1 ggatccccgatgagctaagctagc 25
                                                                                                                 (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                    Cornelissen M,
                                                                                              95EP-0400364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT39339 standard; DNA; 5864
                                                                             96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                      WPI; 1996-402373/40.
                                    WO9626283-A1
                                                                            21-FEB-1996;
                                                                                             21-FEB-1995;
                                                                                                                                    Botterman J,
                                                         29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT39339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT39339/C
ID AAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGS
à
```

```
Plasmid pTCOll3 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-regulatory) gene under control of the Pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterium-mediated transformation using pTCOll3 were male sterile. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of
                                                                                                                                                                                                                                                                                                                  /note= "region containing polyA signal of nopaline synthase gene of Agrobacterium T-DNA" complement (3032, 3367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "promoter of stamen-specific TA29 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "region containing polyA signal of gene 7 of Agrobacterium T-DNA" complement (5840.5864)
                                                                                                                                                                               /note= "promoter of Arabidopsis Rubisco small subunit gene" complement (2659..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "region coding for barstar of Bacillus amyloliquefaciens" 5490..5765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                             /note= "region coding for phosphinothricin
                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Barnase
/note= "Bacillus amyloliquefaciens barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "promoter of nopaline synthase gene
Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "left border of Agrobacterium T-DNA"
                                                                         acetyltransferase"
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 33-3743-47; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botterman J, Cornelissen M, Michiels F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (3368..4877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= Barstar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                        /label= 3'nos
                                                                                                                                  /*tag= d
/label= Pssu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= g
label= PTA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= h
/label= Pnos
/*tag= c
/label= bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= 3'q7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1924..5216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5217..5489
```

σ

```
"note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39-OCT-1999;
                                                                                        misc_feature
                                                                                                                                                misc_feature
                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weston B,
                                                        promoter
                                                                                                               promoter
                                                                                                                                                                                                                                                             3'UTR
                        CDS
                                                                                                                                                                      CDS
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /noté- "promoter from the atSlA ribulose-1,5-biphosphate
carboxylase small subunit gene from Arabidopsis thaliana"
2610..2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "TagI fragment from the 3' untranslated end of the nopaline synthase gene (3'nos) from the T-DNA of pTiT37 and containing plant polyadenylation signals" 2921..2936
                                                                                                                                                                                            T-DNA; plasmid pTC0113; transgenic Brassica plant; transformation event; male-sterility gene; chimeric; tobacco; ds.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Protein encoded by bialaphos resistance
gene (bar) of Streptomyces hygroscopicus"
884..2609
                                                                                                                                                                                                                                                                                  1..25
/*tag= a
/*ote= "Right border repeat from the TL-DNA from
PT1B653"
26..53
/*tag= b
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "Residual seguence from the TL-DNA at the
                                                                                                                                                                                                                                                                                                                                                                                      /______The 3' untranslated end from the TL-DNA gene 7 (3'97) of pTiB6S3" 310...331
                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= h
/note= "Synthetic polylinker derived sequence"
2606.-2920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= j
/note= "Synthetic polylinker derived sequence"
2937..3032
                                       Length 5864;
               Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;
                                                      Indels
                                     Score 25; DB 17;
Pred. No. 0.0079;
Mismatches 0;
                                                                                                                                                                                                                   Chimeric - Streptomyces hygroscopicus.
Chimeric - Arabidopsis thallana.
Chimeric - Bacilius amyloliquefaciens.
Chimeric - Nicotiana tabacum.
Chimeric - Agrobacterium tumefaciens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                  right border repeat
                                                                                                                                                                                                                                                                            Location/Qualiflers
                                                                     Chimeric T-DNA of plasmid pTC0113.
                                                                                                                             AAD06990 standard; DNA; 5865 BP
                                     Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 25; Conservative 0;
barnase in non-stamen tissue.
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  ..883
                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                            Key
misc_feature
                                                                                                                                                             06-AUG-2001
                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                            AAD06990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                                                                                                                                                                                                                                                            3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3'UTR
                                                                                                              RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                     合
                                                                                                                                      SXS
                                                                     ö
```

```
/*tag= o
/note= "Promoter of the nopaline synthase gene from the
T-DNA of pTiT37 of Agrobacterium tumefaciens"
5216.5217
/notes "The 3' untranslated region downstream from the barnase coding sequence of Bacillus amyloliquefaciens" 3033..3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the
                                                                                                                                                          /*tag= m
/note= "bromoter region of the anther-specific gene
TA29 from Nicotiana tabacum"
4879..4924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Residual sequence from the TL-DNA at the right border repeat"
5811..5840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "The 3' untranslated end from the TL-DNA
gene 7 (3'g7) of pTiB6S3"
5767.5773
/*tag= u
                                                                   /product= "Protein encoded by barnase gene from
Bacillus amyloliquefaciens"
3369..4878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= x
/note= "Left border repeat from the TL-DNA from
PTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= w
/note= "Synthetic polylinker derived sequence"
8841..5865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9= u
= "Synthetic polylinker derived sequence"
..5810
                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- p
/note= "Synthetic polylinker derived sequence"
5218..5490
                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= q //product= "Protein encoded by barstar gene of Bacillus amyloliquefaciens" 5491.5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= s
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end
                                                                                                                                                                                                                                                                               sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Sequence from the 3' untranslated end barstar gene from Bacillus amyloliquefaciens" 5531..5554
                                                                                                                                                                                                                                                   /*tag= n
/note= "Synthetic polylinker derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 47-49; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Beuckeleer M;
                                                                                                                                                                                                                                                                                                1925..5215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5555..5766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
```

us-09-698-903b-5.rng

```
3'UTR
                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                       transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic gene, at a specific location in the Brassica genome. Transgenic brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is chimneric T-DNA of plasmid prooll3. This sequence comprises right border repeat, left border repeat and 3' untranslated region (UTR) from TL-DNA of priB653, synthetic polylinker sequences, coding regions of blalaphos resistance gene (bar) from Striptomyces hyproscopicus, barnase gene from Bacillus amyloliquefaciens and promoters of atSIA arabidopsis thallana, the anther-specific gene from the T-DNA of priB37 of Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-DNA; plasmid pTCO113; transgenic Brassica plant; transformation event; male-sterility gene; chimeric; tobacco; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= f //product= "Protein encoded by bialaphos resistance game (bar) of Streptomyces hygroscopicus" /*tag= g /*tag= g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*teg= a
/note= "Right border repeat from the TL-DNA from
pT1B6S3"
                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= d
/note= "The 3' untranslated end from the TL-DNA
gene 7 (3/97) of priB6S3"
                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 22; Length 5865; larity 100.0%; Pred. No. 0.0079; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26..53
**tag~ b
note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= e
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                     Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/note= "Residual sequence from the TL-DNA
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - Streptomyces hygroscopicus.
Chimeric - Arabidopsis thaliana.
Chimeric - Bacilius amyloliquefaciens.
Chimeric - Nicotiana tabacum.
Chimeric - Agrobacterium tumefaciens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                       right border repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric T-DNA of plasmid prcoll3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD06990 standard; DNA; 5865 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD06990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AADO6990/C
XX
AC
AC
AC
AC
AC
AC
ADO6
XX
AC
ADO6
XX
COLIM
COS
COLIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3'UTR
 8$8888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
/*tag= i
/note= "TagI fragment from the 3' untranslated end of the
nopaline synthase gene (3'nos) from the T-DNA of prim37
/note= "Promoter from the atS1A ribulose-1,5-biphosphate carboxylase small subunit gene from Arabidopsis thallana" 2610..2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4925..5215

/*tag= 0

/*note= "Promoter of the nopaline synthase gene from the

FIDNA of prir37 of Agrobacterium tumefaciens"
                                                                                                                                                                                                                                                                       /*tag= k
/note= "The 3' untranslated region downstream from the
barnase coding sequence of Bacillus amyloliquefaciens"
3033..3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= m
/note= "Promoter region of the anther-specific gene
TA29 from Nicotiana tabacum"
4879..4924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / cus- "Sequence from the 3' untranslated end of barstar gene from Bacillus amyloliquefaciens" 5531.5554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= v
/note= "Residual sequence from the TL-DNA at the
                                                                                                                                                                                                                                                                                                                                                             /product= "Protein encoded by barnase gene from
Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "The 3' untranslated end from the TL-DNA gene 7 (3'97) of priB6S3"
                                                          /*tag- h
/note= "Synthatic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= x
/note= "Left border repeat from the TL-DNA from
pTiB6S3"
                                                                                                                                                                                                          /*tag= j
/note= "Synthetic polylinker derived sequence"
2937,.3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= p
/note= "Synthetic polylinker derived sequence"
/note= "Synthetic polylinker derived sequence"
/*tag= q
/*tag= q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag- s
/note- Synthetic polylinker derived sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ^*tag- n
note- "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= u
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= w
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= q
/product= "Protein encoded by barstar gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus amyloliquefaciens"
5491..5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              right border repeat"
5811. selo
                                                                                                  2660..2920
                                                                                                                                                                                                                                                     ..3032
                                                                                                                                                                                                                                                                                                                                                                                                       3369..4878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5555..5766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5774..5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..5840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5841..5865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200131042-A2
                                          misc_feature
                                                                                                  misc_feature
                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                   3'UTR
```

```
The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the transgenic plant with a male-fertile Brassica plant.

The present sequence is chimeric T-DNA of plasmid prcoll3. This sequence comprises right border repeat, left border repeat and 3' untranslated region (UTR) from T-DNA of prises, synthetic polylinker sequences, coding regions of bialaphos resistance gene (bar) from Streptomyces hygroscopicus, barnase gene from Bacillus amyloliquefaciens and promoters of atSiA ribulose-15-biphosphate carboxylase small subunit gene from Arabidopsis thallana, the anther-specific gene from the T-DNA of prir37 of the anther-specific gene from the T-DNA of prir37
                                                                                                                                        Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
                                                                                                                                                                                                                                      Claim 1; Page 47-49; 53pp; English.
(AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Agrobacterium tumefaciens
                                          De Beuckeleer M;
                                                                                        WPI; 2001-300517/31.
                                             Weston B,
```

; Score 25; DB 22; Length 5865; ; Pred. No. 0.0079; 0; Mismatches 0; Indels 0 Query Match 100.0%; Best Local Similarity 100.0%; Matches 25; Conservative 0; g ö

; 0

Gaps

ö

Search completed: February 25, 2002, 18:17:24 Job time: 16682 sec



us-09-698-903b-5.rni

```
February 25, 2002, 18:05:13; Search time 301.6 Seconds (without alignments) 18.773 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                             702406
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    351203 seqs, 113238999 residues
                                                                                                                                                                                                                                      1 ggatcccccgatgagctaagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - nucleic search, using sw model
                                                                                                                                                                                                                                                                           IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                         US-09-698-903B-5
25
                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                             Scoring table:
                                                                              OM nucleic
                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                   Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued_patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Database

		ð			SUMMARIES	
Result	lt 5. Score	Query Match	Length	DB	ID	Description
	1 25	100.0	1303	6	US-08-894-440-2	Sequence 2, Appli
O	2 25		4946	٣	US-08-817-188-1	1,
ပ	3 25	•	5560	m	US-08-817-188-5	Sequence 5, Appli
	4 25		5864	m	US-08-894-440-4	4
ပ	5 25		5864	m	US-08-894-440-4	4
	6 25		6548	m	US-08-894-440-1	Sequence 1, Appli
	7 25	_		r	US-08-817-188-2	7
	8 24			+	US-08-453-104-23	23,
	9 24			~	US-08-694-824-23	23,
, ,			3201	-	US-08-453-104-22	22,
		0.96		~	US-08-694-824-22	22,
. 7	12 24	0.96		7	US-08-232-016-23	23,
• 1		96.0	7	ď	US-08-232-016-22	22,
	14 24	0.96	78	7	US-08-549-680A-5	2,
υ	15 17	68.0		~	US-08-232-016-11	Sequence 11, Appl
. 7	16 17	0.89		4	US-09-080-625-3	'n
	17 17	68.0	3336	4	US-09-080-625-2	Sequence 2, Appli
	18 17	68.0		4	US-09-080-625-5	'n
	19 17	0.89	3877	4	US-09-080-625-4	4
υ	20 17	68.0	~	9	5428147-1	Patent No. 5428147
U	21 16.6		62	~	US-08-790-912-1	Sequence 1, Appli
•			54	~	US-08-503-226B-32	32,
•	23 16	64.0		e	US-08-721-458B-32	32,
υ	24 16	64	٠٠,	7	US-08-209-521-28	28,
. •		61.6	1186	Н	US-08-064-121-2	2, A
• •	26 15.4	61.6	1186	Н	US-08-478-015-2	7
•••		61.6	1186	m	US-08-475-975-2	7

ö

Gaps

ö

Query Match 100.0%; Score 25; DB 3; Length 1303; Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 25; Conservative 0; Mismatches 0; Indels (

1 ggatcccccgatgagctaagc 25

ŏ

Sequence 2, Appli Sequence 46, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	plants	nce: HindIII-EcoRI	osaic Virus strain Bacillus	on signal of gene 7
3 US-09-084-889-2 3 US-08-651-5630-46 3 US-08-65-177A-1 2 US-08-65-177A-1 2 US-08-16-155B-1 3 US-08-04-185-101 1 US-08-044-185-101 1 US-08-046-177A-1 5 US-08-046-182-1 5 US-08-91-1258-1 6 US-09-31-1258-1 7 US-09-31-1256-1 6 US-09-31-1250-1 7 US-08-112-817C-1 1 US-08-112-817C-1 1 US-08-112-817C-1 1 US-08-112-817C-1 1 US-08-112-817C-1 1 US-08-112-817C-1 1 US-08-112-817C-1 1 US-08-112-817C-1 1 US-08-0965-950-3 4 US-08-998-16-591	ALIGNMENTS 08894440 ts obtain male sterile to obtain male sterile 1. US/08/894,440	ence ption of Artificial Sequence: nt of pFS88 nker of pGEM2 (pGEM2)	moter of Cauliflower M (P35S) coding for barstar of quefaciens	ure .287) region containing polyadenylation of Agrobacterium T-DNA (3'97) ure 1303) polylinker of pGEM2
6 1186 6 2143 6 2143 6 10281 6 10281 6 10281 0 1642 0 2352 0 2352 0 7431 2 1377 2 1377 4 699 6 60	ULT 1 08-894-440-2 equence 2, Application US/0889444 atent No. 602546 ENERAL INFORMATION: APPLICANT: PLANT GENETIC SYSTEMS ATTLE OF INVENTION: Method to obt FILE REFERENCE: NMSCOR CURRENT APPLICATION UMBER: US/08 CURRENT FILING DATE: 1997-11-12 SOFTWARE: Patentin Ver. 2.0 EQ ID NO 2	cial Sequence N: Description N: fragment of eature 55) N: polylinker of	NAME/KEY: misc_feature LOCATION: (36)(694) OTHER INFORMATION: 35S pro OTHER INFORMATION: CM1841 FEATURE: NAME/KEY: misc_feature LOCATION: (695)(967) OTHER INFORMATION: region OTHER INFORMATION: amyloli	FEATURE: LOCATION: (968)(1287) OTHER INFORMATION: region con OTHER INFORMATION: of Agrobac FEATURE: NAME/KEY: misc_feature LOCATION: (1288)(1303) OTHER INFORMATION: polylinker 8-894-440-2
611. 651. 660. 660. 671. 672.	Applica 225546 225546 225546 22471 20071 101 DA 101 DA 101 DA	H: 1303 DNA ISM: Artifici RE: INFORMATION: INFORMATION: RE: RE: INFORMATION: INFORMATION: INFORMATION: INFORMATION:	RE: (EY: misc_fea (DN: (36)(6 INFORMATION: INFORMATION: RE: (EY: misc_fea (EY: misc_fea (INFORMATION:	nisc_f (968). RMATIO RMATIO nisc_f (1288) RMATIO
4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	20 CEE FE # BES C	LENGTH: 1303 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: OTHER INFORMATION: Des OTHER INFORMATION: fra FEATURE: NAME: TEATURE: NAME: TEATURE: OTHER INFORMATION: pol: OTHER INFORMATION: pol:	FEATURE: NAME/KEY: misc_feature LOCATION: (36)(694) OTHER INFORMATION: 35S OTHER INFORMATION: CM1) FEATURE: NAME/KEY: misc_feature LOCATION: (695)(967) OTHER INFORMATION: reg OTHER INFORMATION: reg	NAME/KEY: misc_feature LOCATION: (968)(1287) OTHER INFORMATION: regionter information: of A FEATURE: NAME/KEY: misc_feature LOCATION: (1288)(1303) OTHER INFORMATION: 0519
800112m4m9mmmm444444	0.1 0.0 0.1 0.1	LENGT TYPE: ORGAN ORGAN OTHER OTHER FEATU NAME/ LOCAT	FEATU NAME/ LOCAT OTHER OTHER FEATU NAME/ LOCAT COCAT	9
	R D V V V V V V V V V V V V V V V V V V			S

9

```
FEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (5067)..(550
                                                          Q
                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEATURE:

OTHER INFORMATION: Description of Artificial Sequence: T-DNA of PEATURE:

OTHER INFORMATION: plasmid pTHW107

FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((1)..(25))

OTHER INFORMATION: T-DNA right border (RB)

FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((97)..(330))

OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((331)..(882))

OTHER INFORMATION: bolyadenylation signal of gene 7 of Agrobacterium FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((331)..(882))

OTHER INFORMATION: bar: region coding for phosphinotricin acetyl

OTHER INFORMATION: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: DE BLOCK, MARC

TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-01279

CURRENT APPLICATION NUMBER: US/08/817,188

CURRENT FILING DATE: 1997-05-15

EARLIER APPLICATION NUMBER: EP 95401844.6

EARLIER FILING DATE: 1995-09-04

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1

LENGTH: 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEATURE:

NAME/KEY: misc_feature
LOCATION: Complement((2658)..(3031))

OTHER INFORMATION: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: Complement((3368)..(4876))
OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter region of Rubisco small subunit gene
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 25; DB 3; Length 49
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OCTHER INFORMATION: barnase: region coding for barnase
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: Complement((4922)..(4946))
; CTHER INFORMATION: LB: T-DNA left border
US-08-817-188-1
1024 ggatcccccgatgagctaagctagc 1048
                                                                                                                                                               Sequence 1, Application US/08817188 Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                       RESULT 2
US-08-817-188-1/c
```

```
RESULT 3
US-08-817-188-5/C
Sequence 5, Application US/08817188
Patent No. 6074876
Herent No. 6074876
HILDER INFORMATION:
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER REPLICATION NUMBER: PCT-EP96/03366
BARLIER FILING DATE: 1995-08-04
HOUMBER OF SEQ. ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ. ID NO 5
LENGTH: 5560
LENGTH: 5560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(25)
OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (84)...(296)
OTHER INFORMATION: 3/ 97: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium OTHER INFORMATION: T-DNA FRATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (4483)..(4671)
OTHER INFORMATION: IV2: region corresponding to the second intron of
OTHER INFORMATION: the ST-LS1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (5533)..(5560)
OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
OTHER INFORMATION: pTIB6S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU: promoter region of Rubisco small subunit
OTHER INFORMATION: gene of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (3059)..(5056)
OTHER INFORMATION: uida: region coding for beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (318)..(869)
OTHER INFORMATION: bar: region coding for phosphinotricin OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (5067)..(5502)
OTHER INFORMATION: P35S: 35S promoter region of CaMV
```

```
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFOR
US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                         to 20
                                                           to 20
) NAME/KEY: misc_feature
): LOCATION: (5058)...(5059)
): OTHER INFORMATION: region with unknown sequence (may contain up to 2)
): OTHER INFORMATION: nucleotides)
): FEATURE:
): NAME/KEY: misc_feature
): LOCATION: (5077)...(5078)
): OTHER INFORMATION: nucleotides)
): OTHER INFORMATION: nucleotides)
): FEATURE:
): NAME/KEY: misc_feature
): LOCATION: (5476)...(5479)
): OTHER INFORMATION: region with unknown sequence (may contain up to 2)
): OTHER INFORMATION: region with unknown sequence (may contain up to 2)
): OTHER INFORMATION: nucleotides)
): OTHER INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of gene
                                                                                                                                                                                  ಧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTCO113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))

OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 25; DB 3; Length 55
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08894440
Patent No. 6025546
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMATION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                  LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: T-DNA OTHER INFORMATION: plasmid pTC0113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
OTHER INFORMATION: region coding for barnase of Bacillus OTHER INFORMATION: amyloliquefactens
                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %Sequence 4, Application US/08894440

Sequence 4, Application US/08894440

Patent No. 6025546

GENERAL INFORMATION:

APPLICANT: PLANT GENETIC SYSTEMS N.V.

TILLE OF INVENTION: Method to obtain male sterile plants

FILE REFERENCE: NASCOR

CURRENT APPLICATION NUMBER: US/08/894,440

CURRENT FILING DATE: 1997-11-12

NUMBER: PATENTIN ONS: 4

SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA
                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (4924)..(5216)
OTHER INFEMATION: promoter of nopaline synthase gene
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: Complement((5840)..(5864))
OTHER INFORMATION: left border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 3; L ilarity 100.0%; Pred. No. 0.0014; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                      NAME/KEY: misc_feature
```

ö

Page

of rice

```
NAME/KET: misc_feature

LOCATION: (5711)..(6262)

OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
FEATURE:
NAME/KET: misc_feature
LOCATION: (6263)..(6496)

OTHER INFORMATION: region containing polyadenylation signal fo gene 7

US-08-894-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: plasmid PTS172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-01279;
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
FEALLIER APPLICATION NUMBER: PCT/EP96/03366
FEARLIER PILING DATE: 1996-07-31
FEARLIER PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                        NAME/KEY: misc_feature
LOCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: Complement((2019)..(2288))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA.
                                                                                                                 OTHER INFORMATION: of nopaline synthase gene of Agrobacterium FEATURE:
NAME/KEX: misc_feature
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El gene c
OTHER INFORMATION: (PEI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 3; Length 6:
llarity 100.0%; Pred. No. 0.0014;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: Complement((2289)..(2624))
OTHER INFORMATION: barnase: region coding for barnase
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6277 ggatccccgatgagctaagctagc 6301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08817188
Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-817-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of FRATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2559)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: of 3'nos)
OTHER INFORMATION: (3'nos)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana FEATURE:
NAME/KEY: misc_feature
LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene of OTHER INFORMATION: Agacum (PTA29)
OTHER INFORMATION: promoter of nopaline synthase gene of FRATURE:
NAME/KEY: misc_feature
LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene of FRATURE:
NAME/KEY: misc_feature
LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene of FRATURE:
NAME/KEY: misc_feature
LOCATION: (4924)..(5216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FERTURE:
NAME/KEY: misc_feature
LOCATION: (3490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement((5840)..(5864))
OTHER INFORMATION: left border of Agrobacterium T-DNA
US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 25; DB 3; Length 58 Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEX: misc_feature
LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08894440
Patent No. 6025546
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTAME: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)..(2003)
OTHER INFORMATION: pUC19 derived vector sequences
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 GGATCCCCCGATGAGCTAGC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ggatcccccgatgagctaagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-08-894-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

ö

Gaps

ö

S

```
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: CORNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                          ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Plet
APPLICANT: STAM, Marke
APPLICANT: STAM, Marke
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
TITLE OF INVENTION: IN PLANT CELLS
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                            NAME/KEY: misc_feature

NAME/KEY: misc_feature

CATION: Complement((5711)..(6262))

OTHER INFORMATION: bar: region coding for phosphinotricin

OTHER INFORMATION: acetyltransferase
FRATURE:
NAME/KEY: misc_feature

CATION: (6496)

OTHER INFORMATION: 3'q7: 3' untranslated region containing the

OTHER INFORMATION: T-DNA

US-08-817-188-2
                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (4336)..(5170)
OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
OTHER INFORMATION: Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 6548;
NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: PEl: promoter region of El gene of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 3;
ilarity 100.0%; Pred. No. 0.0014;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION UNDBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Rea, Teresa S
REGISTRATION NUMBER: 30, 427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEFANCE: (703) 836-620
TELEFAX: (703) 836-5201
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/453,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-453-104-23
Sequence 23, Application US/08453104
Patent No. 5633446
GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: George Mason Blô
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
```

```
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
CORRESPONDENCE: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                    Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: George Mason Bldg., Washington & Prince St CITY: Alexandria STREET: Virginia CUWTRY: United States 21P: 22313-1404 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: BR PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE STATEM: PC-DOS/MS-DOS SOFTWARE: PATENTING SYSTEM: DS-MG-1996 CLASSIFICATION NUMBER: US/08/694,824 FILING DATE: 09-MG-1996 CLASSIFICATION DATA: APPLICATION NUMBER: US 07/937,869 APPLICATION NUMBER: US 07/937,869
                                                                                                                                                                         NAME/KEY: misc_feature;
CCATION: 2078..2082
CTHER INFORMATION: /note= "Nucleotides 2078-2082
CTHER INFORMATION: wherein N is not known."
US-08-453-104-23
                                                                                                                                                                                                                                                                                                                                                              Query Match 96.0%; Score 24; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,427
JER: 010830-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 2879 GATCCCCGATGAGCTAAGCTAGC 2902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08694824 Patent No. 5877306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 gatcccccgatgagctaagctagc 25
LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Rea, Teresa S
REGISCRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
```

9

ö

```
Sequence 22, Application US/08694824
Patent No. 5877306
GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOFTAET, Piet
APPLICANT: TAM, Maike
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTENTAL BULDARES:
CONTENT BULDARES:
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STRTE: Virginia
STRTE: STRIP
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/937,869
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
BRATCHEREN NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.0%; Score 24; DB 2; Length 3201;
100.0%; Pred. No. 0.004;
Live 0; Mismatches 0; Indels
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 2151.2155

CTHER INFORMATION: /note= "Nucleotides 2151-2155

CTHER INFORMATION: wherein N is not known."
                              ö
                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 836-6620
TELEFAN: (703) 836-620
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                       2952 GATCCCCGATGAGCTAAGCTAGC 2975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2952 GATCCCCCGATGAGCTAAGCTAGC 2975
                                                               2 gatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 gateceeegatgagetaage 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 3201 base pairs
nucleic acid
EDNESS: single
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Rea, Teresa S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                 US-08-694-824-22
                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                             οy
                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CORNELISEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: SOETAERT, Piet
APPLICANT: SOETAERT, Piet
APPLICANT: SOETAM, Malke
APPLICANT: SOETAM, Malke
APPLICANT: SOETAM, Malke
TITLE OF INVENTION: NODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
                                                                                                                                                                                   ó
                                                                                                                                                                                   Gaps
                                                                                                                                                                               ö
                                                                                                                                 DB 2; Length 3200; 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3201;
                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIrginia
COUNTRY: United States
LD: 22313-1404
COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082; OTHER INFORMATION: wherein N is not known."
US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 2151_.2155
OTHER INFORMATION: /note= "Nucleotides 2151-2155
OTHER INFORMATION: Wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 1;
Pred. No. 0.004;
                                                                                                                          96.0%; Score 24; DB 100.0%; Pred. No. 0.0 cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
RECISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   2879 GATCCCCGATGAGCTAAGCTAGC 2902
                                                                                                                                                                                                                                                                                                                               US-08-453-104-22

Sequence 22, Application US/08453104

Patent No. 5633446

; GENERAL INFORMATION:
                                                                                                                                                                                                         2 gatococogatgagotaagotago 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.0%; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                    Ouery Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-453-104-22
                                                                                                                                                                                                                                              a
                                                                                                                                                                                                           ð
```

ő

us-09-698-903b-5.rni

```
NAME/KEY: misc_feature
LOCATION: 3582..4407
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacte
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KET: misc_feature
LOCATION: 7071..7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader wit
US-08-232-016-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 5600.6457
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CORRELESSEN, Marc
APPLICANT: SOETAERT, Plet
APPLICANT: STAM, Maixe
APPLICANT: STAM, Maixe
APPLICANT: DOCKY, Jan
APPLICANT: VAN AARSSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
CORRESPONDENCE: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 96.0%; Score 24; DB 2; Length 7566; Best Local Similarity 100.0%; Pred. No. 0.0045; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-CCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P39,300
ER: 010830-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 1808 GATCCCCCGATGAGCTAAGCTAGC 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/08232016 Patent No. 5952547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 gatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/CDOCKET NUMBER: 0106
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 836-6620
TELEPAN: (703) 836-5221
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-232-016-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Coding region of a truncated modified bt2 (cryIAb) gene, also designated as the
   Sequence 23, Application US/08232016

Patent No. 5952347

GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOCTAERT, Piet
APPLICANT: TAMM, Maike
APPLICANT: VAN AARSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUINS, Doane, Swecker & Mathis
CITY: Alexandia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 2396..2921
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
OS-POST 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: plasmid DNA designated as pPS0212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CF FILING DATE: 25-MAR-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             010830-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cryIAb6 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE.
ATTORNEY/AGENT INFORMATION.
NAME: MGGOWAD, MALODIM K
REGISTRATION NUMBER: p19,300
REFERENCE/DOCKET NUMBER: 01083C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7566 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alexan-CITY: Alexan-STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 1.1785
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 484.684
OTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.0%; Score 24; DB 2; Length 7811;
100.0%; Pred. No. 0.0045;
tive 0; Mismatches 0; Indels
                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Verson #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,680A
FILING DATE: 16 JANUARY 1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 194..218
OTHER INFORMATION: /note= "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: complement (729..1340)
OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
NAME/KEY: promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . LUCATION: 3001..3023
; OTHER INFORMATION: /note= "T-DNA left border; OTHER INFORMATION: sequences"
US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_recomb
LOCATION: 1..7811
OTHER INFORMATION: /label- vector pTRVA3
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-0111P
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8000
TELEFAX: 24845
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: promoter
LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-016-11/c
; Sequence 11, Application US/08232016
; Patent No. 5552547
; GENERAL INFORMATION:
APPLICANT: CORNELISEBN, Marc
APPLICANT: SOCIABLISEBN, Marc
APPLICANT: STAM, Malke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               702 GATCCCCGATGAGCTAAGCTAGC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 gatcccccgatgagctaagctagc 25
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (synthetic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 24; Conservative
                                             22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1877..2110
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: Containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..1869
OTHER INFORMATION: /note= "Coding region of a
OTHER INFORMATION: truncated bt2 (cryIAb) gene, also designated as the bt884 gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 3665.4491
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 5684..6541
OCHER INFORMATION: /note= "Sequence complementary to
nt No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 3006_.3665
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 2480..3005
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.0%; Score 24; DB 2; Length 7639; 100.0%; Pred. No. 0.0045; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08549680A
Patent No. 5962768
GENERAL INFORMATION:
APPLICANT: CORNELISSEN, MARCUS
APPLICANT: CORNELISSEN, WERCUS
APPLICANT: OSSELE, VERONIQUE
APPLICANT: VAN AARSSEN, ROEL
TILE OF INVENTION: MARKER GENE
NUMBER OF SEDORGES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
STREET: VISUINA
                                                                   TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: plasmid DNA designated as pJD884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D 1892 GATCCCCCGATGAGCTAAGCTAGC 1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 gatcccccgatgagctaagctagc 25
LENGIH: 7639 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 24; Conservative
                     TYPE: nucleic acid_
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-549-680A-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

ö

```
APPLICANT: DOCKK, Jan
APPLICANT: VAN AARSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Butns, Doane, Swecker & Mathis
CORRESPONDENCE ADDRESS:
ADRESPEE: P.O. Box 1404
CITY: Alexandria
STATE: VIrginia
CONTRE: United States
IP: 22313-140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BM PC COMPATA:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 30-CCT-1991
FILING DATE: 30-CCT-1991
FRIOR APPLICATION NUMBER: GB 92400820.4
FRIOR APPLICATION NUMBER: GB 92400820.4
FRIOR APPLICATION NUMBER: P99,300
REFERENCE/COCKET NUMBER: O10830-049
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION COMPENSES: SINGLE
TOPOLICE CHARACTERICICS:
LENGTH: 29 base pairs
TTYPE: nucleic acid
STRRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORGINAL SOURCE: CARANISM: Oligonucleotide, designated as PS59 US-08-232-016-11
```

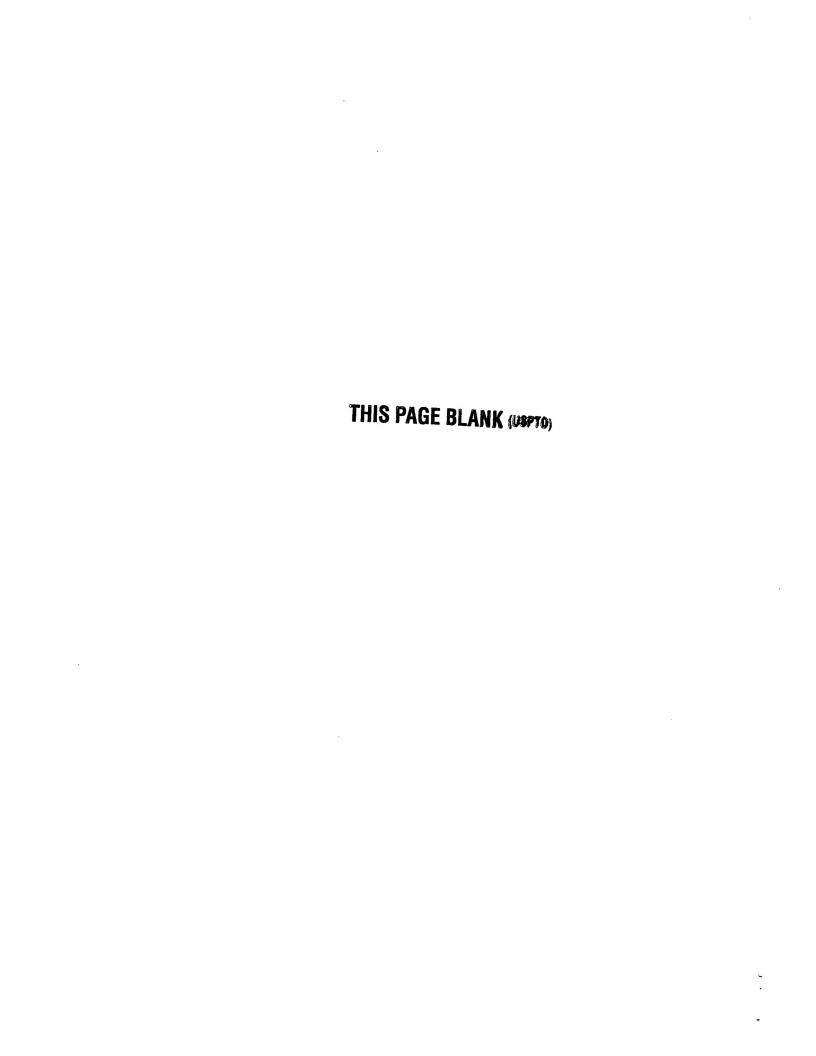
Gaps ö 68.0%; Score 17; DB 2; Length 29; 100.0%; Pred. No. 6.6; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 17; Conservative

ó

õ

g

Search completed: February 25, 2002, 18:05:15 Job time: 18563 sec



qd69g01.x zv49d03.r MR4-ST012

UI-M-BH3-H3120G12-

T. brucei UI-M-BH3-

nbxb0096F

UI-R-CAO-nbeb0031F UI-HF-BP0

BB499943

hr64e06.x L0045H03-

A0867402 r AW501051 d AA429095 a AA429095 a AA429095 a AA429095 a AA489968 d BG073283 b BG073283 b BG073283 b BG073283 b BG0732 a BG073283 b BG13414 d BG3734 a BG3734 d BG3734 d BG3734 d BG3732 d BG3732 d BG035724 b BG035724 b BG035724 b

601060510

602461858 601312066

tc01g05.x 602325804

602624567

601070751

db27g06.x UI-M-BH3-

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum Maximum Database

```
Tel: (206) 616-3818

Tex: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu, Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

Plate: 1074 row: C column: 20
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 498)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. &
                                                                                                                                                                                                                                                                                                 AQ791259 498 bp DNA GSS 03-AUG-1999 HS_5498_A2_B10_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1074 Col=20 Row=C, DNA sequence. AQ791259 GI:5698806
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                             High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                               ALIGNMENTS
                                                          BG073283
TA311E120
BI133671
                                                                                                                                                                      AI344042
BG035724
BG166218
                                                                                                                                                                                                           CNS0333U
 1498
1649
251
400
Homo sapiens
 Hood, L.
                                                                                                                                                                                                                                                                                                                                               human.
RESULT 1
AQ791259
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
 υ
                              00000
                                                                   00 00
                                                                                                              υ
                                                                                                                                 000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ791259 HS_5498_A
AZ028032 RPCI-23-3
AW862033 RC3-CT034
BB455584 BB455584
N24161 yx96d12.s1
BF496895 AT10901.5
BIO38578 MR-NT014
BF877912 MRO-ET010
BE639934 946044B07
AQ834638 HS_5442_A
AL233215 Tetracdon
BE120999 UI-R-CAO-
                                                         (without alignments)
32.517 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                 February 25, 2002, 17:20:57; Search time 8261.74 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                 22703874
              Compugen Ltd
                                                                                                                                  11351937 seqs, 5372889281 residues
                                                                                                                                               Total number of hits satisfying chosen parameters:
       GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                              1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ791259
AZ028032
AW862033
BB453584
                                    OM nucleic - nucleic search, using sw model
                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             П
                                                                                                                                                                                                                                                                                                                                                                          em_gss_other:*
                                                                                                                                                               DB seq length: 0
DB seq length: 200000000
                                                                              US-09-698-903B-5
                                                                                                                                                                                                                                                                                                                 gb_gss:*
em_gss_fun:*
                                                                                                                                                                                                                                                                                                                                             em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                    em_gss_pro:*
em_gss_rod:*
                                                                                                                                                                                                                                                                                                                                em_gss_hum:*
                                                                                                                                                                                                                                                                                                                                      em_gss_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                            133011110013
                                                                                                                                                                                                                        em_estfun:*
em_esthum:*
em_estin:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpo:*
                                                                                                                                                                                                                                                                                                                                                                    em_gss_vrt:
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                           gb_est1:*
gb_est2:*
gb_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           498
303
303
312
312
4494
497
605
605
605
295
                                                                                                                                                                                                                   EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.8
72.8
70.4
70.4
70.4
70.4
70.4
68.8
```

Mus muscu WWS014.El UI-R-CA0-

AL225651 1 BG476758 6 AK016762 A BE419550 W BE119925 U

and

BE639934 AQ834638 CNS038XY BE120999

BF496895 BI038578 BF877912

18.2 118.2 117.6 117.6 117.6 117.6 117.6 117.6

0000

5 6 7 8 8 9 10 11 12

υU

Score

Result õ N24161

a

```
70.48; Score 17.6;
                                                                                                                                                                                                                                                                         247 ATCCACCAATGAGCTTAGCTAGC 225
                                                                                                                                                                                                                                                       3 atcccccgatgagctaagctagc 25
                                                                                                                                                                               72.8%;
87.0%;
                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
                                                                                                                                                                                               Similarity
                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brazil
                                                                                                                                                                             Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                               RESULT 3
AW862033/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                               /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially disested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ028032 562 bp DNA GSS 25-FEB-2000 RPCI-23-373M15.TV RPCI-23 Mus musculus genomic clone RPCI-23-373M15 AZ028032 GI:7103416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 562)
Enbo,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,S., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: szhacetag. Clone the mouse BAC library RPCI-23. For BAC Clones are derived from the mouse BAC library availability, please contact Pieter de Jong (pieter@deJong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) of from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Grgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                           Length 498;
                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1074 Col=20 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Other_GSSS: RPCI-23-373M15.TJ
Contect: Shaying zhoo Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 938 0200
                                                                                                                                                                                                                                                                                                                                     72.8%; Score 18.2; DB 13;
87.0%; Pred. No. 2.9e+02;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .562
/organism="Mus musculus"
               High quality sequence stop: 498.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-373M15"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                   414 ATCCCCCGATGTCCTAAGATAGC 436
                                                                                                                                                                                                                                                                                                                                                                                                               3 atcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                  498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: BAC ends.
Class: BAC ends
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Thes 20; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                               166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ028032/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

```
1. 303
/organism="Homo sapiens"
/do_ref="texton:9606"
/do_ref="texton:9606"
/dov_stage="Adult"
/dev_stage="Adult"
/dev_stage="A
brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2704922
Fax: +55-11-2707001
Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-CT0347-110
300-014-allox1=2000-03-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 303.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 303)
Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., ads SilvayW. Jr., Zago,M.A., Bordin,S., Costa,F.F.F.,
Erunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW862033 303 bp mRNA EST 19-MAY-2000
KS2-CT0347-110300-014-a10 CT0347 Homo sapiens CDNA, mRNA sequence.
AW862033, GI:7957726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.2; DB 13;
Pred. No. 2.9e+02;
0; Mismatches 3;
```

DB 10; Length 303;

à

```
Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.4%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N24161.1 GI:1138311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N24161/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Louise mouse.

House mouse.

Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryotta; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Eukaryotta; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Skonno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Etwidas, S., Fikunishi, Y., Hara, A., Hayatsu, N., Izawa, M., Kadota, K., Kagawa, J., Kagawa, T., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadyan, Y., Kadya, S., Kurihara, C., Kurihara, C., Saluta, R., Shinata, Y., Ono, T., Owa, C., Salito, H., Sato, K., Shibata, Y., Ono, T., Owa, C., Salito, H., Sato, K., Shibata, Y., Shidama, A., Shiraki, T., Sapabe, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tanoda, Y., Watahiki, A., Votca, T., Yamamura, T., Yamanaka, T., Yano, R., Yasunishi, A., Votca, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Contact: Yoshinde Hayashizaki, Y. Contact: Yoshinde Hayashizaki, T. Tagawa, A., Takahashi, R., Yoshino, H., Inpublished (2000)

Contact: Yoshinde Hayashizaki
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoattivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. Automated filitration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                 BB453584 312 bp mRNA EST 21-JUL-2000
BB453584 RIKEN full-length enriched, 12 days embryo spinal ganglion
Mus musculus cDNA clone D130023P09 3' similar to U28724 Mus
musculus DNA mismatch repair (PMS2) mRNA, mRNA sequence.
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D130023P09"
/clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Site 1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                   Gaps
                                   ö
                                   Indels
                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spinal ganglion"
/tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
83.3%; Pred. No. 5e+02;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"DH10B"
                                                                                      2 gatcccccgatgagctaagctagc 25
                                                                                                                                           29 GAGCTCCTTATGAGCTAGC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                BB453584.1 GI:9349077
                                20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-44 (1999)
     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                            RESULT 4
BB453584/c
LOCUS
                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
```

COMMENT

SOURCE

```
RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand CDNA was primed with a primer [5] of the primer [5] of the primer [5] of the prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand CDNA was prepared for full-length by primer adapter of sequence [5] of the primer adapter of sequence [6] of the primer adapter 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 454)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Leh.M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stops: 351
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N24161 454 bp mRNA EST 28-DEC-19
yx96d12.s1 Soares melanocyte 2NbHM Homo sapiens CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares melanocyte 2NbHM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.6; DB 10;
Pred. No. 5e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:3879233"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 351.
Location/Qualifiers
1. 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE: 269591 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:269591"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 GGATCTCCCAAGTAGCTAAGCTAG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ggatcccccgatgagctaagctag 24
```

4

ö

Gaps

ö

Indels

4,

BASE COUNT ORIGIN

ø

RESULT

g ð

LOCUS

BF496895

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_llb-"Wr0143"
/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/inote="Organ: nervous_tumor; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and obnA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 510)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-NT0143-220101-004-h09&t3=2001-01-22&t4=1)

Seq primer: puc I # forward

High quality sequence start: 196

High quality sequence stop: 396.

Location/Qualifiers

1. 510
                                                                                                                                                                                                                                                 BI038578 510 bp mRNA EST 14-JUN-2001
MR4-NT0143-220101-004-h09 NT0143 Homo sapiens CDNA, mRNA sequence.
BI038578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.4%; Score 17.6; DB 11;
83.3%; Pred. No. 5.4e+02;
1ve 0; Mismatches 4;
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                      452 GATCCGCCGAGGAGTTATGCTAGC 475
                                                                     2 gatececegatgagetaagetage 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ggatcccccgatgagctaagctag 24
                        ö
                                                                                                                                                                                                                                                                                                                                          BI038578.1 GI:14445204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     587 bp
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF877912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brazil
                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                BI038578/c
LOCUS
                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                      Matches
                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503
                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
BF877912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                        ð
                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotta; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryotta; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryotta; Neoptera; Endopteryotta; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases i to 497)
S Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Baxter,E., Berman, B., Carlson,J., Change,M., Chavex,C., Chew,M., Dorsett,V., Farfan, D., Erise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Liao,G., Miranda,A., Misra,S., Mungall,C.J., Nunco,J., Pacieb,J., Parages,V. Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin,G.M.

BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11580196.
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone-"AT10901"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_grage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/n.121-AT.319: DH5-alpha TonA"
/note="Organ: ADULT Lestes; Vector: POTB7; Site_1: ECORI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into poTB7: Plasmid cDNA library."
(Pharmacia), Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino." 81 c 61 g 139 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF496895

497 bp mRNA
AT10901.5prime AT Drosophila melanogaster adult testes poTB7
Drosophila melanogaster cDNA clone AT10901 5 similar to CG7235:
FBan0007235 'heat shock protein' located on: 21.25F4-25F4;:
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: hit 9486 6798
hit genomic AE003610: arm:2L [5357975,5614606]
estimated-cyto:25E2-25F4: 04/08/2001
Plate: AT.109 row: A column: 1
High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 497
                                                                                                                                                                                                                                                    Indels

    .497
    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"

                                                                                                                                                                                         70.4%; Score 17.6; DB 11;
llarity 83.3%; Pred. No. 5.3e+02;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.6; DB 11;
Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                          448 GGATCCCCAGGTGAGATTAGCTAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04/08/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                1 ggatcccccgatgagctaagctag 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF496895.2 GI:13694366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                  Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF496895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BDGP
                                                                                                                                                                                       Query Match
Best Local S:
Matches 20,
```

TITLE JOURNAL COMMENT

FEATURES

ö

Gaps

ö

Indels

BASE COUNT ORIGIN

Length 510;

17-JAN-2001

EST

us-09-698-903b-5.rst

```
University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
    REFERENCE
                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ834638
                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..587
/Organism="Homo sapiens"
/db_zere="texton:9606"
/clone_lib="ET0109"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: lung_tumor; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pucl 18 vector. Reverse transcription of tissue mRNA and cubnA amplification were performed under low stringency conditions."
                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 587)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., Bordin,S., Costa,F.F., Nagal,M.A., Bordin,S., Costa,F.F., Brunstein,A., Garvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-ET0109-171100-001-a01&t3=2000-11-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence start: 19
High quality sequence start: 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
MR0-ET0109-171100-001-a01 ET0109 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE539934 605 bp mRNA EST 30-AUG-2000
846044B07.y1 946 - tassel primordium prepared by Schmidt lab Zea
BE539934
                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.4%; Score 17.6; DB 11; Length 587; 83.3%; Pred. No. 5.5e+02; Live 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ggatccccgatgagctaagctag 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 GGATCCCCCGATGAGTCTTG 38
                                        BF877912.1 GI:12268042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:9953351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                          sequence tags
                                                                                                                                                                                                                                                                                                    Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE639934.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                      20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays
                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
BE639934
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average." 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High Throughput Sequencing Center
University of Washington
University of Washington
University of Washington
University of Washington
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="946 - tassel primordium prepared by Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ834638 611 bp DNA GSS 27-AUG-1999 HS_5442_Al_H01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1018 Col=1 Row=O, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
1 (bases 1 to 605)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999).
97380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.6; DB 10; Length 605;
Pred. No. 5.5e+02;
0; Mismatches 5; Indels 0
                                                                                                                                                                                                                          855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotestanford.edu
Plate: 946044 row: B column: 07.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                        Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tassels"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                            1. .605
/organism="2ea mays"
/cultivar="0H43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ggatcccccgatgagctaagctagc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ834638
AQ834638.1 GI:5800700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.4
Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lab"
```

```
ò
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                 /cate_________//sex="mail"
/sex="maile"
/note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoR1 and EcoR1 wethylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoR1 sites"

a 135 c 105 g 175 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNSO38XY 924 bp DNA GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
006G08 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontidae; Tetraodon.

1 (bases 1 to 924)

8 cost.-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the firshwater pufferfish Tetraodon nigroviridis
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
70.4%; Score 17.6; DB 13; Length 611;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1018 Col=1 Row=O"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="006G08"
                                                                                                                    High quality sequence stop: 611.
Location/Qualifiers
1. 611
                         http://www.htsc.washington.edu
Plate: 1018 row: O column: 1
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 GGATCCACCTCTGAGCCAAGCTAG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ggatcccccgatgagctaagctag 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL233215.1 GI:7892350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                          Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS038XY/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enail: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Noti site and the oligo-dr track served to identify it as a clone from the Soares Lab Clone distribution: clones will be available through Soa polyA-Yes.

Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 295)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                             BE120999 295 bp mRNA EST 13-JUN-2000 UI-R-CAO-baf-h-12-0-UI.sl UI-R-CAO Rattus norvegicus CDNA clone BE120999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                     Gaps
/clone_lib="G" / hote="Genoscope sequence ID : C0BG006BD04SP1-end : PUC-Or1"
                                                                                                                                                     ö
                                                                                                                  Length 924;
                                                                                                                                                  Indels
                                                                                                               Score 17.6; DB 13;
Pred. No. 5.9e+02;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site at ratest eng ulowa edu. Th
previously described in (Bonaldo,
Genome Research 6:791-806, 1996)
                                                    ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
                                                    197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_LIB=UI-R-CA0
TAG_TISSUE-hypothalamus
TAG_SEQ-GATGC"
                                                    б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                785 GGCTCCCCGATGAGCACAGCTGG 762
                                                                                                                                                                                 24
                                                  268
                                                                                                                                            ·;
                                                                                                                                                                            1 ggatcccccgatgagctaagctag
                                                                                                             70.4%;
                                                                                                                                                                                                                                                                                                                                                         BE120999.1 GI:8513104
                                                249 c
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 295
                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            Norway rat
                                                  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               discovery
                                                207
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus.
                                                                                                                                                                                                                                                        RESULT 12
BE120999/c
LOCUS
DEFINITION
                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
```

ò

us-09-698-903b-5.rst

```
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.8%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 336)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.4*
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF410724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF410724
                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
BF410724/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 58, 1520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., at and Haysahizaki,Y., Akiyama,J., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Haysahizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I (badawa, T. Akahira, S., Akiyama, J., Arakawa, T., Carninci, F., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horl, F., 18hi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horl, F., 18hi, Y., Hara, J., 18hikawa, T., Itch, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Shibata, Y., Suruki, H., Tagawa, A., Takahashi, T., Togahara, Y., Sunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, RIKEN Mouse ESTS (Konno, H., et al.)

AL Unpublished (2000)

AL Unpublished (2000)

Contact: Yoshihide Hayashizaki, Y.

The Institute of Physical and Chemical Research (RIKEN)

Tel: 81-45-503-9216

Fax: 81-45-503-9216

Fax: 81-45-503-9216

Fax: 81-45-503-9216
                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.

Was musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 326)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length enriched, 0 day neonate kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                             BB499943 326 bp mRNA EST 26-JUL-2000
BB499943 RIKEN full-length enriched, 0 day neonate kidney Mus
musculus cDNA clone D630023P14 3', mRNA sequence.
                                                                                                                                                 Gaps
                                                                                                                                            ö
                                                                                                  Length 295;
                                                                                                                                            Indels
                                                                                             Score 17.2; DB 10;
Pred. No. 7.5e+02;
0; Mismatches 3;
  ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="kidney"
/dev_stage="0 day neonate"
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="D630023P14"
  Б
72
                                                                                                                                                                                                                        237 GGATCCCCCGACCAGCGAAGCT 216
                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                        BB499943.1 GI:9476600
                                                                                             Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                            1 ggatccccgatgagctaagct
  ပ
67
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                         BB499943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
```

```
ö
/note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: msorres@blue.weeg.uiowa.edu
The sequence contained an oligo-df track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-df track served to identify it as a clone from the normalized thalamus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UI-R-CAO-bmc-b-04-0-UI.sl UI-R-CAO Rattus norvegicus cDNA clone UI-R-CAO-bmc-b-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="UI-R-CA0"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.2; DB 10;
Pred. No. 7.6e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CA0-bmc-b-04-0-UI"

    .336
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 TCCCCCGATGAGCCAGGCTGGC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 tececegatgagetaagetage 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF410724.1 GI:11398699
```

us-09-698-903b-5.rst

```
Contact: Wing RA

Clemson University

A BAC Ends

Contact: Wing RA

Clemson University

In Seq prime: TATACACTCACTATAGGG

Class: BAC ends

High quality sequence start: 23

High quality sequence stop: 328.

Location/Qualifiers

Location/Qualifiers

Location/Cualifiers

Location/Cualifiers

Location/Cualifiers

Location/Cualifiers

Location/Cualifiers

Location/Cualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAO Library Is a Subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons hitppocampus. For a detailed description of the library from which this clone was derived, please visit our web previously described in (Bonaldo, The subtraction has been genome Research, 6:791-806, 1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ867402 368 bp DNA GSS 03-NOV-1999 nbb6b031F05f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0031F05f, DNA sequence.
AQ867402 GI:6217859
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                         Score 17.2; DB 11; Length 336;
Pred. No. 7.7e+02;
0; Mismatches 3; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                    TAG_LIB=UI-R-CA0
TAG_TISSUE=thalamus
                                                                                                                                                                                                                                                                                    85 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 GGATCCCCCGACCAGCGAAGCT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ggatccccgatgagctaagct 22
                                                                                                                                                                                                                                                              TAG_SEQ=GATCG"
73 c
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
AQ867402
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
```

ò

```
for genomic studies. In order to facilitate positional clouhing, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using Ecorl as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.8%; Score 17.2; DB 13; Length 368; 86.4%; Pred. No. 7.8e+02; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 25, 2002, 17:21:01 Job time: 16154 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 atcccccgatgagctaagctag 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 ATCACCCAATGAGCTCAGCTAG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.4 Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```



X00431 Agrobacteri A10942 Nucleotide A10943 Nucleotide A10943 Nucleotide A10941 Nucleotide A10941 Nucleotide AR0951 DA used as AR095107 Sequence AR012338 Sequence AR012338 Sequence I4986 Sequence I4986 Sequence I82374 Sequence I82374 Sequence

X05579 Soybean bet V00090 Agrobacter1 AX127753 Sequence AX172462 Sequence

I44104 Sequence 23 I44103 Sequence 22 AJ251014 Transform

Title: Perfect score: Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

sed

Minimum DB s Maximum DB s

Database

```
artificial sequence.

1 (bases 1 to 22)
Weston,B. and de Beuckeleer,M.
Male-sterile brassica plants and methods for producing same Patent: WO 0131042-A 6 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer MDB193"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX127753 22 bp DNA
Sequence 6 from Patent WO0131042.
AX127753
                                                                                                                                                                                                  I82374
TBI251013
I44104
                                                                                                                                                                                                                                     144103
TBI251014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINHYGDNA
                                                                                                                                                                                                                                                                                                                                   A60112
AR098311
AX127748
AX127748
                                                                                                                                                                                                                                                                                                                                                                                            A60109
A76916
AR098308
E31990
                                AX127753
AX172462
ARGMTUB
                                                                                                                                                                                                                                                                                                            AX172440
A71437
                                                                                                                A10943
A10941
A18051
AR095107
AR098313
                                                                                                                                                                           AX012338
149886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR074387
AR078675
                                                                                                                                                                                                                                                              AX172441
                                                                                                                                                                                                                                                                                                 AR098307
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR074388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX063413
                                                                                         A10942
A10939
                                                                                                                                                                                                                                                                         A60108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX127753.1 GI:14134400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetic construct. synthetic construct
           DB
                                                                                                                                                                                                                                                                                   24595
24595
24595
194140
           Length
                                                                                                      1085
1166
11166
11186
11186
11186
11186
11186
3200
                                                                                                                                                                                                                                                             4832
                                                                                                                                                                                                                                                                         4946
                                                                                           1000.00
            Match
           Score
                                  egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
AX127753
LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                     4243
Result
            õ
                                                                                                                                                                                                                                                    0 0 0 0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0000
                                                                                         (without alignments)
155.680 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                              ; Search time 2331.3 Seconds
                                                                                                                                                                                                                                     2944280
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                            1472140 seqs, 8248589755 residues
                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                             February 25, 2002, 18:00:10
                                                                                                                                                    1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_htg_hum:*
em_htg_inv:*
em_htg_rod:*
em_htg_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_sts:*
em_sy:*
em_un:*
em_un:*
em_htgo_hum:*
em_htgo_inv:*
em_htgo_rod:*
                                                                                                                         US-09-698-903B-6
22
                                                                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9b_ro:*
9b_sts:*
9b_sy:*
9b_un:*
9b_vi:*
em_ba:*
em_fun:*
em_fun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_ov: *
em_pat: *
em_ph: *
em_pl: *
                                                                                                                                                                                                                                                                                                                                                         gb_ba:*
gb_ntg:*
gb_on:*
gb_on:*
gb_ov:*
gb_ph:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_om:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_in:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_ro:*
                                                                                                                                                                                                                                                                                                                                               GenEmbl:*
```

AX172441 Sequence 1
A76915 Sequence 1
A76915 Sequence 1
A76915 Sequence 1
A701240 Sequence 1
A717244 Sequence 7
A60112 Sequence 7
A60112 Sequence 5
AX17748 Sequence 5
AX17748 Sequence 5
AX17748 Sequence 2
AX17748 Sequence 2
AX1990 Mutated bar A6010 Sequence 2
A76916 Sequence AX08318 ASQUENCE AX08431 ASQUENCE AX08431 ASQUENCE AX07438 Sequence AX07438 Sequence AX07438 Sequence AX07438 Sequence AX07438 ASQUENCE AX07438 AGUENCE AX0693 AGU

15-MAY-2001

SUMMARIES

```
VOUCAGO. IGT:39180

VOUCAGO. IGT:39180

VOUCAGO. IGT:39180

VOUCAGO. IGT:40180

Agrobacterium tunefaciens.

Agrobacterium tunefaciens.

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizoblaum.

El (bases 1 to 811)

S Dhaese, P., De Greve, H., Gielen, J., Seurinck, J., Van Montagu, M.M.

Identification of sequences involved in the polyadenylation of higher plant nuclear transcripts using Agrobacterium T-DNA genes as models.

IL EMBO J. 2, 419-426 (1983)
                                                                                                                                                              /note="theroretical fusion junction (24) with gene 7 of Ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="transcript 7"
148. .528
Ante="unknown gene (148 is 1st base in codon) (525 is 3rd base in codon)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTRN7 831 bp DNA BCT 02-SEP-1999 Agrobacterium tumefaciens gene encoding 'transcript 7' mRNA for protein with unknown function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 22; DB 12; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct's Ubmission
Submitted (27-MAY-1983) to the EMBL/GenBank/DDBJ
Data kindly reviewed (27-MAY-1983) by Dhaese P.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132. .673 '-'
/note="transcript 7 (alternate)"
132. .672
                  1. .13
/note="beta-1-tubulin sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTA [2]"
                                                                                                                                                                                                                                                                                                                                             88
                                                    14. .28
/note="puc 13 polylinker"
29. .35
                                                                                                                                                                                                                                                                      /note="polyA site"
220. .225
/note="put.polyA signal"
a 47 c 38 g 81
                                                                                                                                                                                                                         /note="put.polyA signal"
198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  revised
                                                                                                        29. .35
/note="Sal I linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="CCA [1] r
/citation=[1]
/citation=[2]
                                                                                                                                                                                                                .178
                                                                                                                                                                                       plasmid"
                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dhaese, P
               misc_feature
                                                        misc_feature
                                                                                                   misc_feature
                                                                                                                                              misc_feature
                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       old_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     old_sequence
                                                                                                                                                                                                                                                       polyA_site
                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
ATTRN7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARGWIUB 249 bp DNA SYN 02-APR-1988

NN Soybean beta-1-tubulin gene fused to Ti plasmid unit 7 3UTR.

X05579.1 GI:58087

X05579.1 GI:58087

SOSTO-1 GI:58087

Synthetic construct.

Synthetic construct

Synthetic construct

Synthetic construct

Synthetic Load Sequence.

E Loases I to 249)

Foaket, D.E.

The expression of a chimeric soybean beta-tubulin gene in tobacco location/Qualifiers

Load Construct

The co
                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                    03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="fusion product (17AA); Protein sequence is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                                              synthetic construct.

artificial sequence.

1 (bases 1 to 22)

de Both, G. and de Beuckeleer, M.

Hybrid winter ollseed rape and methods for producing same Patent: WO 041556-A 23 14.-UN-2001;

Avents CropScience N.V. (BE)

Location/Qualifiers
                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                          Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                    PAT
                                                                                                                                     ;
                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1...22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer 193"
a 7 c 4 9 5 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/protein_id="caa29084.1"
/db_xref="GI:4376141"
/translation="AMAAWASSNWSTDPPMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                 Query Match
100.0%; Score 22; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 22; Conservative 0; Mismatches
         Ŋ
                                                                                                                                                                                                                                                                                                                             AX172462 22 bp DNA
Sequence 23 from Patent W00141558.
AX172462.1 GI:14597574
         б
         4
                                                                                                                                                                       1 teatetacggeaatgtaceage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
      U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserv
    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
VERWORDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                               RESULT
AX172462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARGMTUB
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

27-SEP-1993

١

g ð

```
100.0%; Score 22; DB 6; Length 1037; 100.0%; Pred. No. 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 22; DB 6; Length 1085; 100.0%; Pred. No. 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence 1 from patent number DE3920034.
A10939
A10939.1 GI:492367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 from patent number DE3920034.
                     A10942 1037 bp DNA PAT ;
Nucleotide sequence 4 from patent number DE3920034
A10942.1 GI:492369
                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                   ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                               Patent: DE 3920034-A 4 31-MAY-1990;
Location/Qualifiers
1. 1037
/organism-"unidentified"
/db_xref="taxon:32644"
338 a 174 c 166 g 359
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: DE 3820034-A 1 31-MAY-1990;
Location/Qualifiers
1. .1085
/organism="unidentified"
/db_xref="texon:32644"
369 a 218 c 155 g 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: DE 3920034-A 5 31-MAY-1990;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  837 TCATCTACGGCAATGTACCAGC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               885 TCATCTACGCAATGTACCAGC 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1085 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1160 bp
                                                                                                                                                    (bases 1 to 1037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence
A10943
A10943.1 GI:492370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1160)
                                                                                                                                                                                                                                                                                                                                                                 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified.
unidentified
unclassified.
                                                                                                   unidentified
                                                                                                                  unidentified
unclassified
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A10939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A10943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                   Query Match
                                   DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                  JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
A10939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
A10943
                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                   οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
/transl_table=11
/protein_id="CAA23429.1"
/db_xref="GI:39181"
/db_xref="GI:39181"
/db_xref="GI:39181"
/translation="MHPADTPLASDLDMACEEFIKTYGASPOLETGEVIQTNNGLLY
LYGKGSLSQRIHDTHLKFKEKEELSFTTIKPAEMKAQQSDLTYYVAIFQSNYFLCVSN
PEKGFLRCHNRPELYPIVAHGSMS"
a 176 138 g 255 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tummefaciens
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
1 (bases 1 to 878)
MCPHARSON,J.C.
MCPHARSON,J.C.
BACHARSON,J.C.
LINA Sequence analysis of crown gall tumor T-DNA encoding the 0.7 kb transcript.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MNFADTPLASLDLDWACEEFIKTYGASPOLETGEVIQTNNGLLY
LYGKGSLSQRIHDTHLKFKEKEELSFTTIKPAEMKAQQSDLTYYVAIFQSNYFLCVSN
PEKGFLRCHNRPFLYPIVAHGSMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                               ATTDNA 878 bp DNA BCT 25-MAR-1996
Agrobacterium tumefaciens crown gall tumor T-DNA from Ti (tumor
inducing) plasmid pTiA6.
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                  ö
                                                                                                                                                                             Query Match 100.0%; Score 22; DB 1; Length 831; Best Local Similarity 100.0%; Pred. No. 0.76; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.0%; Score 22; DB 1; Length 878; Best Local Similarity 100.0%; Pred. No. 0.76; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Agrobacterium tumefaciens"
/strain="plasmid pTiA6"
/db_xref="taxon:358"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 12 (5), 2317-2325 (1984)
84169535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109. .489 // /note="unidentified reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Function 659. .664
/note="polyadenylation signal"
- 189 c 139 g 262 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA25129.1"
/db_xref="G1:39151"
/db_xref="SWISS-PROT:P03867"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="TATA-box"
                                                                                                                                                                                                                                                                580 TCATCTACGCAATGTACCAGC 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATCTACGCAATGTACCAGC 562
                                                                                                                                                                                                                                                1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                             X00431
X00431.1 GI:39150
plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68. .613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                              RESULT
ATTDNA
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
```

ö

Gaps

ö

27-SEP-1993

ö

Gaps

ö

27-SEP-1993

g ò

```
/translation="NEIQDEBARLSWIATTGVPCAAVLDVVTEAGRDWLLLGEVPGGD LLSSHLAPAERVSIMADAWRRLHTLDPATCPFDHQAKHRIERARTRWEAGLVDQDDLD ELGSSHLAPAELFARLKARWPDCEDLVVTHGDACLPWINVENORFSGFIDCGRLGVADR YQDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"

1055. 1186

/note="3" regulatory sequence containing the polyadenylation site derived from agrobacterium T-DNA gene?"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 22; DB 6; Length 1186; 100.0%; Pred. No. 0.76; 1.ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 22; DB 6; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1186)
D'Halluin, K. and Gobel, E.
Process for transforming monocotyledonous plants
Patent: US 6002070-A 2 14-DEC-1999;
Location/Qualifiers
1. 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1186)
D'Halluin, K. and Gobel, E.
Process for transforming monocotyledonous plants
Patent: US 6074897-A 2 13-JUN-2000;
Location/Qualifiers
1. .1186
/organism="unknown"
244 a 317 c 325 g 300 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT
                                                                                                                                                                                                                                                                                            300 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
                                                  /prote1n_id="CAA01373.1"
/db_xref="G1:4529900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR095107 1186 bp DNA
Sequence 2 from patent US 6002070.
AR095107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR098313 1186 bp DNA
Sequence 2 from patent US 6074877.
AR098313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
1 317 c 325 a
                                                                                                                                                                                                                                                                                         325 g
                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1029 TCATCTACGGCAATGTACCAGC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR095107.1 GI:10022665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR098313.1 GI:12807570
                                                                                                                                                                                                                                                                                       317 c
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 a
                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
                                                                                                                                                                                            polyA_site
                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
AR098313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="neomycine phosphotransferase gene"
167. 790
/gene="neomycine phosphotransferase gene"
/gene="neomycine prosphotransferase gene"
/gene="neomycine phosphotransferase gene"
/gene="neomycine phosphotransferase gene"
/gene="neomycine"
/gene="ne

    .8
/note="sequence derived from tapetum specific promoter of
Nicotlana tabacum"
    .790

                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1994
                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                 Query Match
100.0%; Score 22; DB 6; Length 1160;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 22; DB 6; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                       A10941 1166 bp DNA PAT 2
Nuclectide sequence 3 from patent number DE3920034.
A10941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A18051 1186 bp DNA PAT DNA used as a probe for neo gene seq ID No:2. A18051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 9209696-A 2 11-JUN-1992,
Location/Qualifiers
1. 1186
/organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                411 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: DE 3920034-A 3 31-MAY-1990,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381
1. .1160
/organism="unidentified"
/db_xref="taxon:32644"
a 194 c 188 g 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unidentified"
/db_xref="taxon:32644"
108 c 196 g 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1066 TCATCTACGCCAATGTACCAGC 1087
                                                                                                                                                                                                                                                                                            960 TCATCTACGCCAATGTACCAGC 981
                                                                                                                                                                                                                                                              1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 1186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A10941.1 GI:492368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A18051.1 GI:583120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified.
unidentified
unclassified.
                                                                           45
                                                                        367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
KEYWORDS
     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                    o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
A18051
                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                à
```

g à

```
Search completed: February 25, 2002, 18:00:10 Job time: 18418 sec
                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown" 317 c 325 g
                                                       0;
                                                                                                                                                                                                         I82374.1 GI:3210671
Query Match 100.0
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.

Best Local Similarity 100.

Matches 22; Conservative
                                                                                                                                                                                                                               .
Unknown.
                                                                                                                                                                                                                                                        Unknown
                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                 LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"coding sequence of neomycine phosphotransferase" 791. -1186
/note-"3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA gene 7"
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö

    .8
hote="sequence derived from tapetum specific promoter of
Nicotiana tabacum"
    .790

                                            Gaps
                                                                                                                                                                             06-SEP-2000
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
            ; Score 22; DB 6; Length 1186; 
; Pred. No. 0.76; 
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 22; DB 6; Length 1186; Best Local Similarity 100.0%; Pred. No. 0.76; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             1 (dases 1 to 1186)
D'Halluin,K. and Goebel,E.D.
Process for transforming monocotyledonous plants
Process for transforming monocotyledonous plants
Patent: EP 095371-A 2 10.NOV-1999;
PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
ce 1.1186
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="DNA used as probe for neo gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (Dases 1 to 1186)
D'Halluin, K. and Gobel, E.
Process for transforming monocotyledonous plants
Patent: US 5641664-A 2 24-JUN-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT
                                                                                                                                                                               PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149886 1186 bp DNA
Sequence 2 from patent US 5641664.
149886
                                                                                                                                                                          AX012338 1186 bp DNA
Sequence 2 from Patent EP0955371.
AX012338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
17 c 325 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 1029 TCATCTACGGCAATGTACCAGC 1050
                                                                       1 tcatctacggcaatgtaccagc 22
            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                       AX012338.1 GI:9998387
                                                                                                                                                                                                                                                   synthetic construct.
synthetic construct
artificial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I49886.1 GI:2472106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
149886
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                RESULT 13
AX012338
                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                        SOURCE
                                                                       ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                              Gaps
                                                                                                                                                                      10-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Length 1186;
100.0%; Score 22; DB 6; Length 1186; 100.0%; Pred. No. 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                              0; Indels
                                                                                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 1186)
D'Halluin,K. and Gobel,E.
Process for transforming monocotyledonous plants
Patent: US 5712135-A 2 27-JAN-1998;
Location/Qualifiers
                                                                                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 22; DB 6; 100.0%; Pred. No. 0.76;
                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                     182374 1186 bp DNA
Sequence 2 from patent US 5712135.
182374
```

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Database

```
Nucleotide sequency T-DNA of plasmid processing equency plasmid processing processing plasmid processing processing plasmid pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer T4 used
Right (5') border
Left (3') border f
Right flanking reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosyl-phosphati
Polynucleotide seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human liver GPI-PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene; fertility restorer gene; barnase gene; barstar gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer for the right flanking region in transgenic plant BN-RF1.
                     Plasmid
Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                       AAZ91097
AAT39336
AAT61394
AAZ91096
AAF86441
AAF25320
AAQ42169
AAQ42159
AAN50226
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA89355
AAZ28157
AAH25428
AAD06996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH25439
AAF08254
AAQ22726
AAQ90583
                                                                                                                                                          AAT39339
AAT39339
AAD06990
AAD06990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD06997
AAD06999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ45415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 60; Page 46; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De Both G, De Beuckeleer M;
    2000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 1000 | 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2000; 2000WO-EP12872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0457037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        7639
24593
24596
3336
3336
33694
44832
52228
53249
53864
6539
6539
6538
6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH25438 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-381419/40.
WO200141558-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
  17.4
17.2
16.4
16.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH25438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
AAH25438
  0000
                                                                                                                                                                       ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
                                                                                                                                                                                                                                                                                                                                                                                                                  υo
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oυ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer for the PCR primer MDB193 USP-Promoter-casse Legumin-signalpept USP-signalpeptide USP-romoter-casse Chimeric neo gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pTS88 Eco
Plasmid DV131 comp
pPS029 Bt ICP codi
pVE36 Bt ICP codin
                                                                                                                                  February 25, 2002, 18:17:24; Search time 716.55 Seconds (without alignments) 26.322 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2. (SIDSZ/gcgdata/geneseq/geneseqn/NA1980.DAT:*
3. (SIDSZ/gcgdata/geneseq/geneseqn/NA1981.DAT:*
4. (SIDSZ/gcgdata/geneseq/geneseqn/NA1992.DAT:*
4. (SIDSZ/gcgdata/geneseq/geneseqn/NA1992.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1992.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1992.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1992.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1998.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1998.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1998.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1998.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1998.DAT:*
5. (SIDSZ/gcgdata/geneseq/geneseqn/NA1999.DAT:*
                 4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                          fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                   930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                 GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                  nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD06995
AAQ04705
AAQ04703
AAQ04704
AAQ04704
AAQ139337
AAZ29122
AAQ14529
AAQ14529
                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                 US-09-698-903B-6
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1085
1160
1166
1186
1303
3153
3201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
```

Result No.

a

ö

Sequence 22 BP; 6 A; 7 C; 4 G; 5 T; 0 other;

g

ó

Gaps

```
The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene (e.g. barnase gene), and the other plant has an expression cassette comprising a fertility restorer gene (e.g. barstar gene), integrated into the genome. The fartility gene. The plant pair is useful for producing hybrid seed and esterility gene. The plant pair is useful for producing hybrid seed genetic stability and adaptability to different genetic backgrounds. The present PCR primer was used to amplify the right flanking region of a vector in a transgenic plant which carries the TA29-barstar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer MDB193 to generate the flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic plant is useful for producing a hybrid seed by crossing the hybrid seed from the transgenic Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is secondary thermal interlaced (TAII)-PCR primer The Brassica at the present sequence is secondary thermal interlaced (TAII)-PCR primer This primer corresponds to position 226-247 of plasmid procilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MS-B2 elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                  Score 22; DB 22; Length 22;
Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                        Sequence 22 BP; 6 A; 7 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 28; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                      1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0430497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD06995 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200131042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-2001
                                                                                                                                                                                                                  transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD06995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAIL; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06995
ID AAD0
×300000000000000x8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                   용
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The unique BglII-Ort (720-725) site is for ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1032-1037) for cloning the cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 22; DB 11; Length 1037; 100.0%; Pred. No. 0.059; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                 Incorporation of DNA into higher plant genome - by specified recombinant DNA techniques.
      Length 22;
                                                                                                                                                                                                            Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; legumin; USP-Pr.17-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1037 BP; 338 A; 174 C; 166 G; 359 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foreign DNA incorporation; recombinant DNA techniques;
                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                            Wobus
 100.0%; Score 22; DB 22;
100.0%; Pred. No. 0.034;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                           Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Legumin-signalpeptide cassette Le-Sig.T7.
                                                                                                                                                                                                                                                                                                                                                        Bassuner R, Baumlein H, Muntz K,
                                                                                                                                                                                       USP-Promoter-cassette USP-Pr.T7.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08; Fr. 0;
                                           AAQ04703 standard; DNA; 1085 BP
                                                                                                                      AAQ04705 standard; DNA; 1037
                                                                                                                                                                                                                                                                                                                                 (PFLA-) VE KOMB PFLANZENZUC.
                                                                                                                                                                                                                                                                                          89DE-3920034
                                                                                                                                                                                                                                                                                                               88DD-0319887
                                                                                                                                                                  (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAQ04703-Q04706
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1990-172459/23.
                                                                                                                                                                  12-OCT-1990
                                                                                                                                                                                                                                                                                        20-JUN-1989;
                                                                                                                                                                                                                                                                                                             19-SEP-1988;
                                                                                                                                                                                                                                           DE3920034-A.
                                                                                                                                                                                                                                                                   31-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transfected
                                                                                                                                            AAQ04705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ04703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                          AAQ04705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
AAQ04703
                                                               Q
                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

Wobus

```
The unique BglII-Ort (720-725) site is for ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1261-1266) for cloning the cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
                                                                                                                                                                                      The unique BglII-Ort (890-895) site is for ligating foreign DNA and the HindIII-Ort in the 3' polyllinker (1155-1160) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected. See also AAO04703-Q04706.
                                                                                                                                                                                                                                                                                                                                                100.0%; Score 22; DB 11; Length 1160; 100.0%; Pred. No. 0.06; Live 0; Mismatches 0; Indels 0
                                                                                                           incorporation of DNA into higher plant genome - by specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Incorporation of DNA into higher plant genome - by specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; legumin; USP-Pr.T7-2; ss.
                                                                                                                                                                                                                                                                                                   Sequence 1160 BP; 369 A; 192 C; 188 G; 411 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1166 BP; 381 A; 208 C; 196 G; 381 T; 0 other;
                                 Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 22;
                                 Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USP-Promoter-cassette USP-Pr.T7.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ04704 standard; DNA; 1166
 (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89DE-3920034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant DNA techniques.
                                                                                                                            recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baumlein H,
                                 Baumlein H,
                                                                                                                                                           Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also AAQ04703-Q04706
                                                             WPI; 1990-172459/23
P-PSDB; AAR05199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-172459/23
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-1989;
                                 Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE3920034-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ04704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ04704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
higher plant genome; legumin; B4 gene; signalpeptide; Le-Sig.T7.; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                 įs
                                                                                                                                                                                                                                                                                                                                                                                                                           The Legumin gene B4 is used. The unique BglII-Ort (815-820) site ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1080-1085) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected. See also AAQ04703-Q04706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 22; DB 11; Length 1085; Best Local Similarity 100.0%; Pred. No. 0.059; Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                Incorporation of DNA into higher plant genome - by specified recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; signalpeptide; USP-Sig.T7.; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other
                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                    Wobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1085 BP; 368 A; 219 C; 155 G; 343 T; 0
                            Location/Qualifiers
747.814
/*tag- a
/product-Legumin-signalpeptide
                                                                                                                                                                                                                                                                      Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /_rag=_a
/product=signalpeptide
747..817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USP-signalpeptide cassette USP-Sig.T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 708..877
                                                                                                                                                                                                                                                                    Baumlein H, Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ04706 standard; DNA; 1160 BP
                                                                                                                                                                       89DE-3920034
                                                                                                                                                                                                       88DD-0319887
                                                                                                                                                                                                                                      (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89DE-3920034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                WPI; 1990-172459/23.
P-PSDB; AAR05198.
                                                                                                                                                                       20-JUN-1989;
                                                                                                                                                                                                       19-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1990
                                                                                                          DE3920034-A
                                                                                                                                                                                                                                                                    Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE3920034-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ04706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ04706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
```

g

Length 1166;

DB 11;

'n

Wobus

ö

Gaps

4

Pred. No.

100.0%;

```
ó
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two transformed corn plants were analysed by means of Southern hybridisation. As a probe, a 1184 bp EcoRI-HindIII fragment derived from another plasmid was used. The sequence of that plasmid is given below. Results showed that at least a chimeric neo gene was integrated into the plant genomic DNA.
                                                                                                                                                                                                     Nicotiana tabacum; neomycine phosphotransferase; Agrobacterium; ss.
                   ö
                                                                                                                                                                                                                                                                                     "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming monocotyledonous plants e.g. cereals - comprises wounding and/or degrading cells of intact plant tissue or embryogenic callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3' regulatory sequence contg. the polyadenylation site derived from Agrobacterium T-DNA gene 7"
                Indels
                                                                                                                                                                                                                                                                                                                      /product neomycine_phosphotransferase 791..1186 /*tag c /*tag c /note= "3' requistor con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1186 BP; 244 A; 317 C; 325 G; 300 T; 0 other;
                ő
              Mismatches
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 60; 76pp; English.
                                               1066 tcatctacggcaatgtaccage 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PLBZ ) PLANT GENETIC SYSTEMS NV.
              ;
                                  1 tcatctacggcaatgtaccage 22
                                                                                                              AAQ25707 standard; DNA; 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90EP-0403332,
91EP-0401888.
                                                                                                                                                          07-DEC-1992 (first entry)
Best Local Similarity 100. Matches 22; Conservative
                                                                                                                                                                                 Chimeric neo gene probe.
                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goebel E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-217075/26.
                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-1990;
08-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                         WO9209696-A.
                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dhalluin K,
                                                                                                                                                                                                                             Synthetic
                                                                                                                                     AAQ25707;
                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                        RESULT
AAQ25707
ID AAQ2
                                                                                                                                                                                                                                                   éy
                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                    ð
```

```
region containing polyadenylation signal of gene 7 og Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                 /function= 35S promoter of cauliflower mosaic virus strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The HindIII-ECORI fragment (AAT39337) of plasmid pTSB8 contains barstar DNA under control of a 35S promoter. The plasmid was used with pTS174 (see also AAT39336) contg. barnase DNA under control of the stamen specific promoter El to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pVEL16 (see also AAT39338) contg. barnase DNA under control of the stamenspecific PG55 promoter to produce male sterile malze plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barnase DNA in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                            Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds.
                                                                                                                                                                                                                                                                                                                                        /*tag= c
/label= barstar
/product= Bacillus amyloliquefaciens barstar
968..1287
                                                                                                                                                                                                         1..35
/*tag= a
/label= pGEMZ
/note="Polylinker of pGEM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- e
/label= pgEM2
/note= "polylinker of pGEM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cornelissen M, Michiels F;
                                                                                                  Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 38; 56pp; English.
                        AAT39337 standard; DNA; 1303 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                       /*tag= d
/label= 3'g7
/function= re
                                                                                                                                                                                                                                                                       /*tag= b
/label= P35s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95EP-0400364.
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       1288..1303
                                                                                                                                                                                                                                                                                                                         695..967
                                                                                                                                                                                                                                                          16..694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-402373/40.
                                                                           22-JAN-1997
                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9626283-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Botterman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-1996
                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                            promoter
RESULT
AAT39337
                                                                                                                                                                                                                                                                                                                         CDS
```

ó

Gaps

ö

Indels

ö

Mismatches

1029 tcatctacggcaatgtaccage 1050

1 tcatctacggcaatgtaccage 22

Similarity

22;

Matches

ð q S

S

g

ò

(first entry)

```
AAQ14529 standard; DNA; 3201 BP
                                                                                                                                                                                                                                                                                          pPS029 Bt ICP coding sequence.
                                                                                                                                                                                                                                                 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                           AAQ14529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ15144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
                                                                                                                                               AAQ14529
                                                                                                                         RESULT
                       ò
                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present DNA sequence is the plasmid DV131, that is used in the generation of GFP:NFTI fusion protein constructs. It contains an generation of GFP:NFTI fusion protein constructs. It contains an gene, the coding sequence of EGFP:NFTI translational fusion, excised from DV126 and the Tr7 terminator. This plasmid is used to carry a chimeric gene, comprising an aleurone-specific promoter like L3, that is operably linked to the gene encoding a screenable marker, like Green fluorescent protein (GFP), luciferase or maize R gene. The gene fusions allow both selection and screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in embryogenic tissues, allowing selection and screening of viable transgenic seeds. Screening of transgenic seeds avoids the need for growing and assaying of seeds for transgenes and allows implementation of automated seed screening techniques for the identification of
                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic seed; marker; aleurone-specific promoter; Plasmid DV131; GFP:NPTII fusion protein construct; L3/EGFP:NPTII/Tr7; maize R gene; expression cassette; maize L3 oleosin gene; chimeric gene; transgene; MGFP:NPTII translational fusion; Tr7 terminator; luciferase gene; assay; Green fluorescent protein; GFP; gene fusion; selection; screening; expression; automated seed screening technique; screenable marker; transformant; embryogenic tissue; implementation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screenable marker genes useful for identification of transgenic seeds
                                                                                                      Gaps
                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid DV131 comprising L3/EGFP:NPTII/Tr7 expression cassette.
                                                         DB 17; Length 1303;
0.061;
hes 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 22; DB 21; Length 3153; Best Local Similarity 100.0%; Pred. No. 0.069; Matches 22; Conservative 0; Mismatches 0; Indels 0
Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3153 BP; 801 A; 857 C; 756 G; 739 T; 0 other;
                                                         Score 22; DB Pred. No. 0.00; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 164-166; 182pp; English.
                                                                                                                                                                1094 tcatctacggcaatgtaccagc 1115
                                                                                                                                                                                                                                                                                     AAZ29122 standard; DNA; 3153 BP
                                                                                                  ö
                                                                                                                                          1 tcatctacggcaatgtaccage 22
                                                       Query Match

Best Local Similarity 100.0%;

Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEKA-) DEKALB GENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0080625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US11023.
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spencer TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-072441/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ransgenic seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9960129-A1
                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kriz AL,
                                                                                                                                                                                                                                                                                                                                AAZ29122;
                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                  AA229122
                                                                                                                                                                                                                                               RESULT
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "n" in the sequence refers to not known nucleotides. ppS029 is identical to pVE36 (AAQ15144), but carries both the terminal modification and the internal modification of the Bt
                                                                                                                                                                                                                                                                                                                                                                                 Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3201;
Bacillus thuringiensis; insecticidal crystal protein; ICP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis; insecticidal crystal protein; ICP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3201 BP; 880 A; 710 C; 720 G; 886 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 22; DB 12;
100.0%; Pred. No. 0.069;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                        Dockx J;
                                                                                                                                                                                                                                                                                                        Stam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 6(c); 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2948 tcatctacggcaatgtaccage 2969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See also AAQ14529, AAQ15142-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ15144 standard; DNA; 3201
                                                                                                                                                                                  91WO-EP00733
                                                                                                                                                                                                                                                                                                        Soetaert P,
                                                                                                                                                                                                                         90EP-0401055
                                                                                                                                                                                                                                                                 (PLAN-) PLANT GENETIC SYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Conservative
                                                                                                                                                                                                                                                                                                                                             WPI; 1991-339820/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sedneuce
                                                                                                                                                                                                                                                                                                        Cornelissen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVE36 Bt ICP
                                                                                                                                                                                  17-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deletion; ss.
                      deletion; ss
                                                                                                                                                                                                                         18-APR-1990;
                                                                                                 WO9116432-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
```

ö

; 0

Gaps

ó

```
ö
                                                                                                                                                                                                                                                      "n" in the sequence refers to not known nucleotides. pPSO29 (AAQ14529) is identical to pVE36, but carries both the aminoterminal modification and the internal modification of the Bt ICP
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transganic seed; marker; aleurone-specific promoter; Plasmid DV130; GFP:NPTII fusion protein construct; L3/MGFP:NPTII/Tr7; maize R gene; expression cassette; maize L3 oleosin gene; chimeric gene; transgene; Green fluorescent protein; Terminator; luciferase gene; Green fluorescent protein; GFP; gene fusion; selection; screening; transformant; expression; automated seed screening technique; assay; screenable marker; embryogenic tissue; implementation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid DV130 comprising L3/MGFP:NPTII/Tr7 expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 3201; 0.069;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                             Sequence 3201 BP; 915 A; 651 C; 700 G; 930 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                        Dockx J;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Score 22;
Pred. No. C
                                                                                                                                        Stam M,
                                                                                                                                                                                                                                Disclosure; Fig 6(c); 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  3021 tcatctacggcaatgtaccagc 3042
                                                                                                                                                                                                                                                                                                                                                                    100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                        See also AAQ14529, AAQ15142-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ29121 standard; DNA; 3336 BP
                                                                                                                                                                                                                                                                                                                                                                                                                 1 tcatctacggcaatgtaccage 22
                                                             91WO-EP00733
                                                                                     90EP-0401055
                                                                                                                                   Cornelissen M, Soetaert P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEKA-) DEKALB GENETICS CORP
                                                                                                           (PLAN-) PLANT GENETIC SYST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US11023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                          WPI; 1991-339820/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kriz AL, Spencer TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-072441/06.
                                                           17-APR-1991;
                                                                                   18-APR-1990;
                                    31-OCT-1991.
            WO9116432-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9960129-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ29121;
                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
ð
```

```
The present DNA sequence is the plasmid DV130, that is used in the generation of GFP:NPTII fusion protein constructs. It contains an expression cassette comprising, a promoter from the maize L3 oleosin gene, the coding sequence of MGFP:NPTII translational fusion, excised from DV127 and the T7 terminator. This plasmid is used to carry a chimeric gene, comprising an aleurone-specific promoter like L3, that is coperably linked to a gene encoding a screenable marker, like Green fluorescent protein (GFP), luciferase or maize R gene. The gene fusions allow both selection and screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in embryogenic tissues, allowing selection and screening of viable transgenic seeds. Screening of transgenes and allows implementation of automated seed screening techniques for the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFP:NPTII fusion protein construct, Lastacti intron/EGFP:NPTII/Trz, expression cassette; maize L3 oleosin gene; chimeric gene; transgene; EGFP:NPTII translational fusion; Tr7 terminator; luciferase gene; Green fluorescent protein; GFP; gene fusion; maize R gene; selection; screenable marker; screening; automated seed screening technique; assay; transformant; expression; embryogenic tissue; implementation; ds.
Screenable marker genes useful for identification of transgenic seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screenable marker genes useful for identification of transgenic seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid DV133 used for construction of GFP:NPTII fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 22; DB 21; Length 3336; 100.0%; Pred. No. 0.069;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present DNA sequence is the plasmid DV133, comprising
                                                                                                                                                                                                                                                                                                                                               Sequence 3336 BP; 888 A; 830 C; 764 G; 854 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic seed; marker; aleurone-specific promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                             Example 1; Page 163-164; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 168-170; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ29124 standard; DNA; 3694 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 tcatctacggcaatgtaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEKA-) DEKALB GENETICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0080625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spencer TM;
               for plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-072441/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for plant breeding
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9960129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ29124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kriz AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

```
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                              AAH25423;
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3'UTR
                                                                                                                                                                                                                                                                                                                      AAH25423/C
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                     g
     δ
                                                                                                                                                                                                                                                                                                                                       ö
L3/rACTI intron/EGFP:NPTII/TT7, that is used in the generation of PEP:NPTII fusion protein constructs. It contains an expression cassette comprising, a promoter from the maize L3 oleosin gene, the rice actin 1 intron, the coding sequence of EGFP:NPTII translational fusion, excised from DV126 and the Tr7 terminator. This plasmid is used to carry a chimeric gene, comprising an aleurone-specific promoter like L3, that is operably linked to a gene encoding a screenable marker, like Green allow both selection and screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in embryogenic tissues, allowing selection and screening of viable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic seed; marker; aleurone-specific promoter; Plasmid Dv132; SPE:NPTII fusion protein construct; L3/ACTI intron/MGFP:NPTII/TT7; expression cassette; maize L3 oleosin gene; chimeric gene; transgene; MGFP:NPTII translational fusion; Tr7 terminator; luciferase gene; Green fluorescent protein; GFP; gene fusion; maize R gene; selection; screenable marker; screening; automated seed screening technique; assay; transformant; expression; embryogenic tissue; implementation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present DNA sequence is the plasmid DV132, comprising L3/rACTI intron/MGFP:NPTII/Tr7, that is used in the generation of GFP:NPTII fusion protein constructs. It contains an expression cassette comprising, a promoter from the maize L3 oleosin gene, the rice actin 1 intron, the coding sequence of MGFP:NPTII translational fusion, excised from DV127 and the Tr7 terminator. This plasmid is used to carry a
                                                                                                                                              transgenic seeds. Screening of transgenic seeds avoids the need for growing and assaying of seeds for transgenes and allows implementation of automated seed screening techniques for the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screenable marker genes useful for identification of transgenic seeds for plant breeding -
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid DV132 used for construction of GFP:NPTII fusion protein.
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                   Score 22; DB 21; Length 3694;
Pred. No. 0.07;
Mismatches 0; Indels 0;
                                                                                                                                                                                                             Sequence 3694 BP; 890 A; 984 C; 914 G; 906 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 166-168; 182pp; English.
                                                                                                                                                                                                                                                                                                                        3216 tcatctacggcaatgtaccage 3237
                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                          1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                  AA229123 standard; DNA; 3877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEKA-) DEKALB GENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0080625.
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.vv
Thes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spencer TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-072441/06.
                                                                                                                                                                                       transgenic seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9960129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ29123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kriz AL,
                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                        AA229123
                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                   g
  88888888888888888888888888888888888
                                                                                                                                                                                                                                                                                                           ò
```

```
ö
chimeric gene, comprising an aleurone-specific promoter like L3, that is operably linked to a gene encoding a screenable marker, like Green fluorescent protein (GPP), luciferase or maize R gene. The gene fusions allow both selection and screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in embryogenic tissues, allowing selection and screening of viable transgenic seeds. Screening of transgenic seeds avoids the need for growing and assaying of seeds for transgenes and allows implementation of automated seed screening techniques for the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene; fertility restorer gene; barstar gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
"right border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "atSlA ribulose-1,5-biphosphate carboxylase small subunit gene from Arabidopsis thallana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= 1
/note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= f
/note= "synthetic polylinker derived sequences"
complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "synthetic polylinker derived sequences'
complement (98..309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "residual sequence from TL-DNA at right
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 22; DB 21; Length 3877; 100.0%; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= e
/note= "3' UTR from TL-DNA gene 7 of pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Streptomyces hygroscopicus bialaphos
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                             Sequence 3877 BP; 977 A; 957 C; 922 G; 1021 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resistance (bar) gene"
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of plasmid pTHW118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 border repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3399 tcatctacggcaatgtaccagc 3420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH25423 standard; DNA; 4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces hygroscopicus. Arabidopsis thaliana. Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310..330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54..90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91..97
```

```
Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                              /*tag= p
/note= "left border repeat from TL-DNA from priB6S3"
                   /note= "faq1 fragment from 3' UTR of nopaline synthase gene from T-DNA of pri37 and containing plant polyadenylation signals"
                                                                                                                                   /*tag~ m
/note= "Barstar gene coding region from Bacillus
amyloliquefaciens"
complement (3254..4762)
                                                                                                  /note= "downstream of Bacillus amyloliquefaciens
                                                             /*tag= k
/note= "synthetic polylinker derived sequences"
2941..2980
                                                                                                                                                                         /*tag= n
/note= "anther-specific gene TA29 promoter from
Nicotiana tabacum"
                                                                                                                                                                                                                 /*tag= o
/note= "synthetic polylinker derived sequences"
4808..4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
                                                                                                               barstar coding region'
complement (2981..3253)
  complement (2659..2919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 80-82; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                          (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                        99US-0457037.
                                                                                                                                                                                                                                                                                                                                                                            De Both G, De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                 06-DEC-2000; 2000WO-EP12872
                                                    2920..2940
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                           WO200141558-A1
                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                      08-DEC-1999;
                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                              14-JUN-2001
                                                                                                                                                               promoter
                                                                               3'UTR
 3'UTR
                                                                                                                       CDS
```

The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to plasmid prHWII8. This plasmid comprises the barstar gene, which acts as a fertility restorer gene. The plasmid is used to create transgenic plants of the invention.

```
Gaps
                                         ó;
 100.0%; Score 22; DB 22; Length 4832;
100.0%; Pred. No. 0.073;
Live 0; Mismatches 0; Indels 0
                                                                1 tcatctacggcaatgtaccage 22
Ouery Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                 à
```

ö

Search completed: February 25, 2002, 18:17:24 Job time: 16682 sec

Appl Appli Appli

```
US-08-064-121-2
00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 23, Appl
Sequence 5, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 6, Appli
                                                                                                                                                                       February 25, 2002, 18:05:15; Search time 301.6 Seconds (without alignments) 16:520 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-084-889-2
US-08-94-440-2
US-08-453-104-23
US-08-694-824-23
US-08-694-824-23
US-08-694-824-23
US-08-694-824-22
US-09-080-625-5
US-09-080-625-4
US-08-817-188-1
US-08-817-188-1
US-08-817-440-4
US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-817-188-2
US-08-232-016-23
US-08-232-016-22
US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                      GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                US-09-698-903B-6
22
1 tcatctacggcaatgtaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY_NUC Gaport 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11186
11186
11186
11186
111186
13303
33200
33200
33200
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
33300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
3300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
300
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o
                                                                                                                         OM nucleic
                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
No.
```

Sequence 4, Appli Sequence 83, Appl Sequence 55, Appl

US-09-446-504-4 US-09-446-504-83 US-09-446-504-55

18.8 16 15.8 15.8

0 0 0 0 0 0

5428147-1

```
Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1.2.

Sequence 1.2.

Patent No. 5641664

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: O'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke

TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS

TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: George Mason Bldg., Washington & Prince Sts.

CITY: Alexandria

STRATE: Virginia

CONTYRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IN PC: Floppy disk

COMPUTER: IN PC: Compatible

COMPUTER: SYSTEM: PC-DOS/MS-DOS

COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,121
FILING DATE: 24-MAY-1993
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
APPLICATION NUMBER: EP 91401888.2
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                  US-08-663-7138-1
US-09-014-888-1
US-08-955-918C-8
US-08-955-918C-6
US-08-955-918C-6
US-08-922-267A-1
US-08-936-707A-1
US-08-936-707A-1
US-08-936-706A-1
US-09-248-203-1
US-09-248-203-1
US-09-248-203-1
US-08-916-703-1
US-08-916-703-1
US-08-916-703-1
US-08-916-703-1
US-08-14-991-1
US-08-14-991-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAR: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1186 base pairs
double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linea
STRANDEDNESS:
```

```
á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                            LOCATION: 791..1186
CTHER INFORMATION: /label= 3'97
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium US-08-064-121-2
                                                 /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USS-UB-478-015-2

Sequence 2, Application US/08478015

Sequence 2, Application US/08478015

GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: D'HALLUIN, Rathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STATE: VIrginia
COMPRES: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: NOT-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: OR-UIN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: OB-UIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
RILING DATE: 23-UNN-1993
ATPLICATION NUMBER: US 08/064,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,340
REFERENCE/DOCKET NUMBER: 010830-088
TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1029 TCATCTACGGCAATGTACCAGC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 teatetaeggeaatgtaeeage 22
                                                                                                                                                                                                                                                                          791..1186
                                                                                                                 NAME/KEY:
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-478-015-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
/label= NPTII /note= "coding sequence of neomycine phosphotransferase ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -

LOCATION: 791..1186

COTHER INFORMATION: /label= 3'97

OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylat

OTHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"

US-08-478-015-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                  /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3

US-08-475-975-2

US-08-475-975-2

Sequence 2, Application US/08475975

Patent No. 6002070

GENERAL INFORMATION:
APPLICANT: O'HALLOIN, Kathleen
APPLICANT: GORLE, Elke
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STRAEE: USTAIN: United States
ZIP: 2213-1404

COMPUTER: LBM PC Compatible
COMPUTER: LBM PC Compatible
COMPUTER: LBM PC Compatible
COMPUTER: THOPPY disk
COMPUTER: TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
FILING DATE: 07-JUN-1995
CLASSIPICATION NUMBER: US 08/064,121
FILING DATE: 23-MAY-1993
APPLICATION NUMBER: EP 94401888.2
FILING DATE: OB-JUL-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: OB-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 22; DB 1; Length 1186; Best Local Similarity 100.0%; Pred. No. 0.02; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1029 TCATCTACGGCAATGTACCAGC 1050
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAMBE/KEY:
NAMBE/KEY:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                   NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
```

```
NAME/KEY: -
LOCATION: 791.1186
COTHER INFORMATION: /label- 3'g7
COTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium GTHER INFORMATION: T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI OTHER INFORMATION: fragment of pTS88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 22; DB 3; Length 1186; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,121
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
APPLICATION NUMBER: EP 91401888.2
ATTORNEY AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 35,113
REFERENCE/DOCKET NUMBER: 010830-043
TELEPHONE: (703) 836-620
TELEFAX: (703) 836-620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1029 TCATCTACGCAATGTACCAGC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08894440
; Patent No. 6025546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tcatctacggcaatgtaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: 9..790
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-894-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- 3'97
/note= "3' regulatory sequence containing the
polyadenylation site derived from Agrobacterium
T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 22; DB 3; Length 1186; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/084,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09084889
Patent No. 6074877
GENERAL INFORMATION:
APPLICANT: GOBEL, BIRe
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
INTILE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMUNICATION INFORMATION:
TELEFONE: (703) 836-620
TELEFAN: (703) 836-5021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: 1inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1029 TCATCTACGCCAATGTACCAGC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tcatctacggcaatgtaccagc 22
                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.(
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-475-975-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 791..1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 9..790
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1.8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-084-889-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

Gaps

ö

0; Indels

```
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                          Best Local Similarity 100. Matches 22; Conservative
; TOPOLOGY: linear
US-09-080-625-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-453-104-23
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (36)..(694)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 22; DB 3; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GERERAL INFORMATION:
APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
TITLE OF INVENTION: IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (695)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 77210-4433
COMPUTER REABABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARRE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
                                            LOCATION: (1)..(35)
OTHER INFORMATION: POLYLINKEr Of PGEM2 (PGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

: LOCATION: (1288)..(1303)

: OTHER INFORMATION: polylinker of pGEM2

US-08-894-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (512) 418
TELEPHONE: (513) 418
TELEPHONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arnold White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09080625
Patent No. 6307123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold Whit
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
             : misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-080-625-3
                                                                                                                                      FEATURE:
```

```
| US-09-080-625-3 | The Content of t
```

```
APPLICANT: SOSTAERT, Piet
APPLICANT: STAM, Malke
APPLICANT: STAM, Malke
APPLICANT: STAM, Malke
APPLICANT: TALE OF LINVENTION: UNDIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
COMMITMED ADDRESS: 222131-4404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOFTAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 22; DB 1; Length 3201; 100.0%; Pred. No. 0.024; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Nucleotides 2151-2155 OTHER INFORMATION: wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
RELCOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
RELEFAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08694824
Patent No. 5877306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3021 TCATCTACGCCAATGTACCAGC 3042
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 2151..2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-453-104-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-694-824-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CORNELLSSEN, MATC
APPLICANT: SOFTHERT, Plet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 2; Length 3200;
Pred. No. 0.024;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STATE: Virginia COUNTRY: United States ZIP: 22313-1404 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTONINY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: /note= "Nucleotides 2078-2082; OTHER INFORMATION: wherein N is not known." US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,427
REGISTRATION NUMBER: 010830-032
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-08-453-104-22
: Sequence 22, Application US/08453104
                                                                                                                                                                Sequence 23, Application US/08694824 Patent No. 5877306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2948 TCATCTACGCCAATGTACCAGC 2969
                        2948 TCATCTACGCAATGTACCAGC 2969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Sc
100.0%; Pr
tive 0;
  1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature rocation: 2078..2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Rea, Teresa S
REGISTRATION NUMBER:
                                                                                                              RESULT 8
US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ор
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
õ
```

```
Ouery Match
100.0%; Score 22; DB 4; Length 3336;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-080-625-5

Sequence 5, Application US/09080525

Sequence 5, Application US/09080525

GENERAL INFORMATION:

APPLICANT: Kriz, Alan L.

APPLICANT: Sencer, T. Michael

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSCENE

TITLE OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/09/080,625
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Robert E.
REGISTRATION NUMBER: P-42,628
REFERENCE/DOCKET NUMBER: DEKM:161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
FILING DATE:
                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HAARE: HAASON, RODERT E.
REGISTRATION NUMBER: P-42,628
REFERENCE/POCKET NUMBER: DEKM:16
TELEPHONE: (512) 414-3000
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 2858 TCATCTACGCAATGTACCAGC 2879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-09-080-625-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-09-080-625-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 22; DB 2; Length 3201;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09080625
Patent No. 6307123
GENERAL INFORMATION:
APPLICANT: KTLS. Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: DENTIFICATION
TITLE OF INVENTION: DENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold White & Durkee
STREET: P.O. Box 4433
CONTY: HOUSTON
                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
                                                                                                                                                                                                       CITY: ALEXAULIAGE
STATE: VITGINIA
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPALDIS
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
CLASSIFICATION 536
PRIOR APPLICATION DATE: 16-DEC-1992
RILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
ATPOREY AGENT INDERRATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REEERRENCE/DOCKET NUMBER: 010830-032
REGISTRATION NUMBER: 030,427
REEERRENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
FEMALICATION FOR SEQ ID NO: 22:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
CCATION: 2151..2155
COTHER INFORMATION: /note= "Nucleotides 2151-2155
COTHER INFORMATION: wherein N is not known."
US-08-694-824-22
       FITLE OF INVENTION: IN PLANT CELLS NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3021 TCATCTACGCCAATGTACCAGC 3042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tcatctacggcaatgtaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-080-625-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

Gaps

us-09-698-903b-6.rni

```
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((97)..(330))
OTHER INFORMATION: 3'97: 3' untranslated region containing the
LOCATION: Complement((97)..(330))
OTHER INFORMATION: 3'97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: bar: region coding for phosphinotricin acetyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: Complement((3368)..(4876))
OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KER: misc_feature
LOCATION: Complement((2658)..(3031))
COTHER INFORMATION: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter region of Rubisco small subunit gene OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        % Sequence 5, Application US/08817188

Sequence 5, Application US/08817188

Patent No. 6074876

GENERAL INFORMATION:

APPLICANT: DE BLOCK, MARC

TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR

FILE REPERENCE: 2121-01279

CURRENT APPLICANO NUMBER: US/08/817,188

CURRENT FILING DATE: 1997-05-15

EARLIER APPLICATION NUMBER: PCT/EP96/03366
                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 22; DB 3; Length 49
100.0%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature:
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: Complement((4922)..(4946))
; OTHER INFORMATION: LB: T-DNA left border
US-08-817-188-1
         95401844.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tcatctacggcaatgtaccagc 22
EARLIER APPLICATION NUMBER: EP EARLIER FILING DATE: 1995-08-04 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PATENTIN VEY. 2.0 SEQ ID NO 1 LENGTH: 4946
                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3877;
                         DB 4; Length 3694; 0.024;
                                                                                                                                                                                                                                                                Sequence 4, Application US/09080625
Patent No. 6307123
GENERAL INFORMATION
APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
TITLE OF INVENTION: IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTAL. CONTINER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22;
Pred. No. 0
                       100.0%; Score 22;
ilarity 100.0%; Pred. No. 0
Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:

NAME: Hanson, Robert E.

REGISTATION NUMBER: P-42,628

REFERENCE/DOCKET NUMBER: DEKM:161

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 474-757

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 3877 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08817188; Patent No. 6074876; GENERAL INFORMATION:
                                                                                                                                        3216 TCATCTACGCCAATGTACCAGC 3237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                 1 tcatctacggcaatgtaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-09-080-625-4
                                               Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-817-188-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                    US-09-080-625-4
                            Query Match
                                                                                                                 à
                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
```

of

ö

Gaps

us-09-698-903b-6.rni

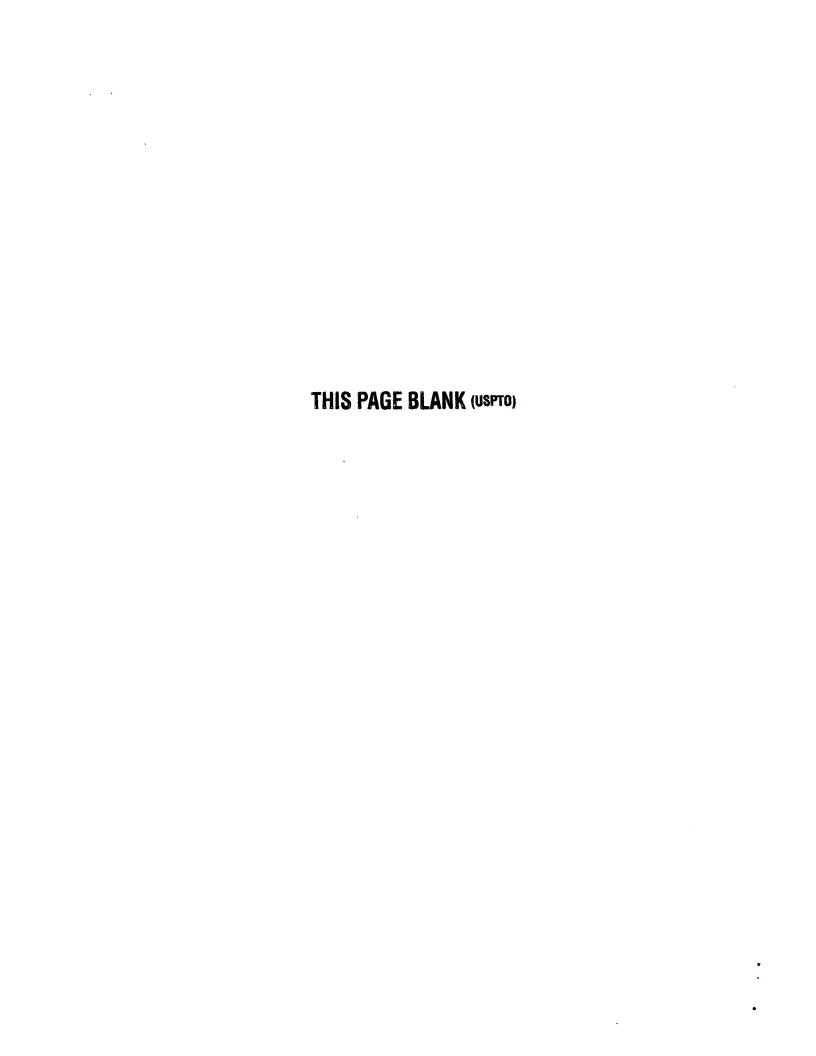
```
CCATION: (318)...(869)
OTHER INFORMATION: bar: region coding for phosphinotricin of the information: bar: region coding for phosphinotricin of the information: bar: region coding for phosphinotricin feature: name/KEr: misc_feature
LOCATION: (830)..(2760)
OTHER INFORMATION: 958U: promoter region of Rubisco small subunit of the INFORMATION: 958U: promoter region of Rubisco small subunit of the information: 960 of Arabidopsis thaliana
NAME/KEY: misc_feature
LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript reaminer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | NAME/KEY: misc_feature
| LOCATION: (5533)..(5560)
| OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
| OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
| FEATURE: | NAME/KEY: misc_feature
| LOCATION: (5058)..(5059)
| OTHER INFORMATION: region with unknown sequence (may contain up to 20
| FEATURE: | NAME/KEY: misc_feature
| LOCATION: (5077)..(5078)
| OTHER INFORMATION: region with unknown sequence (may contain up to 20
| FEATURE: | NAME/KEY: misc_feature
| LOCATION: (5077)..(5078)
| OTHER INFORMATION: nucleotides)
| CATURE INFORMATION: region with unknown sequence (may contain up to 20
| OTHER INFORMATION: region with unknown sequence (may contain up to 20
| OTHER INFORMATION: region with unknown sequence (may contain up to 20
| OTHER INFORMATION: region with unknown sequence (may contain up to 20
| US-08-817-188-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
NAME/KEY:
NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (84)...(296)
OTHER INFORMATION: 3' g7: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (4483)...(4671)
OTHER INFORMATION: IV2: region corresponding to the second intron of
OTHER INFORMATION: the ST-LS1 gene
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5067)...(5502)
OTHER INFORMATION: P35S: 35S promoter region of CaMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MISC_feature
NAME/KEY: (3059)..(5056)
OTHER INFORMATION: uldA: region coding for beta-glucuronidase
EARLIER FILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
EARLIER FILING DATE: 1995-08-04
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 5560
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
```

```
ó
                                          Gaps
                                         ö
    Score 22; DB 3; Length 5560;
Pred. No. 0.026;
; Mismatches 0; Indels
Query Match

Ouery Match

Best Local Similarity 100.0%; Pred. No. 0.0

Matches 22; Conservative 0; Mismatches
                                                                                                                                                       Search completed: February 25, 2002, 18:05:16 Job time: 18564 sec
                                                                              1 tcatctacggcaatgtaccage 22
                                                                                          q
                                                              δ
```



-

```
Eukaryota: Metazoa; Nematoda: Chromadorea; Rhabditida; Rhabditoldea; Eukaryota; Metazoa; Nematoda: Caenorhabditis.

1 (bases 1 to 568)
1 (bases 2 to 568)
1 (bases 3 to 568)
1 (bases 3 to 568)
1 (bases 4 to 568)
1 (bases 4 to 568)
1 (bases 5 to 568)
1 (bases 6 to 568)
1 (bases 6 to 568)
1 (bases 7 therry-Mieg, 7., Thierry-Mieg, 7., Thierry-Mieg, 7., Brasch, M.A., Vandenhaute, 7., Lamesch, P.E., Hill, D.E. and Vidal, M. Opener, 17, 300 genes in C. elegans
1 (bases 17, 300 genes in C. elegans bases 17, 300 genes in C. elegans
       AA458389 V949FID.

BEI88752 VV1-HTO51

AZ319004 1M0038H21

AZ319004 1M0038H21

AA637160 VZ13003.T

AA637160 VZ13003.T

AA637160 VZ13003.T

AA637180 VZ13003.T

AA68889 AV668989

MC2524 ZA408.51

AA78256 OCCIO.4.S

AA25624 ZT79b11.T

AA87825 OCCIO.4.S

AA25624 ZT79b11.T

AA87825 COCIO.4.S

AA574351 N112h10.S

BG730070 GeO9409.X

AI33411 SD05212.S

AI53411 SD05212.S

AI53411 SD05212.S

AI53411 SD05212.S

AI580125 tx16f08.X

BE367010 PT1_42_A1

BE367010 PT1_42_A1

BE367010 PT1_42_A1

BE367017 PT1_42_A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Jerome_Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
Politape_vaglio@dfci.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                          BI174209 568 bp mRNA EST 09-JUL-2001
OSTF013F8_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
7el: 617 632 5180
Fax: 617 632 2425
                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
         AA458389
BE168752
TA105D12Q
AZ319004
                                                                                                                                                                                          BI234655
AZ720352
AI862985
                                                                                                                                                                                                                         AI533411
AI580125
BE367030
BE367017
                                                                               AI593113
AI280109
                                                                                                                                        AA256224
AA574351
BG730070
                                                                                                                                                                                                                                                                                   BG049365
AW953929
BE542678
BF177958
BE393004
                                                                    AA637160
                                                                                                          AV668989
                                               AW789094
                                                                                                                                                                                                                                                                           BE819452
                                                                                                                                                                       AI449899
                                                                                                                                                                               AI338197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                             C46F11.2, mRNA sequence.
B1174209
B1174209.1 GI:14640012
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Caenorhabditis elegans
 RESULT 1
BI174209/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
υ
                                                                                                                                                                                                      ပပ
                                                                                                                                                                                                                                      000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW358852 43779 MAR
AA475114 vg95a03.r
BE032643 132077 MA
BE924637 EST428407
AA212655 MW78e01.r
AQ72420 HS_2119_A
AZ851447 2M0153M11
BG592665 EST491343
BG9664119 602832063
BG400800 602446016
AZ474239 1M0290J11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI174209 OSTF013F8
                                                                            (without alignments)
28.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    ; Search time 8261.74 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                   22703874
         4.5
Compugen Ltd
                                                                                                                                                                               11351937 segs, 5372889281 residues
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
       GenCore version Copyright (c) 1993 - 2000
                                                                 February 25, 2002, 17:21:01
                                                                                                                             1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW358852
AA475114
BE032643
AA212655
AQ724420
AZ851447
BG592665
BG592665
BG400409
AZ474239
                                                sw model
                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Π
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_gss_other:*
                                              nucleic search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                        em_gss_fun:*
em_gss_hum:*
em_gss_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
                                                                                                         US-09-698-903B-6
22
                                                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_gss_pln:*
                                                                                                                                                                                                                                                                                                               em_esthum: *
em_estin: *
em_estom: *
em_estol: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_estfun:*
                                                                                                                                                                                                                                                                                                                                                        em_estba:*
em_estro:*
em_estov:*
em_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                gb_est1:*
gb_est2:*
gb_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                dp_gss:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330
352
352
355
355
355
721
721
721
162
                                                                                                                                                                                                                                                                                              EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55...
1111...
1122...
1143...
116...
116...
```

sed

99 09

Minimum I Maximum I

Database

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Location/Qualifiers 1..568

source

FEATURES

17.4 117.2 117.2 117.2 117.2 117.2 117.2 117.2 117.2 117.2

O

4007

Score

Result g

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                            AA475114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
                       /strain="N2"
/db_xref="taxon:6239"
/db_xref="taxon:6239"
/clone_lib="#AD-wrmcDNa"
/sex="Hermaphrodite and male"
/sex="Hermaphrodite and male"
/fissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNa library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into ppc86"
46 a 116 c 159 g 147 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 436
Fax: 402 762 436
Fax: 402 762 430
Fax: 402 762 762
Fax: 402 762
Fax: 402 762 762
Fax: 402 762
Fax: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="Vector: pChW SPORT6; Site_1: Xbai; Site_2: Xhoi;
Inbrary made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

118 c 108 g 50 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW358852 330 bp mRNA EST
43779 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
AW358852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
/organism⊶"Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.4; DB 11;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
79.1%; Score 17.4; Esst Local Similarity 94.7%; Pred. No. 3.8e
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
Plate: 25 row: A column: 16
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW358852.1 GI:6863502
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 TCTACGCAATATACCAGC 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 tctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scrofa
                                                                                                                                                                                                                                                                                                                                                                                           146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW358852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

Score 17.2; DB 10; Length 330; Pred. No. 4.2e+02;

78.2%; 86.4%;

Best Local Similarity

Query Match

```
Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                          AA475114 352 bp mRNA EST 18-JUN-1997 vg95a03.r1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA AA475114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This soloe is available royally-free through LinL; contact the IMAGE Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Fils clone is available royalty-free through LinL; contact the
MGI:513156
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 346.
Location/Qualifiers
1. 352
/organism="Mus musculus"
/strain="FVB/N" musculus"
/strain="FVB/N" 10090"
/clone="IMAGE:873676"
/clone="IMAGE:873676"
/clone=Lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 352;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.2%; Score 17.2; DB 10;
86.4%; Pred. No. 4.2e+02;
.ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                190 TCATCCACGCGTTGTACCAGC 211
ö
                                  1 tcatctacggcaatgtaccagc 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 TCATCTACCGGATTGTACCAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                               AA475114.1 GI:2199644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
BE032643
```

m

```
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5', mRNA sequence.
AA212655
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                       110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
AA212655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potato.
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Solanaceae; Solanum;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
I (basea I to 355)
Van der Hoeven,R.S., Bezzerides,J., Holt,I.E., Liang,F., Cho,J., Utterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E., Tanksley,S.D. and Baker,B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)
Contact: Cathy Ronning
                                                                                                                                                                                            Casas, E.,
                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Cetartiodactyla, Suina, Suidae, Sus. 1 (bases, 1 to 355)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)
CONTACT: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE924637 355 bp mRNA EST 02-OCT-2000 EST428407 potato leaves and petioles Solanum tuberosum cDNA clone cSTB30G22 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pcMv SPORT6; Site_1: Xba1; Site_2: Xho1;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embrace "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
  09-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 355;
BE032643 355 bp mRNA EST 0
132077 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.2; DB 10;
Pred. No. 4.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC IPIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 63 row: L column: 13
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and 30 embryos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE924637
BE924637.1 GI:10450713
                                    BE032643.1 GI:8327652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 c
                                                                                                                Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                  pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                  DEFINITION
                                                                                                                ORGANISM
                                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE924637
                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 432)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA212655 432 bp mRNA EST 18-FEB-1997 mw78e01.rl Soares mouse NML Mus musculus cDNA clone IMAGE:676824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
The Institute for Genomic Research For clone request: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.2; DB 11;
Pred. No. 4.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:416528
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 357.
Location/Qualifiers
1. .432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                        118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:676824"
                                                                                                                                                                                                                                                                                                                                                                                liquid nitrogen."
62 c 65 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 TCATCTACGACAATTTACCTGC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA212655.1 GI:1811317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 78.2%;
1 Similarity 86.4%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 tcatctacggcaatgtaccagc
```

```
AZ851447 567 bp DNA GSS 21-FEB-2001
2M0153M11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCZM0153M11 R, DNA sequence.
AZ851447 GI:13037453
             438 TCATCTACGCCACTGTGCCAGC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                              RESULT 8
AZ851447/c
                                                                                                           DEFINITION
                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                              ACCESSION
                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                             SOURCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammala; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 562) Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                              AQ724420 562 bp DNA GSS 14-JUL-1999
HS_2119_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo
Sapiens genomic clone Plate=2119 Col-14 Row=E, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Fax: (206) 616-3818
Email: jWallace@u washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2119 row: E column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="Plate=2119 Col=14 Row=E"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                         Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.2; DB 13; Length 562;
Pred. No. 4.7e+02;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                    Score 17.2; DB 10;
Pred. No. 4.4e+02;
0; Mismatches 3;
                                                                                                                                       88 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 562.
Location/Qualifiers
1. .562
                                                                                                                                    125 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 g
                                                                                                                                                                                                                                                                                  94 TCATCTACCGGATTGTACCAGC 115
                                                                                                                                                                                                                                                                   1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                               AQ724420
AQ724420.1 GI:5484089
                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                     148 c
                                                                                                                  Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saptens
                                                                                                                                  71 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juman.
                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                             RESULT
AQ724420
                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                             g
```

22

1 tcatctacggcaatgtaccagc

à

```
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil47321H gib]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xi10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                 Logass I to 36/)

Journ, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longare, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R.,

Musis, Rose, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

University of Utah

University of Utah

Weiss

University of Utah

Baill2, USA

Baill2, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 567)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .567
/organism="Mus musculus"
/strain="c57BL/G1"
/strain="c57BL/G1"
/clone="UGC2M0153M11"
/clone=lUGC2M0153M11"
/clone_lib="Mouse lOkb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.2; DB 13;
Pred. No. 4.7e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0153 row: M column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 567.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.28;
86.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 86.4;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                Mus musculus
house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

þe

```
/Organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="lamAGE:4592474"
/clone=lib="NHL MGC 75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/fil (ggcgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="lMAGE:4986807"
/clone="lMAGE:4986807"
/lab_host="bH10B (Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 932)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLAM10996 row: m column: 16
High quality sequence stop: 718.
Location/Qualifiers
I. 738

//Strain="Mus musculus"
//Strain="FWB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inge.lln.gov
Plate: LLCM1330 row: o column: 03
High quality sequence stop: 230.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602464016F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592474 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.2; DB 11; Length 721;
Pred. No. 4.9e+02;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    611 TCATCTACCGGATTGTACCAGC 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BG400800
BG400800.1 GI:13294248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.2%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tcatctacggcaatgtaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         932 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG400800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
BG400800/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG964419 721 bp mRNA EST 12-JUN-2001
602832063F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4986807 5',
                                                                                                                                                                                                                                                                                                          Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 721)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
Generations of ESTS from sprouting potato eyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (abass 1 to 721)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                             BG592665 721 bp mRNA EST 12-APR-2001
EST491343 cSTS Solanum tuberosum cDNA clone cSTS2C3 5' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Butision tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lb="csrsc".
/clone_lb="csrs".
/tissue_type="sprouting eyes from tubers"
/dev_stage="l2-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.2; DB 11;
Pred. No. 4.9e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Solanum tuberosum"
/cultivar="Rennebec"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 g
  300 TCAACTACAGCAATGAACCAGC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 TCGTCCACCGCAATGTACCAGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                          BG592665.1 GI:13610805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG964419.1 GI:14352056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tcatctacggcaatgtaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tubers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BG964419
                                                                                                                                                                                              mRNA sequence.
BG592665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
                                                                                                                                                                                                                                                                                      potato.
                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                       BG592665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG964419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                 RESULT
                                                                                                                                                                                                                                                                                      SOURCE
                          合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

ö

Gaps

ö

12-MAR-2001

g ð

```
source
                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG669143
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Jab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//nab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
5'-ATTCTAGAGGCGGGCGGCGGATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 162)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A2474239 162 bp DNA GSS 04-OCT-2000
1M0290J11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0290J11"
/clone_llb="Mouse 10kb plasmid UUGC1M library"
/xm="mail"
                                                                                                                                                                                                                                         Length 932;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                         Score 17.2; DB 11;
Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0290 row: J column: 11
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone UUGC1M0290J11 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: CACACAGGAACAGGTATGACC Class: plassid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 162.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                       301 TGATCCACGCAATGGACCAGC 280
                                                                                                                                                                                                                                                                                                                              1 tcatctacggcaatgtaccage 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ474239
AZ474239.1 GI:10632364
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                             212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS
                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ474239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
```

```
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zhang Xu.
Laboratory of Sensory System
Laboratory of Sensory System
Institute of Neuroscience
102 Yue Yang Road, Shanghai 200031, P.R.China
103 Yue Yang Road, Shanghai 200031, P.R.China
104 186-21-6471846
105 106 18 186-21-6471846
106 186 186 186 186 186
107 186 186 186 186 186
108 186 186 186 186
108 186 186 186 186
108 186 186 186 186
108 186 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186 186
108 186
108 186
108 186
108 186
108 186
108 186
108 186
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xiao, H.S., Han, Z.G., Zhang, F.X., Huang, O.H., Lu, Y.J., Bao, L., Pu, G., Guo, C., Yan, Q., Jin, S.X., Zhu, Z.D., Xu, X.R., Li, N.G., Chen, Z. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG669143 855 bp mRNA EST 30-APR-2001
DRN05H06 Rat DRG Library Rattus norvegicus cDNA clone DRN05H06 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Distinct gene expression profiles of rat dorsal root ganglion induced by peripheral nerve axotomy Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="dorsal root ganglion"
/dev_stage="adult" 246 t 5 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.4%; Score 16.8; DB 13; 90.0%; Pred. No. 5.6e+02; live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.4%; Score 16.8; DB 11;
90.0%; Pred. No. 7.8e+02;
Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .855
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sprague-Dawley"
/db.xref="taxon:10116"
/clone="DRN05H06"
/clone_lib="Rat DRG Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG669143.1 GI:13891050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 TTATCTACTGCAATGTACCA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tcatctacggcaatgtacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BG669143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: T3
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: T3
BACKWARD: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
```

```
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVI-HT0516-140
300-107-e07x13-2000-03-14xt4=1)
Seq primer: puc 18 forward
High quality sequence stop: 216.
1. 216
                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Coldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J. and Simpson, A.J. and Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A min1:library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) pofiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
                                             BE168752 216 bp mRNA EST 21-JUN-2000
QVI-HT0516-140300-107-e07 HT0516 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0516"
/dev_stage="Adult"
                                                                                      BE168752
BE168752.1 GI:8631473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rel: +55-11-2704922
                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brazil
                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
    RESULT 15
BE168752/c
                                                               DEFINITION
                                                                                   ACCESSION
VERSION
                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
                                                                                                                              KEYWORDS
SOURCE
                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 479)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theisling, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HIMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                AA458389 479 bp mRNA EST 06-JUN-1997 vg45f10.r1 Scares_mammary_gland_NbAMG Mus musculus cDNA clone IMAGE:864715 5 similar to gb.J03040 SPARC PRECURSOR (HUMAN); gb:M20692 Mouse osteonectin (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra MyMouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_mammary_gland_NbWMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 10;
Pred. No. 1.1e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOISON CO. 1. Send 1 rev2 ET from Amersham Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 441.

Location/Qualifiers
1. .479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:864715"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 g
                      673 ATCTAGGGCAATGTCCCAGC 692
                                                                                                                                                                                                                                                        AA458389.1 GI:2181109
  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.5%;
llarity 94.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 TCATCCACGCCAATGTAC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo."
a 125 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tcatctacggcaatgtac 18
    atctacggcaatgtaccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                         AA458389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
                                                                                                                                                                                                                                                                                    EST
                                                                                                        RESULT 14
AA458389/c
                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
  m
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
ò
                                    음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
```

```
ö
                               Gaps
                               ò
 Length 216;
                               Indels
Score 16.2; DB 10;
Pred. No. 1.1e+03;
0; Mismatches 3;
                                                                                                                                                      Search completed: February 25, 2002, 17:21:04 Job time: 16157 sec
                                                             21
                                                                                       26
Query Match 73.6%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                             1 tcatctacggcaatgtaccag
                                                                                        46 TCAGCCACGCCAAGTACCAG
```

y conditions. 59 g 40 t

AX127757 Sequence AX127748 Sequence AX063413 Sequence E31991 Mutated bar A60109 Sequence 2 A76916 Sequence 2 A76916 Sequence 2

AX127755 Sequence AX127757 Sequence

E31990 Mutated bar AR078675 Sequence I44104 Sequence 23

us-09-698-903b-8.rge

Sequence:

Run on:

Searched:

Minimum Maximum

Database

```
1. .415
/organism="synthetic construct"
/db.xref="taxon:32650"
/note="5' border flanking region of elite event MS-B2"
                                                                                                                                                                                                                                                                                                                                                                                                                             artificial sequence.

1 (bases 1 to 415)
Weston, B. and de Beuckeleer, M.
Male-sterile brassiac plants and methods for producing same Patent: WO 0131042-A 8 03-MAY-2001;
Aventis CropScience N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                             AX127755 415 bp DNA
Sequence 8 from Patent WO0131042.
AX127755
                                                                                                                                                                                                                   TBI251013
TBI251014
A18051
                                                                                                                                                                                                                                                                   182374
BINHYGDNA
                                                                                                                                                              AR074388
A24782
AR074387
                                                                                                                                                                                                                                      AR095107
AR098313
AX012338
                                                                                                                                                AX127748
A24783
                  AX127755
AX127757
AX127748
AX063413
                                                                                                                                                                                               A10943
AX172463
                                                                                                               AR098307
                                                                                                                                                                                                                                                                                                                   AF242881
                                                                                                                                          AR098311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                              144103
                                                                                                                                                                                                                                                            149886
                                                                                                                                                                                                                                                                                               ATACH5
                                                                                                                                                                                                                                                                                 ATTRN7
                                                                                                                                                                                                                                                                                                                                                                                                  AX127755.1 GI:14134402
                                                                                                                                                                                                             6
12
12
6
                                                                                                                                                                                                                                                                                                                                                                                                                synthetic construct. synthetic construct
      DB
                                                                                                                                                                                                                                                                                                    24595
24595
194140
249
                                5865
7599
6539
6548
6548
6548
6548
7811
                                                                                            4832
49946
49946
49946
49946
73560
7566
7766
1033
1033
10037
                                                                                                                                                                                                             3201
2476
3236
3236
1186
1186
1186
1186
1186
                                                                                                                                                                                                                                                                                       878
24595
      Match Length
                                             Query
                                                                                                                                                                                                                           11253
11253
11466
11466
11466
11466
       Score
                                                                                           188.4
188.4
188.4
188.4
188.4
                                                                                                                                   188.4
188.4
188.4
188.4
188.4
                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                 RESULT
AX127755
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                     Result
       õ
                                                                                                                                                         0000000
                                                                                                                                                                                                              O
                                                                                                                                                                                                                                  0000000000
                                            ; Search time 2331.3 Seconds (without alignments) 2936.700 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                     1 gtcgagtttggtgttcatga.......agctggtacattgccgtag 415
                                                                                                                                    2944280
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                      1472140 segs, 8248589755 residues
                                                                                                                                   Total number of hits satisfying chosen parameters:
                                            February 25, 2002, 18:00:10
                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                nucleic search, using sw model
                                                                                                  IDENTITY_NUC Gapoxt 1.0
                                                                                                                                                                                                                                                                                                                                                                                                  em_v1:*
em_htgo_hum:*
em_htgo_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                       em_htgo_rod:*
em_htg_hum:*
em_htg_inv:*
em_htg_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_htg_other:*
                                                                                                                                                DB seq length: 0
DB seq length: 200000000
                                                                       US-09-698-903B-8
                                                                                                                                                                                                                                                                   gb_ro:*
gb_sts:*
gb_sy:*
gb_un:*
gb_vi:*
em_ba:*
                                                                                                                                                                                                                                                                                                                                             em_ov: *
em_pat: *
em_ph: *
em_pl: *
                                                                                                                                                                                                                                                                                                                                                                       em_ro:*
em_sts:*
em_sy:*
                                                                                                                                                                                                                                                                                                                  em_hum:*
                                                                                                                                                                                                                                                                                                                        em_in:*
em_om:*
em_or:*
                                                                                                                                                                                                                         gb_om:*
gb_ov:*
gb_pat:*
gb_ph:*
gb_pl:*
                                                                                                                                                                                                             gb_htg:*
gb_in:*
                                                                                                                                                                                                                                                                                                                                                                                            еш_un:*
                                                                                                                                                                                                       gb_ba:*
                                                                                                                                                                                                GenEmbl:*
                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                  Scoring table:
                                OM nucleic
```

AX172441 Sequence 1
A76916 Sequence 1
A76915 Sequence 1
A7712440 Sequence 1
A7712440 Sequence 1
A717241 Sequence 7
A71437 Sequence 5
AR098311 Sequence 5
AR098311 Sequence 5
AR07438 Sequence 5
AR07438 Sequence 5
AR07438 Sequence 2
A172463 Sequence 22
AR07438 Sequence 22
A172463 Sequence 22
A172463 Sequence 22
A172463 Sequence 22
A17251013 Transform
A18251014 Transform
A18251014 Transform
A18251015 Sequence 2
AR095107 Sequence 2
AR095107 Sequence 2
AR09610 Aprobacteri
X00431 Agrobacteri
X00431 Agrobacteri
E00546 DNA fragmen
AE242881 Agrobacteri
E00546 DNA fragmen

X05579 Soybean bet

ALIGNMENTS

PAT

SUMMARIES

~

```
tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                             ๙
                                                                                                                                                                                                                                                                                                                                                                                           1849
                                                                                                                                                                                                                                     RESULT 3
AX127748/C
                                                                                                                                                                                                                                                          DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                              source
                          409
                                        29
           7
                                                                       126
                                                                                                     186
                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                  306
                                                                                                                                                                                110
                                                                                                                                                                                               366
                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5633
                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                   LOCUS
                       g
                                       ò
                                                     qq
                                                                                    QQ
                                                                      δ
                                                                                                    ò
                                                                                                                   g
                                                                                                                                   δ
                                                                                                                                                 셤
                                                                                                                                                                               Q
                                                                                                                                                                 ð
                                                                                                                                                                                              δ
                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                á
                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                             gtatatatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggggcacc 180
                                                                                                                                                                                          tgataaaataacaagtcaggtattatagtccaagcaaaacataaatttattgatgcaag 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            event MS-B2"
                                                                                                                                                                                                                                                                         360
                                                                                    Gaps
                                                                                                   9
                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                            15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                            synthetic construct.

synthetic construct

synthetic construct

a (base) to 416)

Weston, B. and de Beuckeleer, M.

Male-sterile brassics plants and methods for producing same Patent: WO 0131042-A 10 03-MAY-2001;

Avents CropScience N.V. (BE)

Location/Qualifiers
                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416;
                                                                     Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elite
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 416
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="3' border flanking region of
                                                                                                                                                                                                                                                                                                                                            PAT
                                                                 Query Match
100.0%; Score 415; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.2e-64;
Matches 415; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 380.8; DB 6;
Pred. No. 2.5e-58;
                                      u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ų
                                      136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152
                                                                                                                                                                                                                                                                                                                                     AA127757 416 bp DNA Sequence 10 from Patent WO0131042.
1. .234
/note="plant DNA"
235. .415
                                      Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194. .416
/note="plant DNA"
72 c 54 <
                      235. .415
/note≂"T-DNA"
                                                                                                                                                                                                                                                                                                                                                               AX127757.1 GI:14134404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.8%;
98.5%;
                                   55 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                    154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
      misc_feature
                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S:
Matches 404)
                                                                                                                                                                                                                                                                                                                         RESULT 2
AX127757/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Source
                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                              a
                                                                                                à
                                                                                                                              à
                                                                                                                                             g
                                                                                                                                                                         g
                                                                                                                                                           å
                                                                                                                                                                                          õ
                                                                                                                                                                                                      염
                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                g
```

```
ö
125
                                                                 245
                                                                                                                                                                                    171
                                                                                                                                                                                                        402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       same
                                                  tgagaacaactcacaagcattaatcatgttcatataaatatatgtacattatac-gtata
                                                                                                    tatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggggacccatggt
                                                                                                                                                      ttcaagtattatatatattataattataattatggtaggatgtacatggccgataagaaaa
                                                                                                                                                                    223 gaigtacaiggccgataagaaaaggcaaiitgiagaigitaaiicccaiciigaaagaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 5865)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing Patent: WO 0131042-A 1 03-MAY 2001;
Aventis Cropscience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5865;
                                                                                                                                                                                                                                                                                                                 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                             attcagaaatatttcaataactgattatatcagctggtacattgccgtag
                                                                                                                                                                                                                                                                                                                                                                                                         PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.1%; Score 191.4; DB 6;
99.5%; Pred. No. 5.7e-25;
live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="synthetic construct"
/db_xrsf="texon:32630"
/db_tref="T-DNA of plasmid pc0113"
/ 1095 c 1149 g 1772 t
                                                                                                                                                                                                                                                                                                                                                                                                  AX127748 5865 bp DNA
Sequence 1 from Patent W00131042.
AX127748
AX127748.1 GI:14134395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.1
Best Local Similarity 99.5
Matches 192; Conservative
```

 \sim

ö

```
6353 ACATTGCCGTAG 6342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid PTS172.
Plasmid PTS172
                                                                                                                                                                                                                                                                                                                                             404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 acattgccgtag 415
             source
                                                                                    1755 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1756 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmids.
FT
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT (A60109/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  rocus
                                                                                                                                                                                       δλ
                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAZUYUKI HAMADA,FUMIO NAKAKIDO
C12N15/09,A01H5/00,C12N5/10,C12N9/22//(C12N5/10,C12R1:91), PC
                                                                                                                    artificial sequence.

(bases 1 to 7599)

Hoffmann, B., Mollier, P. and Pelletier, G.

Promoter expressed specifically in the cells of plant roots,
recombinant vectors and host cells comprising same and transgenic
plants obtained
plants obtained
Patent: WO 0100833-A 5 04-JAN-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 tatagittamatatttatigatamaatamcaagicaggitattatagiccaagcamaaca 342
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2001
                                   24-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                             Length 7599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutated barnase gene and transgenic plant thereof patent: JP 2000041682-A 4 15-FEB-2000;
JAPAN TOBACCO INC.
OS Escherichia coli LE392
PN JP 2000041682-A/4
PD JF 2000041682-A/4
PP 04-AUG-1998 JP 1998220060
PF AAUG-1998 JP 1998220060
PR RAZUKUKI HAMADA, FUMIO NAKAKIDO
PC C12N15/09, A0115/00, C12N5/10, C12N9/22//(C12N5/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutated barnase gene and transgenic plant thereof.
E31991
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                   PAT
                                                                                                                                                                                                                                                                                                                                          46.1%; Score 191.4; DB 6;
99.5%; Pred. No. 5.6e-25;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                 /organism="synthetic construct"
/db_xref="taxon:32630"
/note="ADN-T de PGKB5"
1938 c 1937 g 1752 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C12N15/00,
PC C12N5/00, (C12N5/00,C12R1:91)
CC
                                 AX063413 7599 bp DNA
Sequence 5 from Patent WO0100833.
AX063413
                                                                                                                                                                                                                   Location/Qualifiers
1. .7599
                                                                      AX063413.1 GI:12541201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E31991.1 GI:13021588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 6539)
Kazuyuki, H.F.N.N.
                                                                                               synthetic construct. synthetic construct
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.5
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP 2000041682-A/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified unclassified.
                                                                                                                                                                                                                                                                                            O
                                                                                                                                                                                                                                                                                         1972
                                          DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
DEFINITION
ACCESSION
VERSION
SERVORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                         source
         RESULT 4
AX063413/c
                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                             AUTHORS
                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                KEYWORDS
SOURCE
                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
E31991/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
6414
                                                                                                                                                                                                                                                                                                        6354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 6548;
                      /organism='Escherichia coll LE392'
Location/Qualifiers
                                                                                                                                Length 6539;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic transformation using a PARP inhibitor Patent: WO 9706267-A 2 20-FEB-1997; PLANT GENETIC SYSTEMS NV (BE) LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 45.5%; Score 188.8; DB 6; Best Local Similarity 99.0%; Pred. No. 1.6e-24; Matches 190; Conservative 0; Mismatches 2;
                                                                                                                               Score 188.8; DB 6;
Pred. No. 1.6e-24;
0; Mismatches 2;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      A00109 6548 bp DNA circular
Sequence 2 from Patent W09706267.
                                                                                 ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1690 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .6548
/organism="Plasmid PTS172"
/db_xref="taxon:106340"
a 1579 c 1523 g 1690
                                                                                 1687
                                            1. .6539
/organism="unidentified"
/db_xref="taxon:32644"
a 1578 c 1519 g 168
                                                                                                                               Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i (bases 1 to 6548)
De,B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A60109.1 GI:3715125
```

09:11:49 2002

Tue Feb 26

```
1756 a
                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                   344
                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                         E31990/c
LOCUS
                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                       ŏ
                                                          g
                                                                                 δλ
                                                                                                     g
                                                                                                                            ò
                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                             6482 ATAGTTTAAATATTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACAT 6423
                                                                                                                                                                                                                                                                                                                                                                                                                  atagittaaatatitatigataaaataacaagicaggiatitatagiccaagcaaaaacat 343
                                                                                                                                                                                                                                                                                                                Gaps
                                                          22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                        DB 6; Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
45.5%; Score 188.8; DB 6; Length 6548;
Best Local Similarity 99.0%; Pred. No. 1.6e-24;
Matches 190; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                         Coation (BE)

Loads 1 to 6548)

De, B.M.

GENETIC TRANSFORMATION USING A PARP INHIBITOR PATENT: EP 0757102-A 2 05-FEB-1997;

PLANT GENETIC SYSTEMS NV (BE)

Location/Qualifiers

1. 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic transformation using a PARP inhibitor Patent: US 6074876-A 2 13-JUN-2000; Location/Qualifiers 1.6548
                                               A/b916 6548 bp DNA circular PAT Sequence 2 from Patent EP0757102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT
                                                                                                                                                                                                                                                                                     Query Match
45.5%; Score 188.8; DB 6;
Best Local Similarity 99.0%; Pred. No. 1.6e-24;
Matches 190; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                    /organism="Plasmid PTS172"
/db_xref="taxon:106340"
1 1579 c 1523 g 1690 f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2 from patent US 6074876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
1579 c 1523 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR098308.1 GI:12807565
                                                                                     A76916.1 GI:6088713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6548 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 6548)
De Block, M.
                                                                                                          Plasmid PTS172.
Plasmid PTS172
plasmids.
 6362 ACATTGCCGTAG 6351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6362 ACATTGCCGTAG 6351
                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.
                                                                                                                                                                                                                                           1756 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR098308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown
                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                          SOURCE
                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
AR098308/c
LOCUS
DEFINITION
                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                          284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SASE COUNT
                                                                                                                                           REFERENCE
                                                                                                                                                                           JOURNAL
                                RESULT
A76916/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                PEATURES
                                                      rocus
8
                                                                                                                                                                                                                                                                                                                                                   음
                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
ô
                                                                                                                                                                                                                                                                                  KAZUYUKI HAMADA, FUMIO NAKAKIDO
C12N15/09,A01H5/00,C12N5/10,C12N9/22//(C12N5/10,C12R1:91), PC
aaatttattgatgcaagtttaaattcagaaatatttcaataactgattatacegctggt 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .6548
/organism='Escherichia coli LE392'
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6548;
                                                                                                                                   E31990 6548 bp DNA DAT Mutated barnase gene and transgenic plant thereof.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 188.8; DB 6;
Pred. No. 1.6e-24;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .6548
/organism="unidentified"
/db_xref="taxon:32644"
a 1579 c 1523 g 1690
                                                                                                                                                                                                                                                                                                                                                                                        1690
                                                                                                                                                                                                                                                                                                           C12N5/00, (C12N5/00,C12R1:91)
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                             6362 ACATTGCCGTAG 6351
                                                                   404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C12N15/00,
PC C12N5/0
CC
FH Key
FT source
                                                                                                                                                                                                                                                                                                                                     source
```

S

```
346 atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-1998
                                                                                                                                                                              03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 agtttaaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methods for producing same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4832;
                                                                                                                                                                                                                                                                                                                                                                                                                              others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic transformation using a PARP inhibitor
Patent: WO 9706267-A 1 20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:32630"
/note="T-DNA of plasmid pTHW118"
1883. 4065
/note="Hpal restriction fragment"
a 883 c 932 g 1488 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                                                                                                                                      1. .4832
/organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 188.4; DB Pred. No. 2e-24;
                                                                                                                                                                                                                                                    synthetic construct
artificial sequence.
1 (bases 1 to 4832)
de Both,G. and de Beuckeleer,M.
Hybrid winter oilseed rape and method
Patent: WO 0141558-A 2 14-JUN-2001;
Aventis CropScience N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                             AX172441 4832 bp DNA
Sequence 2 from Patent WO0141558.
AX172441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abul08 4946 bp DNA
Sequence 1 from Patent WO9706267.
A60108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          artificial sequence; vectors.
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                  AX172441.1 GI:14597553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformation vector
Transformation vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A60108.1 GI:3715124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 4946)
De,B.M.
                                                                                                                                                                                                                                         synthetic construct.
                                                                                                       406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 ATTGCCGTAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                               1528
                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                     RESULT 1
AX172441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
A60108
                                                                                                                                                                              LOCUS
                                                                g
                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 3200)

Cornelissen,M., Soetaert,P., Stam,M. and Dockx,J.

Modified Bacilius thuringlensis insecticidal-crystal protein genes and their expression in plant cells
Patent: US 5633446-A 23 2-MAY-1997;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacat 343
                                                                                                                                                                                                                                                                                                                                                                              286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                             31-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-0CT-1997
                                                                                                                            1 (bases 1 to 7811)
Cornelissen,M., Reynaerts,A., Gossele,V. and Van Aarssen,R.
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                 45.5%; Score 188.8; DB 6; Length 7811; 99.0%; Pred. No. 1.6e-24; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 others
                            PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 188.4; DB
Pred. No. 2e-24;
0; Mismatches
                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ų
                                                                                                                                                    Marker gene
Patent: US 5962768-A 5 05-OCT-1999;
                                                                                                                                                                                                                  2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5633446
                                      5962768
                                                                                                                                                                                                    /organism="unknown"
1906 c 1873 g
                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unknown"
710 c 720 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 from patent US E
                         AR078675 7811 bp DNA
Sequence 5 from patent US 5:
AR078675 GI:10005421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         720 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.4%;
ilarity 99.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I44104.1 GI:2469202
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.0
Matches 190; Conservative
                                                                                                                                                                                          .7811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                  đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         đ
                                                                                      Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
                                                                                                                                                                                                                  1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                           source
                                     DEFINITION
                                                                                                   ORGANISM
                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                  ACCESSION
VERSION
                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                         498
                                                                                                                                                                                                                                                                                                                                                                                                                                        558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226
                                                                                                                                                                                                                                                                                                                                                                 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618
                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                   344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404
RESULT 1
AR078675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1:
I44104/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                          KEYWORDS
SOURCE
                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
```

g

q

ð g

ð

ä

g

ó

ö

Gaps

us-09-698-903b-8.rge

```
Search completed: February 25, 2002, 18:00:20 Job time: 18428 sec
                                                                                                                                                                                                                                                   Query Match
                                                   DEFINITION
ACCESSION
                                                                                                                                                                                     source
                                                                                                          ORGANISM
                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                       AUTHORS
TITLE
JOURNAL
                   RESULT 1:
AR098307
LOCUS
                                                                        VERSION
KEYWORDS
                                                                                                                               REFERENCE
                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                        286 agittaaatattatigataaaataacaagicaggiattatagiccaagcaaaaacataa 345
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                         19-OCT-1999
                                                                                                                            ó
                                                                                                      Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
45.4%; Score 188.4; DB 6; Length 4946;
Best Local Similarity 99.5%; Pred. No. 2e-24;
Matches 189; Conservative 0; Mismatches 1; Indels 0;
          Location/Qualifiers'
1. 4946
/organism="Transformation vector pTHWIO7"
/db_xref="transformation" vector pTHWIO7"

# 891 c 963 g 1523 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .4946
/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
a 891 c 963 g 1523 t
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETIC TRANSFORMATION USING A PARP INHIBITOR PATENT: EP 0757102-A 1 05-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                       PAT
                                                                                                Query Match
45.4%; Score 188.4; DB 6;
Best Local Similarity 99.5%; Pred. No. 2e-24;
Matches 189; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                               A76915 4946 bp DNA
Sequence 1 from Patent EP0757102.
A76915
PLANT GENETIC SYSTEMS NV (BE)
                                                                                                                                                                                                                                                                                                                                                                                                      Transformation vector pTHW107.
Transformation vector pTHW107
artificial sequence; vectors.
1 (bases 1 to 4946)
De, B.M.
                                                                                                                                                                                                                                                                                                                                                                                   A76915.1 GI:6088712
                                                                                                                                                                                                                                                                     406 attgccgtag 415
                                                                                                                                                                                                                                                                                            234 ATTGCCGTAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11111111
234 ATTGCCGTAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1569
                                                                                                                                                                                                                                                                                                                                                 LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                             RESULT
A76915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                 ORIGIN
                                                                                                                                         ð
                                                                                                                                                                                                     g
                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                  윱
                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
14-FEB-2001
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                      Length 4946;
                                                                                                                                                                                                                                            Indels
                                                                                                              Genetic transformation using a PARP inhibitor Patent: US 6074876-A 1 13-JUN-2000; Location/Qualifiers
         PAT
                                                                                                                                                                                                                    Score 188.4; DB 6;
Pred. No. 2e-24;
0; Mismatches 1;
                                                                                                                                                                                                                                          1;
ARU98307 4946 bp DNA
Sequence 1 from patent US 6074876.
AR098307
                                                                                                                                                           /organism="unknown"
1 891 c 963 g
                                     AR098307.1 GI:12807564
                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                               Unclassified.
1 (bases 1 to 4946)
De Block, M.
                                                                                                                                                  .4946
                                                                                                                                                                                                                                                                                                                                                                                              406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                    234 ATTGCCGTAG 243
                                                                                                                                                                       1569 a
                                                          Unknown.
                                                                        Unknown
```

•

.

THIS PAGE BLANK (USPTO)

Plasmid pTS88 (Eco pPS029 Bt ICP codi Nucleotide sequenc T-DNA of plasmid p

Plasmid pPS0212 co Plasmid pJD884 con USP-Promoter-casse

```
Legumin-signalpept
USP-signalpeptide
Right flanking reg
pVB36 Bt ICP codin
Chimeric neo gene
Plasmid DV131 comp
Plasmid DV131 used
Plasmid DV133 used
Sequence of opine
Complete nucleotide
Digonucleotide DI
Oligonucleotide DI
                                                Nucleotide sequenc
T-DNA of pTTS24.
Plasmid pTCO113 T-
Chimeric T-DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MS-B2 elite event; transgenic Brassica plant; transformation event; male-sterility gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Right (5') border flanking region of elite event MS-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..234
/*tag= a
/ntag= "Corresponds to plant DNA"
235..415
/*tag= b
/note= "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                 AAQ42160

AAQ42160

AAQ4703

AAQ04703

AAQ04706

AAQ25707

AAZ29122

AAZ29123

AAZ29123

AAZ29123

AAZ29124

AAZ29124

AAZ29124

AAZ29124

AAZ29124

AAZ29123

AAF58259

AAF58259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVET ) AVENTIS CROPSCIENCE NV
 AAD06997 standard; DNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Agrobacterium sp.
- Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
1303
3201
4832
4946
4946
5349
5864
7566
                                                                                                                7639
1037
1085
11085
11077
3201
1186
3153
3336
                                                                                                                                                                                                                                               3877
24593
24596
936
444444444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-2001
                                                  188.4
188.4
188.4
188.4
188.4
                                                                                                                                                                                                                                                                                                               107.6
107.6
107.6
                                                                                                                                                                                                                                                                                                                                                  100.4
106.4
106.4
106.4
106.4
                                                                                                                             182.4
182.4
182.4
179.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD06997;
                                                                                                                                                                                                                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD06997
υU
                                                                                                     00000 000000
                                                                                                                                                                                                                                                                                        000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid prolls T.
Chimeric T-DNA of
Nucleotide sequenc
Plasmid prs. Zdelt
E. coli plasmid pr
Plasmid prs. 72, 4 use
Plasmid prs. 72, C
E. coli plasmid pr
Plasmid prs. 72, C
                                                                                     ; Search time 716.55 Seconds (without alignments) 496.532 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Right (5') border
Left (3') border f
Plasmid pTC0113 T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                   1 gtcgagtttggtgttcatga......cagctggtacattgccgtag
                                                                                                                                                                                                                                                                                                                                                                                    **Sides Signature of the control of 
          4.5
Compugen Ltd.
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                 930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
          GenCore version
Copyright (c) 1993 - 2000
                                                                                     February 25, 2002, 18:17:24
                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD06999
AAT39339
AAD06990
AAF86439
AAT391097
AAT39336
AAT391096
AAT6441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD06997
                                                                                                                                                                                           IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΩI
                                                                                                                                                                                                                                                                                   length: 0
length: 2000000000
                                                                                                                                         US-09-698-903B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5864
5865
75865
7589
5228
6539
6548
6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0
91.8
466.1
466.1
465.1
455.5
455.5
455.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110...
1111...
1111...
1111...
1111...
1111...
1111...
1111...
```

380.8 191.4 191.4 191.4 188.8 188.8 188.8 188.8 188.8

0000000000

Result . 9

sed

DB DB

Minimum Maximum

Database

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

N

```
tgagaacaactcacaagcattaatcatgttcatataaatatatgtacattatac-gtata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 tatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggggcaccatggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 tttggtgttcatgattttgggttttgactcttcaccattacatattgaaactcttacgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 TATACACGTATACAAATAGTAGCGGAGAAATCCATGTAAAGCAGCAGCGGGGCACCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 ttcaagtattatataattataattataattatggtaggatgtacatggccgataagaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggcaatttgtagatgttaattcccatcttgaaagaaatatagtttaaatattttattgata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 98.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50
             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
                                                                                   ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtatatatacacgtatacacaatagtagcgaagaaatccatgtaaagcagcagggggcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tacggatgagaacaactcacaagcattaatcatgttcatataaatatgtacattatac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gtcgagtttggtgttcatgattttgggttttgactcttcaccattacatattgaaactct 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MS-B2 elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atggtttcaagtattatataattataattataattatggtaggatgtacatggccgataa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgataaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 415;
                                                                                                                                                                               present invention relates to a transgenic Brassica plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tttaaattcagaaatatttcaataactgattatatcagctggtacattgccgtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Left (3') border flanking region of elite event MS-B2
                                                                                                                                                                                                                                                                                                                                                                Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 415; DB 22;
Pred. No. 3.5e-76;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                               Page 51; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Sc
100.0%; Pr
:ive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Agrobacterium sp. - Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
     Beuckeleer
                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 100.
415; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD06999/c
ID AAD06999 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     male-sterility gene; ds.
                                   WPI; 2001-300517/31.
   ρe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2001
 B
                                                                                                                                             Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
Matches 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD06999;
   Weston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                 The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TE STATE OF STATE OF
```

ñ

Gaps 99

. .

Indels

Length 416;

22;

Score 380.8; DB 22; Pred. No. 3.2e-69; 1; Mismatches 3;

91.8%;

350 125 290 185 245

171 305 365

51

415

```
The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is left (3') border flanking region of elite event
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;
                                                                                                                                                to plant DNA"
                                                          to T-DNA'
                  /*tag= a
/note= "Corresponds
194..416
                                                                                                                                          /note= "Corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 52; 53pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                         (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                       26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Beuckeleer M;
                                                                                                                     /*tag=
1..193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-300517/31.
                                                                                                                                                                                                     WO200131042-A2
misc_feature
                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                           29-0CT-1999;
                                                                                                                                                                                                                                                            03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weston B,
```

m

```
Key
 g
                                                                                                                                                                                                                                                                                                   合
                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                           synthase gene of Agrobacterium T-DNA" complement (3032..3367)
                                                                                                                                                                                                                                                                                                                 /note= "Bacillus amyloliquefaciens barnase coding
                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "region containing polyA signal of gene of Agrobacterium T-DNA" complement (5840..5864)
                                                        Plasmid pTC0113 T-DNA used to obtain male sterile oilseed rape.
                                                                      Plasmid pTCO113; male sterile; barnase; ribonuclease; barstar; transgenic plant; oilssed rape; canole; Brassica napus; ds.
                                                                                                                                                                                                                                                                                                                                                    stamen-specific TA29 gene
                                                                                                                                                                                                                                                                                                                                                                                       /note= "promoter of nopaline synthase gene of
Agrobacterium T-DNA"
5217..5489
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "region coding for barstar of Bacillus amyloliquefaciens" 5490..5765
                                                                                                                                                                                                                                          promoter of Arabidopsis Rubisco small
                                                                                                                                     /note= "right border of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= k
/label= LB
/note= "left border of Agrobacterium T-DNA"
                                                                                                                                                                                                     /note= "region coding for phosphinothricin
acetyltransferase"
complement (883..2608)
                                                                                                                                                                   oţ
                                                                                                                                                                 /note= "region containing polyA signal
of Agrobacterium T-DNA"
complement (331..882)
                                                                                                                                                                                                                                                                                                                                                    /note= "promoter of stamer
Nicotiana tabacum'
                                                                                                                                                                                                                                                  subunit gene"
complement (2659..3031)
                                                                                                                                                                                                                                                                                                                               complement (3368..4877)
                                                                                                                                            complement (98.330)
                                                                                                         Cocation/Qualifiers
                                                                                                                complement (1..25)
              AAT39339 standard; DNA; 5864 BP
                                                                                                                                                                                                                                                                                                          Barnase
                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Barstar
                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                                       3'nos
                                                                                                                                                                                                                                                                                                                                             /label= PTA29
                                                                                                                                                           3, d1
                                                                                                                                                                                                                                   /label- Pssu
                                                                                                                                                                                                                                                                                                                                                                          /*tag= h
/label= Pnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= j
/label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                  1924..5216
                                         (first entry)
                                                                                                                                                                                                                                          /note= "
                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                           /label=
                                                                                                                                                                                                                             *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9626283-A1
                                                                                                                misc_feature
                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                         polyA_signal
                                          22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-1996
                                                                                           Synthetic
                            AAT39339;
                                                                                                                                                                                                                     promoter
                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                   promoter
RESULT 3
                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                      CDS
```

```
T-DNA; plasmid pTCO113; transgenic Brassica plant; transformation event; male-sterility gene; chimeric; tobacco; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 tatagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaaca 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 taaatttattgatgcaagtttaaattcagaaatattcaataactgattatatcagctgg 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid prcoll3 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-requiatory) gene under control of the Pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterium-mediated transformation using prcoll3 were male sterile. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5692 TAAATITATIGGAAGCAAGITIAAAATICAGAAATATITCAATAACIGATIATATATATCAGCIGG
                                                                                                                                                                                                                                                                                             Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 191.4; DB 17; Length 5864; Pred. No. 1.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression of barstar counteracted any low level expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 33-3743-47; 56pp; English.
                                                                                                                                                                         Cornelissen M, Michiels F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Streptomyces hygroscopicus.
Chimeric - Arabidopsis thaliana.
Chimeric - Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Nicotiana tabacum.
Chimeric - Agrobacterium tumefaciens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric T-DNA of plasmid pTC0113.
                                                                                                                   ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                   (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          barnase in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06990 standard; DNA; 5865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 46.1%;
Best Local Similarity 99.5%;
Matches 192; Conservative
                                                        95EP-0400364
96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5632 TACATTGCCGTAG 5620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 tacattgccgtag 415
                                                                                                                                                                                                                                    WPI; 1996-402373/40.
                                                                                                                                                                            Botterman J,
                                                        21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD06990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06990/c
```

us-09-698-903b-8.rng

```
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                  /*tag= 1
/note= "TagI fragment from the 3' untranslated end of the nopaline synthase gene (3'nos) from the T-DNA of pri137 and containing plant polyadenylation signals"
                                                                                                                                                                               /*tbg= g
//note= Promoter from the atSIA ribulose-1,5-biphosphate
carboxylase small subunit gene from Arabidopsis thaliana"
2610..2659
                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= Office of the nopaline synthase gene from the T-DNA of pTiT37 of Agrobacterium tumefaciens" 5216..5217
                                                                                                                                                                                                                                                                                              /*tag= k
/notae= The 3' untranslated region downstream from the
barrase coding sequence of Bacillus amyloliquefaciens"
3033..3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                 product= "Protein encoded by bialaphos resistance
lene (bar) of Streptomyces hygroscopicus"
184..2609
1..25
/*tag- a
/*tag- a
/note- "Right border repeat from the TL-DNA from
PT.18653"
26..53
                                                             /*tag= c
//note= "Residual sequence from the TL-DNA at the
right border repeat"
98..30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Sequence from the 3' untranslated end of
barstar gene from Bacillus amyloliquefaciens"
5531.5554
                                                                                           /*tag= d /note= "The 3' untranslated end from the TL-DNA gene 7_(3'97) of priB6S3"
                                       /*tag= b
/note= "Synthetic polylinker derived seguence"
                                                                                                                          /*tag= e
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                            *tag- h
note- "Synthetic polylinker derived sequence"
(660..2920
                                                                                                                                                                                                                                                                        /*tag= j
/note= "Synthetic polylinker derived sequence"
1937..3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note- "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                       /*tag- n
note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= p
/note= "Synthetic polylinker derived sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rtag= q
/product= "Protein encoded by barstar gene
Bacillus amyloliquefaciens"
5491.5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= r
                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 5490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..5554
                                                                                                                                                                                                                                                                                                                                                                                                     ..5215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isss..s766
                                                                                                                                         332..883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
 misc_feature
                              misc_feature
                                                      misc_feature
                                                                                                                  misc_feature
                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                   3'UTR
                                                                                                                                                                                                                                                                                      3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3'UTR
                                                                                                                                        cos
                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
```

```
The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic Diant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant. The present sequence is chimeric T-DNA of plasmid procoll3. This sequence comprises right border repeat, left border repeat and 3' untranslated region (UTR) from TL-DNA of prib653, synthetic polylinker sequences, coding regions of blalahos resistance gene (bar) from Streptomyces hygroscopicus, barnase gene from Bacillus amyloliquefaciens and barstar gene from anther-specific gene TA29 from Arabidopsis thaliana, the anther-specific gene TA29 from the T-DNA of pri137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                        /*tag= u
/note= "Synthetic polylinker derived sequence"
/774..5810
/*tag= v
/note= "Residual sequence from the TL-DNA at the
right border repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 tatagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= x
/note= "Left border repeat from the TL-DNA from
                                                                                                                                                                                                                       5811.5840
/*tag= w
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.1%; Score 191.4; DB 22; Length
99.5%; Pred. No. 1.4e-30;
.1ve 0; Mismatches 1; Indels
gene 7 (3'97) of pTiB6S3"
5767..5773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 47-49; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                5841..5865
                                                                                                                                                                                                                                                                                                                                                                                                oTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.5:
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200131042-A2
                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1999;
                                                                                                             misc_feature
                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weston B,
```

ö

'note= "The 3' untranslated end from the TL-DNA

S

BP.

(first entry)

```
Male sterile plant; RNAase inhibitor; plasmid pTS172delta; ds
                               AAF86439 standard; DNA; 5228
                                                                                            Plasmid pTS172delta
                                                                                                                                     Unidentified
                                                                       25-JUN-2001
                                                    AAF86439
          RESULT 6
AAF86439/c
                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                      Plant promoter; root cell; root-specific expression; parasite resistance; nematode resistance; fungal resistance; water stress; salt stress; sugar content; nitrogen transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a plasmid PGKB5. The plasmid contains a plant promoter that directs expression of a selected sequence in root cells at all stages of development of a plant. The plant promoter is used to control expression of genes in a root-specific manner, especially genes that provide resistance to parasites, pests (nematodes or fungl), water and salt stress, or alter sugar content or nitrogen transport. Fragments of the promoter are useful as probes or primers to detect or amplify at least part of the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                   New constitutive plant promoter active specifically in roots, useful for controlling expression of pest or drought resistance genes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7599 BP; 1972 A; 1938 C; 1937 G; 1752 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.1%; Score 191.4; DB 22; Length Best Local Similarity 99.5%; Pred. No. 1.4e-30; Matches 192; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                       (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                    Nucleotide sequence of a plasmid PGKB5
                                                                                                                                                                                                                                                                                                                          Mollier P, Pelletier G;
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9; 92pp; French.
                                                                      AAF25320 standard; DNA; 7599
                                                                                                                                                                                                                                                             23-JUN-2000; 2000WO-FR01768
                                                                                                                                                                                                                                                                                  99FR-0008185
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         related transgenic plants
          403 tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-102893/11.
                                                                                                                                                                                                                    WO200100833-A1
                                                                                                                                                                                                                                                                                  25-JUN-1999;
                                                                                                               30-APR-2001
                                                                                                                                                                                                                                                                                                                          Hoffmann B,
                                                                                                                                                                                                                                          04-JAN-2001
                                                                                                                                                                                                 Synthetic
                                                                                           AAF25320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                            AAF25320/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403
ð
                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
```

```
The present invention relates to a method for producing male sterile plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 atagittaaatatttattgataaaataacaagicaggiattatatagiccaagcaaaaacat 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                 Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5228 BP; 1384 A; 1307 C; 1263 G; 1274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Similarity 99.0%; Pred. No. 4.6e-30; 90; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 14-17; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ91097 standard; DNA; 6539
                                                                                      12-SEP-2000; 2000WO-JP06222
                                                                                                                                  99JP-0279307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-2000 (first entry)
                                                                                                                                                                               (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                         Hamada K, Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5042 ACATTGCCGTAG 5031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 acattgccgtag 415
                                                                                                                                                                                                                                                                   WPI; 2001-266212/27
WO200124616-A1.
                                                                                                                                  30-SEP-1999;
                                            12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ91097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ91097/C
ID AAZ910
XX
AC AAZ910
XX
DT 06-JUN
```

9

```
Sequence 6548 BP; 1757 A; 1578 C; 1523 G; 1690 T; 0 other;
         rice; Oryza sativa; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                SOS
        ô
                                                                                                                                                                                                     Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undesirable characters by specifically expressing the gene alone in anther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 atagtitaaatatitatigataaaataacaagicaggiattatagiccaagcaaaacai 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pTS174; male sterile; barnase; ribonuclease; transgenic plant;
                                                                                                                                                                                                                                                      The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AA291095) for expression specifically in the anther of a plant. This sequence represents the E. coli/Agrobacterium shuttle vector plasmid pTS172 which contains the mutated barnase gene (AA291095) under control of the cauliflower mosal virus 35s promoter. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell. The transformed plant is used in plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                  224 atgtacatggccgataagaaaaggcaatttgtagatgttaattcccatcttgaaagaat 283
                            Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Length 6539;
                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                  Sequence 6539 BP; 1755 A; 1578 C; 1519 G; 1687 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                Score 188.8; DB 21; Length
Pred. No. 4.7e-30;
0; Mismatches 2; Indels
         coli plasmid pTS431 containing mutant barnase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pTS174 used to obtain male sterile rice.
                                                                                                                                                                                                                                       Example 3; Page 23-27; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT39336 standard; DNA; 6548 BP.
                                                                                                                                                                                                                                                                                                                                                                              45.5%;
                                                                                                                                98JP-0220060
                                                                                                             99WO-JP04167
                                                                                                                                                (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 190; Conservative
                                                                                                                                                                  Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATTGCCGTAG 6342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 acattgccgtag 415
                                                                                                                                                                                    WPI; 2000-195581/17.
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                       WO200008176-A1.
                                                                                                             03-AUG-1999;
                                                                                                                               04-AUG-1998;
                                                                                           17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-1997
                                                       Synthetic.
                                                                                                                                                                  Hamada K,
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT39336;
                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6353
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . EXXEXEX
```

```
Plasmid pTS174 (AAT39336) contains Bacillus barnase DNA under control of the stamen-specific PEI promoter. Embryogenic callus from rice cv. Kochihibitiki was transformed with pTS174 alone or with pTS88 (see also AAT3937), a plasmid contq. barstar DNA under control of a 35S promoter. With pTS174 alone, I male sterile line was recovered from 48 electroporation cuvettes. With both plasmids, 7 normal male sterile lines were recovered from 40 cuvettes. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= e
/label= P35S
/function= 35S promoter of cauliflower mosaic virus
5711..6262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function= region containing polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= promoter of the stamen-specific El gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                               /note- "region containing polyadenylation signal nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                /product= Bacillus amyloliquefaciens barnase complement (2625..4313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= phosphinothricin acetyltransferase
6263..6496
                                                                                                  /+tag= a
/label- Vector
/note= "pUC19 derived vector sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cornelissen M, Michiels F;
                                                                                                                                                                                      complement (2019..2283)
                                                                                                                                                                                                                                                                                                                                                       complement (2284..2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 33-37; 56pp; English.
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/label= Barnase
                                                                                                                                                                                                                                                                                                                             T-DNA"
                                                                                                                                                                                                                  /*tag= b
/label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= g
/label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= PE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= f
/label= bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-0400364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4336..5710
                                                                                 .2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-402373/40.
                                                                           misc_feature
                                                                                                                                                                                      polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Botterman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09626283-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-1996
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter
```

45.5%; Score 188.8; DB 17; Length 6548;

~

```
04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                       AAZ91096;
                                  De Block
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                             copies
                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                    ά
                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                          å
       ö
                                                            6423
                                                                        284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacat 343
                    0; Gaps
                                                     /note= "35S promoter region of cauliflower mosaic virus"
                                                                                                                                                                                                                                                                                               /note= "3' untranslated region contg. the poly-A signal of Agrobacterium T-DNA nopaline synthase gene" complement (2289..2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      '3' untranslated region contg. the poly-A signal of gene 7 of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "phosphinothricin acetyltransferase'
                                                                                                                                                                                                         Transgenic plant; poly-(ADP-ribose) polymerase inhibitor;
niacinamide; Agrobacterium; T-DNA; male sterile; barnase;
ribonuclease; RNase; cereal; wheat; Triticum aestivum;
       Indels
                                                                                                                                                                                                                                                                                                                                                             /note= "promoter region of rice El gene"
complement (4336.5710)
Pred. No. 4.7e-30;
; Mismatches 2;
       0; Mismatches
                                                                                                                                                                                                                                                                    Location/Qualifiers
complement (2019..2288)
                                                                                                                                                                                                                                                                                                                                         complement (2625..4313)
                                                                                                                                                                                                                                         Chimeric Agrobacterium sp.;
Chimeric Oryza sativa;
Chimeric cauliflower mosalc virus.
                                                                                                                                                                                                                                                                                                                                   /product- barnase
                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                          3'nos
                                                                                                                                                                                                                                                                                                                                                                                  P35S
                                                                                                                                                   AAT61394 standard; DNA; 6548
99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95EP-0401844.
                                                                                                                                                                                                                                                                                                                                                        /label= PE1
                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Bar
                                                                                                                                                                                                                                                                                                                                                                                                                                6243..6496
                                                                                                                                                                                                                                                                                                                                                                                                       5711..6262
                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag- f
/label- 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "3'
                                                                                                                                                                               (first entry)
       Matches 190; Conservative
                                                                                                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                 6362 ACATTGCCGTAG 6351
                                                                                                    acattgccgtag 415
Best Local Similarity
                                                                                                                                                                                                                      ribonuclease; RNase
                                                                                                                                                                                           Plasmid pTS172.
                                                                                                                                                                              07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP757102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-1997
                                                                                                                                                                 AAT61394;
                                                                                                                                                                                                                                                                                                                                         promoter
                                                                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                                                                                                                                                                                     Key
3'UTR
                                                                                                    404
                                                                                                                                            AAT61394/c
                                                                                                                                                                                                                                                                                                                                                                                                                                 3'UTR
                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                           g
                                                                                    q
                                                                                                   οy
                                                                                                                q
                                                                                                                                                         g
                                              à
                                                                         à
```

```
6422 AAATTATTGATGCAGGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT 6363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pTS172 (AAT61394) contains the barnase coding sequence under control of the rice El gene stamen-specific promoter and a phosphinothricin acetyltransferase coding sequence under control of the CaMW 355 promoter. Plasmid pTS172 and plasmid pTS772 (see also AAT61395) were used to transform wheat spring variety Pavon calli via particle bombardment. Some calli were treated with the poly-(ADP-ribose) polymerase inhibitor nlacinamide before, or before and after, bombardment. Healthy, male sterile plants were regenerated only from bombarded calli that were treated with niacinamide. This was believed to be due to more faithful expression characteristics of the integrated stamen-selective batnase gene in these calli and regenerated shoots. For plants transformed with pTS172, foreign DNA was stably incorporated in the wheat genome in 2-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacat 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 aaatttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggt 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
                                                                                                                                                                                                                                                                        Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 188.8; DB 18; Length 6548;
Pred. No. 4.7e-30;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E. coli plasmid pTS172 containing synthetic barnase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 17-20; 25pp; English.
                                                                  (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ91096 standard; DNA; 6548
95EP-0401844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.03
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 acattgccgtag 415
                                                                                                                                                                                                      WPI; 1997-111050/11
                                                                                                                                                                                                                                                                                                                                                  reduces metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200008176-A1.
```

```
Hamada K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT39337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AAZ91095) for expression specifically in the anther of a plant. This sequence represents the E. coll/Agrobacterium shuttle vector plasmid pTS172 which contains mosaic virus 35s promoter. The vector plasmid pTS172 which contains mosaic virus 35s promoter. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell. The transformed plant is used in plant breeding.
                                                                                                                                                                                                                              Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undestrable characters by specifically expressing the gene alone in anther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
45.5%; Score 188.8; DB 21; Length
Best Local Similarity 99.0%; Pred. No. 4.7e-30;
Matches 190; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Male sterile plant; RNAase inhibitor; plasmid pTS346; ds.
                                                                                                                                                                                                                                                                                                                       Example 3; Page 19-23; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
       99WO-JP04167.
                                                  98JP-0220060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
AAF86441/c
TD AAF86441 standard; DNA; 7492
                                                                                           (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2000; 2000WO-JP06222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NISB ) JAPAN TOBACCO INC.
                                                                                                                                          Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6362 ACATTGCCGTAG 6351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acattgccgtag 415
                                                                                                                                                                                   WPI; 2000-195581/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pTS346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200124616-A1
    03-AUG-1999;
                                                  04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1999;
                                                                                                                                          Hamada K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404
NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
```

```
ö
                                                                                                                                                          an
                                                                                                                              The present invention relates to a method for producing male sterile plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                     284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacat 343
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                        Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- P35S
/function= 35S promoter of cauliflower mosaic virus
strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds.
                                                                                                                                                                                                                                                                                                     Length 7492;
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/label= barstar
/product= Bacillus amyloliquefaciens barstar
968..1287
/*tag= d
                                                                                                                                                                                                                                                Sequence 7492 BP; 1987 A; 1801 C; 1752 G; 1952 T; 0 other;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                               Score 188.8; DB 22;
Pred. No. 4.7e-30;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= pgEM2
/note= "polylinker of pGEM2"
                                                                                                  Disclosure; Page 19-23; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT39337/c
ID AAT39337 standard; DNA; 1303 BP.
                                                                                                                                                                                                                                                                                               1 45.5%;
Similarity 99.0%;
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/label= P3!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695..967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7306 ACATTGCCGTAG 7295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 acattgccgtag 415
Nakakido
                          WPI; 2001-266212/27
                                                                                                                                                                                                                                                                                                             Best Local Sim
Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
```

9

```
coding sequence
                                                                                                                                             Cornelissen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2001
                                                                                       17-APR-1991;
                  deletion; ss
                                                                                                         18-APR-1990;
                                                    WO9116432-A
                                                                      31-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                    Synthetic.
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                            346
                                                                                                                                                                                                                                                                                                                                                                                                                                                              406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH25423
  à
                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   region containing polyadenylation signal of gene 7 og Agrobacterium T-DNA
                                                                                                                                                                                                                                                         The HindIII-ECORI fragment (AAT39337) of plasmid pTS88 contains barstar DNA under control of a 355 promoter. The plasmid was used with pTS174 (see also AAT39336) contg. barnase DNA under control of the stamen-specific promoter El to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pVEI36 (see also AAT39338) contg. barnase DNA under control of the stamen-specific PCA55 promoter to produce male sterile maize plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible
                                                                                                                                                                                              Prodn. of male sterile plants by transforming with a chimaeric construct - comperising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 1303;
                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                           low level expression of barnase DNA in non-stamen tissue
                                                                                                                                                                                                                                                                                                                                                            Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      Score 188.4; DB
Pred. No. 5e-30;
0; Mismatches
                                   /*tag= e
/label= pGEM2
/note= "polylinker of pGEM2"
                                                                                                                                                             Ē
                                                                                                                                                             Michiels
                                                                                                                                                                                                                                           Example 1; Page 38; 56pp; English.
                                                                                                                                           GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                   ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pPS029 Bt ICP coding sequence
                                                                                                                                                             Cornelissen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ14529 standard; DNA; 3201
/label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                      45.4%;
ilarity 99.5%;
Conservative
                                                                                                                         95EP-0400364
                                                                                                        96WO-EP00722
         /function=
                          1288..1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGCCGTAG 1098
                                                                                                                                                                             WPI; 1996-402373/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attgccgtag
                                                                                                                                           (PLB2 ) PLANT
                                                                                                                                                             Botterman J,
                           misc_feature
                                                                                                        21-FEB-1996;
                                                                                                                         21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1992
                                                                                      29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ14529
                                                                                                                                                                                                                                                                                                                                                                                                                                                              286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1107
                                                                                                                                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ14529/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                          පි
                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EX DX SX S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
```

```
hybrid seed; male-sterility gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3021 ATTTATTGATGCAAGTTTAAATTCAGAAAATTTCAATAACTGATTATATATCAGCTGGTAC 2962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.4%; Score 188.4; DB 12; Length 3201; 99.5%; Pred. No. 5.3e-30; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "n" in the sequence refers to not known nucleotides. pPS029 is identical to pVE36 (AAQ15144), but carries both the terminal modification and the internal modification of the Bt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
Bacillus thuringiensis; insecticidal crystal protein; ICP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3201 BP; 880 A; 710 C; 720 G; 886 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Dockx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic plant; winter oilseed rape; fertility restorer gene; barstar gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of plasmid pTHW118.
                                                                                                                                                                                                                                                                                                                                                                                                                   Stam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 6(c); 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH25423 standard; DNA; 4832 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAQ14529, AAQ15142-44.
                                                                                                                                                                                                                                                                                                                                                                                                                   Soetaert P,
                                                                                                                                                                                                                                               91WO-EP00733
                                                                                                                                                                                                                                                                                                      90EP-0401055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces hygroscopicus.
Arabidopsis thaliana.
Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                             (PLAN-) PLANT GENETIC SYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11111111
2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-339820/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attgccgtag 415
```

ó

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                     AAT59531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3'UTR
                                                                                                                                                                                                                                                                                                                                                AAT59531
                                                                                                                                                                                                                                                                                                                                         RESULT
         õ
                                                                                                                                                                                                                           임
                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                             "right border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                            /note- "atSlA ribulose-1,5-biphosphate carboxylase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag- p
/note- "left border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                               /note= "Taq1 fragment from 3' UTR of nopaline synthase gene from T-DNA of pTiT37 and containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                  /*tag= 1
/note= "downstream of Bacillus amyloliquefaciens
barstar coding region"
complement (2981..3253)
                                                                                                                                                                                                                                                                                                                                                /*tag= m
/note= "Barstar gene coding region from Bacillus
amyloliquefaciens"
complement (3254..4762)
                                                                                                       /*tag= d
/note= "synthetic polylinker derived sequences"
complement (98..309)
                                                           /note= "synthetic polylinker derived sequences"
                                                                                  /note "residual sequence from TL-DNA at right border repeat"
                                                                                                                                                          /note= "synthetic polylinker derived sequences"
complement (331.882)
                                                                                                                                                                                                                              /note= "synthetic polylinker derived sequences"
complement (2659.2919)
                                                                                                                                                                                                                                                                                              *tag- k
/note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= 0
/note= "synthetic polylinker derived sequences"
1808..4832
                                                                                                                                     "3' UTR from TL-DNA gene 7 of pTiB6S3"
                                                                                                                                                                                /note= "Streptomyces hygroscopicus bialaphos resistance (bar) gene" complement (883.2608)
                                                                                                                                                                                                                                                                                                                                                                            /*tag= n
/note= "anther-specific gene TA29 promoter
Nicotiana tabacum"
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2000; 2000WO-EP12872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0457037
                                                                                                                                                                                                                            2609..2658
                                                                                                                                                                                                                                                                                       2920..2940
                                                                                                                                             310..330
                         1..25
/*tag=
                                                                  54..90
/*tag=
                                                    /*tag=
                                                                                                                              /*tag=
                                       /note=
                                                                                                                                                     /*tag=
                                                                                                                                                                           /*tag=
                                                                                                                                      /note-
                                                                                                 91..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-381419/40.
 Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                    40200141558-A1
                       misc_feature
                                              misc_feature
                                                                   misc_feature
                                                                                                misc_feature
                                                                                                                                            misc_feature
                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Both G,
                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                                     3'UTR
                                                                                                                                                                                                                                                 3'UTR
                                                                                                                                                                                                                                                                                                           3'UTR
                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                        CDS
```

```
ö
                                                                                                                                           The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. The present sequence represents plasmid primylls. This plasmid comprises the barstar gene, which acts as plants of the invention.
Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 agittaaatattattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP; niacinamide; Agrobacterium; T-DNA; male sterile; barnase; ribonuclease; RNase; cereal; wheat; oilseed rape; Brassica napus; plasmid pTHW107; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           °;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 4832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               '3' untranslated region contg. the poly-A signal of gene-7 of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 188.4; DB 2:
Pred. No. 5.5e-30;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/label= RB
/note= "T-DNA right border"
complement (97.330)
                                                                                           Example 1; Page 80-82; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers complement (1..25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT59531 standard; DNA; 4946 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Agrobacterium sp.;
Chimeric Arabidopsis thaliana;
Chimeric Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/label= 3'g7
/note= "3' unt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-DNA of plasmid pTHW107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 attgccgtag 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1997
```

Page 11

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid pTHW107 is a vector carrying T-DNA (AAT59531) comprising a barnase coding sequence under control of the tobacco TA29 gene stamen specific promoter and a phosphinothricin acetyltransferase coding sequence under control of an Atabidopsis Rubisco small subunit gene promoter. Oilseed rape hypocotyl explants were subunit gene promoter. Oilseed rape hypocotyl explants were infected with Agrobacterium tumefaciens CSBCIRif carrying vector PTW107 and helper Ti plasmid pMP60. In some treatments, the hypocotyls were treated with the poly-(ADF-ribose) polymerase inhibitor niacinamide (250 mg/l) 4 days prior to infection. Plants regenerated from miacinamide-treated transformed calli had a low copy number and displayed less variation in the expression profile of the transgenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and reduces metabolism
                                                                                                        promoter region of Rubisco small subunit
                                                                                                                                                                             Anotes "3' untranslated region contg. the poly-A signal of the nopaline-synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.4%; Score 188.4; DB 18; Length 4946; 99.5%; Pred. No. 5.5e-30; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                    /note= "promoter region of tobacco TA29 gene" complement (4822..4946)
                                        /product- phosphinothricin acetyltransferase
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;
                                                                                                                      gene of Arabidopsis thaliana complement (2658..3031)
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "T-DNA left border"
                                                                                                                                                                                                                              complement (3032..3367)
                                                                                                                                                                                                                                                                                          complement (3368..4876)
 complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 13-16; 25pp; English.
                                                                                                                                                                                                                                                                             'product- barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                            /label= Barnase
                                                                                                                                                                       nos
                                                                                                                                                                                                                                                                                                                        /label= PTA29
                                                                                         PSSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95EP-0401844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95EP-0401844.
                                                                                                                                                     /*tag= e
/label= 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 189; Conservative
                                                                                         /label=
                                                                                                        /note= "
                                                                                                                                                                                                                                                                                                                                                                                  /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-111050/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                              EP757102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Block M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                           promoter
                                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                    misc_RNA
                                                                                                                                    3'UTR
                                                                                                                                                                                                                              CDS
```

g ç

286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa 345

Search completed: February 25, 2002, 18:17:34 Job time: 16692 sec

•

```
(without alignments)
311.633 Million cell updates/sec
                                                                                                                        February 25, 2002, 18:05:16; Search time 301.6 Seconds
                                                                                                                                                                                                                                                 1 gtcgagtttggtgttcatga......cagctggtacattgccgtag
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        351203 seqs, 113238999 residues

    nucleic search, using sw model

                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                                                                                                         US-09-698-903B-8
                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                 OM nucleic
                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                        Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* 5 5 .. .

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*

Database

Sequence 3, Appli Sequence 2, Appli Sequence 5, Appli Sequence 4, Appli Patent No. 5428147 Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 23, Appl Sequence 1, Appli Sequence 1, Appli Sequence 23, Appli Sequence 24, Appli Sequence 22, Appli Sequence 22, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 4, Appl: Description US-08-549-680A-5 US-08-894-440-2 US-08-894-840-2 US-08-694-824-23 US-08-817-1188-1 US-08-817-1188-5 US-08-232-016-22 US-08-232-016-22 US-08-453-104-22 US-08-453-104-22 US-08-478-015-2 US-08-478-015-2 US-08-478-015-2 US-09-084-889-2 US-09-080-625-3 US-09-080-625-5 US-09-080-625-5 US-09-080-625-4 5428147-1 US-08-920-812-6 US-08-921-1177-6 US-08-921-1177-6 SUMMARIES DB Length Query Match 1 Score 191.4 188.8 188.8 188.8 188.4 188.4 188.4 188.4 188.4 188.4 188.4 188.4 188.4 188.4 177 153 153 153 146 Result Š. 0000000000 000 000

NAME/KEY: misc_feature LOCATION: Complement((98)..(330)) OTHER INFORMATION: region containing polyadenylation signal of gene 7 OTHER INFORMATION: of Agrobacterium T-DNA (3'97)

NAME/KEY: misc_feature LOCATION: Complement((331)..(882)) OTHER INFORMATION: region coding for phosphinothricin acetyl OTHER INFORMATION: transferase (bar)

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTCO113 FEATURE:

NAME/KEY: misc_feature LOCATION: Complement((1)..(25)) OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)

OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA OTHER INFORMATION: (3'nos)

misc_feature
Complement((2659)..(3031))

NAME/KEY: I

FEATURE

FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
FEATURE:

Rubisco of

οţ

FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene
OTHER INFORMATION: Arabidopsis (Pssu)

		28	44	œ	10.	8	8654	7	US-08-920-828-6	
	ບ	29	44	9	10.	۲.	5526	m	US-08-751-359-21	Seguence 21, Appl
		30	43.	9	10.	Ŋ	19124	~	US-08-487-826B-13	13,
	υ	31	4	2	50.	4	19124	7	US-08-487-826B-13	13,
		32	42.	9	10.	٣	8920	7	US-08-446-855A-1	1,
		33	42.	9	10.	٣	8920	4	US-09-150-741-1	1,
	υ	34	42	2	10.1	٦.	1316	7	US-08-871-924A-1	~
	ပ	35	40.	4	ó	7	1588	m	US-09-058-489-45	45,
		36	39.	80	o,	٥	15397	~	US-08-673-768-1	٦,
	υ	37	39.	8.	ď	و	15397	N	US-08-673-768-1	-
	υ	38	39.	80	ó	ڡ	24595	9	5428147-1	
	υ	39	39.	4.	9	Z,	80595	4	US-09-078-294-3	m
	υ	40	39	~	9	4	658	4	US-08-998-416-595	
	O	41	38.	8	6	٣	636	4	US-08-998-416-1137	
		42	38	œ	6	m	660	-	US-07-991-867B-32	
		43	38	8	6	· ~	099	-	US-08-107-755A-32	
		77	0 00	ο α	. σ	~	999	۱ ۵	IIS-08-544-332-32	
			9 0				1511	- ۱	TG-07-001-0675-0	
		.			'n	,	TTCT	4	-9/00-T66-/0-	
дВкки	RESULT US-08- ; Sequ ; Pate ; GENE	RESULT 1 US-08-894-440-4/c ; Sequence 4, Applicat Patent No. 6025546 ; GENERAL INFORMATION:	-44(0 4,	0-4/ API 602:	c plic 5546	sati	A. SULT 1 1 -4/c Sequence 4, Application US/08894440 GENERAL INFORMATION:	088	ALIGNMENTS 94440	
•		APPLICA	INT	PL	EV.	GE?	NETIC S	YST		
		TITLE OF INVENTION: Me)F]	INVE	NITIO	è	Method	t C	TITLE OF INVENTION: Method to obtain male sterile plants	nts
•	4 (TIPPENT	3 2	100		í i	NITMORE	:	FILE REFERENCE: NMSCON	
	ے ر	TIRRENT	<u> </u>	Ž	בול בי	Z E	1997 -	1.	3/08/034,440	
	, 24	UMBER	9	SEO	ដូ	Š	NUMBER OF SEO ID NOS: 4	1	3	
		SOFTWARE:	Œ:	Pate	ent]	-	Patentin Ver. 2.	0		
	SE	SEQ ID NO	Š 4	_						
•		LENGTH:		5864						
••		TYPE: DNA	DN2	_						
•		ORGANI	(SM:	Ari	tifi	cia	ORGANISM: Artificial Sequence	enc	v	
		FEATURE:	Œ:	E:	F		1	1		

```
404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-817-188-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
UCCATION: Complement((3368)..(4877))

COTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana OTHER INFORMATION: tabacum (PTA29)

FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: promoter of nopaline synthase gene of OTHER INFORMATION: promoter of nopaline synthase gene of OTHER INFORMATION: promoter of nopaline synthase gene of STEATURE:
NAME/KEY: misc_feature
COCATION: (5217)..(5489)

OTHER INFORMATION: region coding for barstar of Bacillus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5490)..(5765)

OTHER INFORMATION: region containing polyadenylation signal of gene 7
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5490)..(5765)

OTHER INFORMATION: of Agrobacterium T-DNA (3/97)

FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((5840)..(5864))

OTHER INFORMATION: left border of Agrobacterium T-DNA
US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5752 TATAGTTTAATGTTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAAAA 5693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5692 TABATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGG 5633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 gatgiacaiggccgataagaaaggcaattigiagaigttaattcccatcttgaaagaaa 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1).(2003)
OTHER INFORMATION: pucl derived vector sequences (vector)
FEATURE:
LOCATION: complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tatagtttaaatatttattgataaaataacaagtcaggtattatagtccagcaaaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 taaatttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08894440
| Patent No. 6025546
| GENERAL INFORMATION:
| APPLICANT: PLANT GENETIC SYSTEMS N.V.
| TITLE OF INVENTION: Method to obtain male sterile plants
| FILE REFERENCE: NMSCOR
| CURRENT APPLICATION NUMBER: US/08/894,440
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO: 1 | LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.1%; Score 191.4; DB 3; Length 192.5%; Pred. No. 2.7e-37; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5632 TACATTGCCGTAG 5620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 192; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-08-894-440-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ದ್ದ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
6423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6422 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGGT 6363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: plasmid PTS172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
MAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El gene of rice OTHER INFORMATION: (PEI)
NAME/KEY: misc_feature
NAME/KEY: misc_feature
NAME/KEY: misc_feature
OCHER INFORMATION: (5710)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 aaatttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
CURRENT APPLICATION UNBER: US/08/817,188
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER PTLING DATE: 1996-07-31
EARLIER PTLING DATE: 1996-08-04
NUMBER OF SEQ ID NOS: 20
SEG ID 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
COCATION: (5711)..(6262)
COTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (6205)..(6496)
COTHER INFORMATION: region containing polyadenylation signal fo (US-08-094-440-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6548;
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                 FEATURE:
NAME/KRY: misc_feature
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 188.8; DB 3;
Pred. No. 1.1e-36;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08817188 Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.5%;
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
```

```
NAME/KEY: misc_feature
LOCATION: 484..684
OCHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
                              PatentIn Release #1.0, Verson #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 188.8; DB 2;
Pred. No. 1.2e-36;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 194..218
OTHER INFORMATION: /note= "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: complement (729..1340)
OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

COCATION: 3001..3023

OTHER INFORMATION: /note= "T-DNA left border

US-08-549-680A-5

US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_recomb
LOCATION: 1..7811
OTHER INFORMATION: /label- vector pTRVA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: promoter
LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
                         SOFTWARE: Patentin Release #1.0, Versigner APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 16 JANUARY 1996
CLASSIFICATION: 800
ATTONEY, AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 3121-0111P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELERX: (703) 205-8050
TELERX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618 ACATTGCCGTAG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEATURE:
NAMEKREY misc_feature
NAMEKREY misc_feature
CATION: (6263)..(6496)
COTHER INFORMATION: 3'47: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
US-08-817-188-2
                            untranslated region containing the ation signal of the nopaline synthase
                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (4336)..(5170)
OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
OTHER INFORMATION: Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement(5711)...(6262))
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
LOCATION: Complement((2019)..(2288))
OTHER INFORMATION: 3' nos: 3' untranslated region contain
OTHER INFORMATION: 3' nos: 3' untranslated region contain
OTHER INFORMATION: polyadenylation signal of the nopaline
OTHER INFORMATION: gene of Agrobacterium T-DNA.
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2289)..(2624))
OTHER INFORMATION: barnase: region cding for barnase
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: PEl: promoter region of El gene of ric-
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%; Score 188.8; DB 3 99.0%; Pred. No. 1.1e-36; Live 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: CORNELISSEN, MARCUS
APPLICANT: REYNAERTS, ARLETTE
APPLICANT: GOSSELE, VERONIQUE
APPLICANT: VAN AARSSEN ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08549680A Patent No. 5962768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.0 Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

ö Gaps 284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacat 498 ATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAAACAT ö Length 7811; Indels

4

```
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
TUBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
45.4%; Score 188.4; DB 1;
Best Local Similarity 99.5%; Pred. No. 1.3e-36;
Matches 189; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFTCATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 010830-032
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEO ID NO: 23.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                        STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                  CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11111111
2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 attgccgtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                 PERTURE:
OTHER INFORMATION: bescription of Artificial Sequence: HindIII-ECORI
OTHER INFORMATION: fragment of pTS88
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
FEATURE:
NAME/KEX: misc_feature
LOCATION: (36)..(694)
OTHER INFORMATION: Dolylinker of Cauliflower Mosaic Virus strain
OTHER INFORMATION: (365)..(694)
OTHER INFORMATION: (365)..(697)
OTHER INFORMATION: CAPION
OTHER INFORMATION: region coding for barstar of Bacillus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (365)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
FEATURE:
NAME/KEY: misc_feature
LOCATION: (369)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
FEATURE:
NAME/KEY: misc_feature
LOCATION: (368)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
FEATURE:
NAME/KEY: misc_feature
LOCATION: (368)..(1387)
OTHER INFORMATION: pelylinker of pGEM2
UCAFION: (1288)..(1383)
CHER INFORMATION: polylinker of pGEM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 gtacatggccgataagaaaggcaatttgtagatgttaattcccatcttgaaggaaatat 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 agtttamatatttattgatamaatamcaagtcaggtattatagtccaagcamaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 188.4; DB 3; Length 1303;
Pred. No. 1.1e-36;
0; Mismatches 1; Indels 0;
                                                                GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
LENGTH: 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08453104
Patent No. 5633446
GENERAL INFORMATION:
APPLICANT: CORNELISSEN, MAIC
APPLICANT: SCETARRY, Plet
APPLICANT: STAM, MAIKe
                        Sequence 2, Application US/0889440 Patent No. 6025546
                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1107 ATTGCCGTAG 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 attgccgtag 415
US-08-894-440-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-453-104-23/c
                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-08-694-824-23/C
; Sequence 23, Application US/08694824
; Patent No. 5877306
```

Ŋ

```
LOCATION: Complement((97)...(330))
OTHER INFORMATION: 3/97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                             GENERAL INVOICES, MARC

TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: POT/EP96/03366
EARLIER PILING DATE: 1996-07-31
EARLIER PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter region of Rubisco small subunit gene of
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: Complement([3368]..(4876))
OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotlana
OTHER INFORMATION: tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: Complement((2658)..(3031))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: bar: region coding for phosphinotricin acetyl
OTHER INFORMATION: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%; Score 188.4; DB 3; Length 4946; 99.5%; Pred. No. 1.4e-36; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; LOCATTON: Complement((4922)..(4946))
; OTHER INFORMATION: LB: T-DNA left border
US-08-817-188-1
                                                                Sequence 1, Application US/08817188 Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: Complement((3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Sim
Matches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                APPLICANT: CORRELISSEN, MAIC
APPLICANT: SOBTABER; Piet
APPLICANT: STAM, MAIK
APPLICANT: STAM, MAIK
APPLICANT: STAM, MAIK
APPLICANT: STAM, MAIK
APPLICANT: SOBTABER; Piet
APPLICANT: SOBTABER; Piet
APPLICANT: SOBTABER;
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
TITLE OF INVENTION: IN PLANT CELLS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia
COUNTRY: United States
STREET: Virginia
COUNTRY: United States
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMM FC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
CLASSIFICATION NUMBER: DATE-ING DATE: DATE-ING DATE-ING DATE: DATE-ING DATE-IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 2078.2082
OTHER INFORMATION: /note= "Nucleotides 2078-2082
OTHER INFORMATION: wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.4%; Score 188.4; DB 2
99.5%; Pred. No. 1.3e-36;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 836-6620
TELEFAX: (703) 886-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 3200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rea, Teresa S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 attgccgtag 415
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
```

Tue Feb 26

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa 345
                       FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW142
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1). (25)
OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCHERINFORMATION: 3' untranslated region of the CaMV 35S transcript
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DE BLOCK MARC
TITLE OF INVORVATION:
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT APPLICATION NUMBER: PS-15
EARLIER APPLICATION NUMBER: PS-15
EARLIER APPLICATION NUMBER: PS-105-03-04
EARLIER FILING DATE: 1995-06-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5
LENGTH: 5560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
CACTION: (84)..(296).
OTHER INFORMATION: 3' 97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the second intron of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU: promoter region of Rubisco small subunit
OTHER INFORMATION: gene of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (3059)..(5056)
OTHER INFORMATION: uidA: region coding for beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (318)..(869)
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (4483)...(4671)
OTHER INFORMATION: IV2: region corresponding
OTHER INFORMATION: the ST-LS1 gene
FRATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08817188 Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (4483)..(467
                                                                                                                                                                                                   234 attgccgtag 243
                                                                                                                                                              406 attgccgtag 415
                                                                                                                                                                                                                                                                                  US-08-817-188-5
                                      8
                                                                                                                   a
  à
                                                                               ò
                                                                                                                                                            à
                                                                                                                                                                                                 셤
```

```
ô
                                                       NAME/KEY: misc_feature
LOCATION: (5533)..(5560)
GTHER INFORMATION: LB: left border sequence of octopine TL-DNA from OTHER INFORMATION: pTIB6S3
FEATURE:
FRATURE:
LOCATION: (5058)..(5059)
GOTHER INFORMATION: region with unknown sequence (may contain up to 20 OTHER INFORMATION: nucleotides)
FRATURE:
NAME/KEY: misc_feature
LOCATION: (5077)..(5078)
GOTHER INFORMATION: region with unknown sequence (may contain up to 20 OTHER INFORMATION: region with unknown sequence (may contain up to 20 OTHER INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ç
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
CCATION: (5476)..(5479)
CTHER INFORMATION: region with unknown sequence (may contain up
US-08-817-188-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08232016
Patent No. 5952547
GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAER, Plet
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: VAN AALSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
BUTTS, DOANE, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
ION: (5067)..(5502)
INFORMATION: P35S: 35S promoter region of CaMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
45.4%; Score 188.4; DB 3;
Best Local Similarity 99.5%; Pred. No. 1.4e-36;
Matches 189; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
CITY: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 attgccgtag 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-232-016-23/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
```

us-09-698-903b-8.rni

```
LOCATION: 1.1869
OTHER INFORMATION: /note= "Coding region of a
OTHER INFORMATION: truncated bt2 (cryIAb) gene, also designated as the bt884
                                                                              346 atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                     286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOFTAER, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: VAN ARSSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
COUGRE: COURCE:
ORGANISM: plasmid DNA designated as pJD884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STRATE: Virginia
CCUNTRY: Uniqinia
ZIP: 222313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 7639 base pairs
LENGTH: 7639 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
CLASSIPECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ER 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/08232016
Patent No. 5952547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                 1890 ATTGCCGTAG 1881
                                                                                                                                                                                                                                                406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-232-016-22/c
                                                                                                                                                                                              q
                                                                                                                                                                                                                                                δ
                                                     ò
                                                                                                  a
                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 3582..4407
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.1785

VOTER INFORMATION: /note= "Coding region of a OTHER INFORMATION: truncated modified bt2 (cryIAb) gene, also designated as the OTHER INFORMATION: cryIAb6 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 5600_.6457
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 2396..2921
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.4%; Score 188.4; DB 2; Best Local Similarity 99.5%; Pred. No. 1.5e-36; Matches 189; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: plasmid DNA designated as pPS0212
               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION DATA:
PAPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K
REGISTRATION NUMBER: p39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7566 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
03-NOV-1994
V: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 5600..6457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION:
US-08-232-016-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
```

NAME/KEY: misc_feature

ò

```
NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: tabacum (FTA29)
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 agittaaatatitatigataaaataacaagicaggiatiatagiccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 atttattgatgcaagtttaaattcagaaatatttcaataactgattatcagctggtac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (5490)...(5765)
OTHER INFORMATION: region containing polyadenylation signal of gene
FEATURE: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: Complement((2659)...(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3) noa)
                                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 5864;
                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         barnase of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                  LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : LOCATION: Complement((5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.0%; Score 186.8; DB 3
Best Local Similarity 98.9%; Pred. No. 3.4e-36;
Matches 188; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for
OTHER INFORMATION: amyloliquefacters
                  INFORMATION: plasmid pTC0113
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: Complement(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ģ
              OTHER INFORMATION: /note- "3' regulatory sequence OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                         NAME.KEY: misc_feature
LOCATION: 3666.4491
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2154 GTACATGGTCGATAAGAAAAGGCAATTTGTAGATGTTAATTCCCATCTTGAAGAAAATT 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2094 AGTTTAAATATTTTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2034 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 attiatigatgcaagittaaattcagaaatatttcaataacigattatatcagciggiac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 3006..3665
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
                                                                                                                          LOCATION: 2480.3005
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derlyed from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.4%; Score 188.4; DB 2; Length 7639;
99.5%; Pred. No. 1.5e-36;
Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08894440

Batent No. 6025546
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARFE PARENT VET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 5684..6541
OTHER INFORMATION: /note= "Sequence complementary it No. 5952547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                       NAME/KEY: misc_feature
LOCATION: 2480..3005
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.5
Matches 189; Conservative
1877..2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1974 ATTGCCGTAG 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
LENGTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
APPLICANT: CORNELISEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: SOETAERT, Piet
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: SOETAERT, Piet
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: BUTNS, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                            3081 AGTITAAATTCAGAAATATTCAATAACTGATTATATCAGCTGGTACATTGCCGTAG 3025
    359 agtttaaattcagaaatatttcaataactgattatatcagctggtacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.7%; Score 177; DB 2; I
Best Local Similarity 100.0%; Pred. No. 6.5e-34;
Matches 177; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-620
TELEFAX: (703) 836-5201
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                 Sequence 22, Application US/08694824; Patent No. 5877306; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Rea, Teresa S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                           RESULT 14
US-08-694-824-22/c
                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                           APPLICANT: SOFTABET: The APPLICANT: STAM, Maike APPLICANT: STAM, MOIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
STREED: Burns, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

| CCATION: 2151..2155

| OTHER INFORMATION: /note= "Nucleotides 2151-2155

| OTHER INFORMATION: wherein N is not known."

US-08-453-104-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.7%; Score 177; DB 1;
100.0%; Pred. No. 6.5e-34;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY AGGNT INFORMATION:
NAME: Rea, Teresa S
REGISTATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              Sequence 22, Application US/08453104
Patent No. 5633446
GENERAL INFORMATION:
                                                                                                                                                                                                                CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.7
Best Local Similarity 100.
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
406 attgccgtag 415
                                         234 attgccgtag 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                             US-08-453-104-22/C
                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
  à
                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
```

ö

õ

```
NAME/KEY: -
LOCATION: 791..1186
OTHER INFORMATION: /label= 3'g7
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                              RESULT 15
US-08-064-121-2/C
Sequence 2, Application US/08064121
Sequence 2, Application US/08064121
Setent No. 5641664
GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
CORRESPONDENCE 3, S
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
STREET: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEMPY disk
COMPUTER: TBM PC Compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,121
CLASSIFICATION DATA:
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION DATE: 23-NOV-1990
PRIOR APPLICATION DATE:
APPLICATION DATE: BP 91401888.2
FILING DATE: 08-JUL-1991
ATONNEY/AGENT INFORMATION:
NAME: CALLOS: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: -
LOCATION: 1.8
OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: - - COCATION: 9.790 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
FEATURE:
        ò
```

```
ö
                                                                     Gaps
                                                            .;
0
                                          Length 1186;
                                                          Indels
                                  Query Match
36.9%; Score 153; DB 1; I
Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 153; Conservative 0; Mismatches 0;
                                                                                                                                             Search completed: February 25, 2002, 18:05:27 Job time: 18575 sec
; OTHER INFORMATION: T-DNA gene 7" US-08-064-121-2
                                                                      ŏ
                                                                                       qq
                                                                                                        ò
                                                                                                                           g
                                                                                                                                              à
```

THIS PAGE BLANK (USPTO)

Drosophi] Drosoph1]

AL105023 I AL098595 I AL106896 I AL099163 I

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Maximum

Database

```
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 734)

2 (anoscope.

2 Direct Submission

3 Direct Submission

3 Direct Submission

4 Direct Submission

5 Direct Submission

6 Direct Submission

7 Web: www.genoscope.cns.fr)

8 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence T7 end of BAC BACN04L20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL099163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fruit fly.
Plasmid Drosophila melanogaster
                        CONSO182A
CONSO155H
CONSO1616X
CONSO10MP
CONSO10MP
CONSO1990
CONSO1800
CONSO
                                                                                                                                                                                                                                                                                                                                                                                            AQ326762
BH126604
CNS014PQ
                                                                                                                                                                                                                                                                                                  AL566565
CNS00CYH
                                                                                                                                                                                                                                                                                                                                                      CNS003BB
CNS016C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL099163.1 GI:5610774
 734 bp
                                                                                                                                                                                                                                                            1001
1101
854
963
1101
11101
1200
681
563
788
987
678
pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS010MP
                                                                         500.0
500.6
500.6
500.6
500.6
500.6
500.6
            53.4
53.2
53.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
CNS010MP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
LOCUS
                                                                             υυ
                                                                                                                                                                                                                                                 O
                                                                                                                                                                                                                                                              U
                                                                                                                                                                                                                                                                                            υυ
                                                                                                                                                                                                                                                                                                                                         O
                                                                                                                                                                                                                                                                                                                                                                                  0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL055440 Drosophil
AL238491 Tetraodon
AL03832 Drosophil
AL106896 Drosophil
AL106896 Drosophil
AL04456 Drosophil
AL064091 Drosophil
AL065706 Drosophil
AL065706 Drosophil
AL063706 Drosophil
                                                                                                   (without alignments)
539.777 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL099163 Drosophil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    February 25, 2002, 17:21:04; Search time 8261.74 Seconds
                                                                                                                                                                   415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                  1 gtcgagttttggtgttcatga......cagctggtacattgccgtag
                                                                                                                                                                                                                                                            22703874
                        Compugen Ltd
                                                                                                                                                                                                                                11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNSO0238
CNSO16LI
AQ506817
CNSO14PQ
CNSO03BD
                                                             nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNS004 ZW
CNS03D01
CNS000B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS010MP
                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_gss_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_est2:*
gb_htc:*
gb_gss:*
em_gss_fun:*
                                                                                                                                        US-09-698-903B-8
415
                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_gss_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_gss_inv:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_gss_pro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_gss_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_estfun:*
em_esthum:*
em_estin:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_gss_vrt
                                                                                                                                                                                                                                                                                                                                                                                                                               em_estom: *
em_estpl: *
em_estba: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_estov:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11101
844
11101
1101
1101
537
987
1101
1101
893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_htc:*
                                                                                                                                                                                                                                                                                                                                                                                EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.2
13.8
13.8
113.8
113.3
113.2
113.2
113.2
113.2
```

26-JUL-1999

/organism="Drosophila melanogaster" /plasmid="pBeloBAC11" /db_xxef="faxon:7227" /clone_lib="DrosBAC" /clone="BACN04L20"

Location/Qualifiers

source

CNS00JG1 CNS00EVL CNS013XE

000000

Score

Š

FEATURES

AL075824 Drosophil AL065493 Drosophil AL167541 Tetraodon AL172458 Tetraodon AL071865 Drosophil AL070972 Drosophil AL070972 Drosophil AL067940 Drosophil AL0637529 Drosophil AL0637529 Drosophil AL069706 Drosophil AL069706 Drosophil AL065706 Drosophil AL060100 Drosophil AL06100 Drosophil AL064089 Drosophil AL106578 Drosophil AL106568 Drosophil

38.88;

~

```
Conservative
              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sedneuce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNS03D0I/c
                                    Matches
                                                                                 14
                                                                                                                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                         δ
                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submitseion

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EYNZ cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA, provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Quallifiers

| Content of the Content of Content Cancer Cancer
                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO042W 1101 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR11E08 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                      189 aagtattatataattataattataattatggtaggatgtacatggccgataagaaaggc 248
                                                                                                                                                                                                                                                                                               249 mattigtagaigitaaticccaicitigaaagaaataiagittaaatattiitigataaaa 308
                                                                                                                                                                                                                               taacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaaatt 368
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophija melanogaster
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota: Neoptera: Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                    ö
                                                                                                                     Length 734;
                           171 others
                                                                                                                ; Score 63; DB 13; Length 73; Pred. No. 0.0079; 43; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism~"Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
                           u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ų
                           211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 cagaaatattcaataactgattatat 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 AWAMAATATWWMAAAAAWWWWWWWTAT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="RPCI-98"
                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 g
                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="BACR11E08"
: T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="end : T7"
                                                                                                         Query Match
Best Local Similarity 41.1%;
Matches 85; Conservative 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL055440.1 GI:4932241
  /note="end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.78;
                        62 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
CNS004ZW/C
                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                          309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

Length 1101;

DB 13;

61;

Score

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNSO3DOI 844 bp DNA GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
015L14 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 844)

2 (boset-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 844)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat analysis of the compact genome of the
                                                                                                 tatacaaatagtagcgaagaaatccatgtaaagcagcagggggacaccatggtttcaagta 193
                                                                                                                                                                                                                                                                                                             ttcatgattttgggttttgactcttcaccattacatattgaaactcttacggatgagaac 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                      AAAAYAWAAATAWTTTTTAWTAWATATAAATWTWWAWTTAWWTTTTTATWWATATAWA
                                                                                                                                                                                                                                                                                                                                                                              ttatataattat-aattataattatggtaggatgtacatggccgataagaaaaggcaatt
                                                                                                                                                                                                                                                                                                                                                                                                              313 aagtcaggtattatagtccaagcaaaacataaatttattgatgcaagtttaaattcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
Pred. No. 0.018;
; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL238491.1 GI:7897626
GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 aatatttcaataactgattatatc 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charaterization and re
freshwater pufferfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
```

m

```
Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS00Z38
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
CNSO0Z38/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                    163
                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web: www.genoscope.cns.fr

Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffallo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2s on bw sp, the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence TET3 end of BAC # BACROLA24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL063632 GI:4938680
                                                                                                                                                                                                           56 actettacggatgagaacaacteacaageattaateatgtteatataaatatatgtacat 115
                                                                                                                                                                                                                                                                               tatacgtatatatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggg 175
                                                                                                                                                                                                                                                                                                                                              176 gcaccatggtttcaagtattatatatatatataattataattatggtaggatgtacatggcc 235
                                                                                                                                                                                                                                                                                                                                                                              295
                                                                                                                                                                                                                                                                                                                                                                                                                                       296 tttattgataaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgat 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pteryyota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
/clone_11b="G"
/clone_11b="G"
/note="Genoscope sequence ID : COBG015DF07SP1-end
                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                        40 others
                                                                                                                                                                           Indels
                                                                                                                                        Score 57.2; DB 13;
Pred. No. 0.099;
6; Mismatches 169;
                                                                        ų
                                                                        484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 gcaagtttaaattcagaaatatttcaataa 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            б
                                                                        89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fruit fly.
Drosophila melanogaster
                                                                                                                                      Query Match 13.8%;
Best Local Similarity 47.0%;
Matches 155; Conservative
                                                                        79 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                     PUC-Ori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                           487
                                                                                                                                                                                                                                                                               116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS000B8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@enoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Hummain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN01A24 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL097166.1 GI:5608777
                                                                                                                                                                                                                                                                                                                                                849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 attacatattgaaactcttacggatgagaacaactcacaagcattaatcatgttcatata 102
                                                                                                                                                                                                                                                                                                                                                                                            aatatatgtacattatacgtatatacacgtatacaaatagtagcgaagaaatccatgt 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tatagtttaaat---atttattgataaaataacaagtcaggtattatagtccaagcaaaa 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Arthrópoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                    Length 1101;
                                                                                                                                    others
                                                                                                                                                                                                                                                              Indels
                              melanogaster"
                                                                                                                                    137
                                                                                                                                                                                                                        0.094;
                                                                                                                                                                                                                      DB 13;
                                                                                                                                    u
                                                                                                                                                                                                                    Score 57.2; D
Pred. No. 0.09
56; Mismatches
                                                                                                                                    512
1. .1101
/organism="Drosophila m./db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR01A24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fruit fly.
Plasmid Drosophila melanogaster
                                                                                                            : TET3"
110 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                      13.8%;
39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1101 bp
                                                                                                            /note="end
                                                                                                                                    114 c
                                                                                                                                                                                                                                               Best Local Similarity 39.5
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 tggtacattgcc 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTAWATTHCM 717
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DBeloBAC11
```

4

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
           96;
                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
AQ506817/c
                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                      à
                                                           g
                                                                                         à
                                                                                                                g
                                                                                                                                            à
                                                                                                                                                                    g
                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.ons.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · This Drosophila melanogaster BAC library (Dross BAC) was made by Alain Billaud at CEPH (Centre project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence T7 end of BAC BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit AL106896
                                                                                                                                                                                     186 ttcaagtattatataaattataattatagtaggatgtacatggccgataagaaaa 245
                                                                                                                                                                                                                                                           979
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                  aaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaa
                                                                                                                                                                   ő
                                                                                                                                         Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 1101;
                                                                                     others
                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                others
     melanogaster"
                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/plasmid="bBeloBAC11"
/db_xref="taxon:7227"
/clone_llb="brosBAC"
/clone="BACN16D22"
                                                                                                                                  ; Score 57.2; DB 13;
; Pred. No. 0.094;
38; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436
                                                                                   ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.4; DB
No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ų
                                                                                   386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
/organism="Drosophila m
/plasmid="pBeloBACII"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN01A24"
                                                                                                                                                                                                                                                                                                                                                  366 attcagamatatttcaataactgattatat 395
                                                                                                                                                                                                                                                                                                                                                                    *: | : : | | | : : : : : : : | | | | : : | WIWWITWITTITMMMHHHHAYTAWAWT 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                162 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score Pred. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 g
                                                                 /note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL106896.1 GI:5624374
                                                                                                                                    th 13.8%; Similarity 41.4%; 87; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                               1101 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.3%;
                                                                                152 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 c
                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS016LI
                                                                                308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
                                                                                                                                  Query Match
                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                             CNS016LI/c
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                             306
                                                                                                                                                                                                                                                                                                                                                                             828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                             8
                                                                                                                                                                                       à
                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                  음
                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                  à
```

Best Local Similarity

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUJUDELY 537 bp DNA GSS 29-APR-1999
RPCI-11-281J17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-281J17
AUS Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building Chipublished (1997)

Other_GSSS: RPCI-11-281J17.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                     43 attacatattgaaactcttacggatgagaacaactcacaagcattaatcatgttcatata 102
                                                                                                                           103 aatatatgtacattatacgtatatatacacgtatacaaatagtagcgaagaagta
                                                                                                                                                                                                                                            /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                              283 tatagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaaca 342
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                              163 aaagcagcagggggaaccatggtttcaagtattatataattataattataatta
                                                                                                                                                                                                                                                                                                                                            ö
    Indels
  138;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .537
/organism="Homo sapiens"
/db_xref="GDB:7607752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="RPCI-11-281J17"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ506817.1 GI:4711564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hbe@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 537)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 taaatttattgat 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          750 ATMAATTTTTWT 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sed primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
```

```
Library Submission of the Sequence of Sequences of Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoryo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcokI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://pacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS003BD 1101 bp DNA GSS vs control Drosophila melanogaster genome survey sequence TET3 end of BAC #
                                                                                                                                                                                                                                                                                                                                     243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363
                                                                                                                                                       64 ggatgagaacaactcacaagcattaatcatgttcatataaaatatatgtacattatacgta 123
                                                                                                                                                                                                                                             124 tatatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggggcaccatg 183
                                                                                                                                                                                                                                                                                    710 ТИТТТТТТТТТТАВМАВАВМАВАВМАВАВМТИТТАВМИТТТАВАВСАВАВИТАТТАВА 769
                                                                                                                                                                                                                                                                                                                                                                               829
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                               gagtttggtgttcatgattttgggttttgactcttcaccattacatattgaaactcttac
                                                                                                          590 RRBKKBNKKKKKKKKKTKTTTTTKAYMWCTBKCCCCCCCCCCCCMMAMAMAMAAMA
                                                                                                                                                                                                650 AWWACWAAAATTAGAATAAAAAWAWAAAAAAAAAAAATAAWTATWWAWNTWYTWWWW
                                                                                                                                                                                                                                                                                                                                   184 gtttcaagtattatataattataattataattatggtaggatgtacatggccgataagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 taaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             890 имаааамаишимокаамоишишимиштаамаааааааааааааамишиши
                         ö
                       103; Conservative 100; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xxef="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BACROBKO8"
    0.27
    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DACKUBEOR OF RPCI-98 library f. fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaattcagaaatatttcaataactg 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      950 WWWWTTTTTTTTTKAWKTTKNKG 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL064091.1 GI:4941847
  26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope.
Direct Submission
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS003BD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                          8
                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                             유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                       ŏ
                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk ... This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNSO14PQ 987 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN12P22 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL104456
AL104456.1 GI:5616067
                                                                                                                                                       tacatattgaaactcttacggatgagaacaactcacaagcattaatcatgttcatataaa 104
                                                                                                                                                                                                                                          tatatgtacat-tatacgtatatatacacgtatacaaatagtagcgaagaaatccatgta 163
                                                                                                                                                                                                                                                                                  aagcagcagggggcaccat---ggtttcaagtattatatatattataattataggt 220
                                                                                                                                                                                                                                                                                                                                                                                                                         aggatgtacatggccgataagaaaaggcaatttgtagatgttaattcccatcttgaaaga 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                     aatatagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaa 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                              TATATATATATATATATATATATATATACATATATAAATATATATATATATATATATATATATAAA 394
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthrópoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cataaatttattgatgcaagtttaaattcagaaatatttcaataactgattatat 395
                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 others
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                                                                                                          0; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                 DB 13;
                                                                                        0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.8;
                                                                 Score 55;
                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="DrosBAC"
/clone="BACN12P22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : SP6
                                                              13.3%;
51.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="end
                                                            Ouery Match 13.3°
Best Local Similarity 51.0
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1, .987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNT
                                                                                                                                                    45
                                                                                                                                                                                              453
                                                                                                                                                                                                                                          105
                                                                                                                                                                                                                                                                                                                                164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341
                                                                                                                                                                                                                                                                                                                                                                                                                      221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
CNS014PQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                      å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
```

合

à

ð

g

à a

g à

g

õ

g

ò g

ò

9

```
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL069706.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope
                                                                                                                                                 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNSOOEVL
                                                                                                                                                                                                                                                Best Local Sim
Matches 100;
                                                                                                                                                                                                                              Query Match
                                  source
                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dp
                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDCP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovy Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-8 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the language of the BDGP is and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR38J18 of RPCI-98 library from Drosophila melanogaster (fruit AL076232 GENOME SEQUENCE).
                                                                                                                                                                                                                                                88 aatcatgitcatataaatatatgtacattatacgtatatacacgtatacaegtatacaaatagtag 147
                                                                                                                                                                                                                      607
                                                                                                                                                                                                                                                                                    608 TITITITITITITITITITITITANITITINATAINITIMITAATITITIAAATAAMAITITAA 667
                                                                                                                                                                                                                                                                                                                           208 ttataattatggtaggatgtacatggccgataagaaaaggcaatttgtagatgttaattc 267
                                                                                                                                                                                                                                                                                                                                                                                                                                          268 ccatcttgaaagaaatatagtttaaatatttattgataaaataacaagtcaggtattata 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               giccaagcaaaaacaitaatttaattgatgcaagtittaaattcagaaatatttcaataact 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 tittgactottcaccattacatattgaaactcttacggatgagaacaactcacaagcatt 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                          ö
                                                                                                     Length 1101;
                      149 others
                                                                                                                                         Indels
                                                                                          Query Match
13.2%; Score 54.8; DB 13;
Bast Local Similarity 39.8%; Pred. No. 0.27;
Matches 146; Conservative 32; Mismatches 189;
                        ų
                        334
                        б
/note="end : TET3"
120 c 103 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dq 086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                      ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 gattata 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908 AAAAAA 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope
                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS00JG1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
```

```
"Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila denome Project (BDCP).

The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutcoyo Osocgaw and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial isogenic strain y2; on bw sp. the same strain used for the BDCP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be located.of the library found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit AL069706
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephquidaa, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgataaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaag
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                   DB 13; Length 980;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                    69
                                                       melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29B23"
                                                                                                                                                                                                                                                                                                                                 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 tttaaattcagaaatatttcaataactgattatat 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                         13.2%; Score 54.6; Di
ilarity 46.5%; Pred. No. 0.3;
Conservative 20; Mismatches
                                                                                                                                                                               297
                                               /organism="Drosophila
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR38J18"
Location/Qualifiers
1. .980
                                                                                                                                                                            102 g
                                                                                                                                               'note-"end : T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:4949849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1101 bp
                                                                                                                                                                               112 c
```

1

ö

g

ò 셤 ò g

ð QQ õ

ò

Q

```
Direct Submissions

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUSSUNKHX 905 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACRITYNG of FRECI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                          189 aagtattatataaattataattataattatggtaggatgtacatggccgataagaaaggc 248
                                                                                                                                                                                                                                                                                                                                                                                aatttgtagatgttaattcccatcttgaaagaaatatagtttaaattttattgataaaa 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 taacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaaatt 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agaacaactcacaagcattaatcatgttcatataaatatatgtacattatacgtatatat 128
                                                                                                                                        129 acacgtatacaaatagtagcgaagaaatccatgtaaagcagcaggggggacccatggtttc 188
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fruit fly.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Medezoa; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                    244 ATTATTTTTTAAAATANCTAAAAATTTAATAMAAAATTAAAATTAAAATAATAATAMAA
                                                                                                                                                                                                                                                                                                                                                                                                          ;
                       893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 others
                       Length
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
                  13.1%; Score 54.4; DB 13;
illarity 41.1%; Pred. No. 0.33;
Conservative 26; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 cagaaatatttcaataactgattatacage 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 AAATTTAATTTTTTAATWTTTTTTCATANC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="BACR17N06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:4957174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL077798.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
                                                               Matches 136;
                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNS00KHX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                              ò
                                                                                                                                                   ద
                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNSO13XE 893 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN10102 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        971 WAWTWTATAWTTWTATWTATWWTAWTAWAATATTTATTAAWWTATATTTTAWAAA 1030
                                                                                                                                                                                                                                                                                     129 acacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggggaccatgtttc 188
                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                                                                      taacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaaatt 368
                                                                                                                                                                                                  agaacaactcacaagcattaatcatgttcatataaatatatgtacattatacgtatatat 128
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 893)
                                                                                                                                                                                                                                                                                                                 189 aagtattatataattataattataattatggtaggatgtacatggccgataagaaaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                              Length 1101;
                     232 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    others
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                                                                                                         ; Score 54.6; DB 13;
; Pred. No. 0.29;
62; Mismatches 156;
                     ىد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ų
                     299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1031 WTAATATATWATAWWTAWATATAWAWWA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cagaaatatttcaataactgattatatca 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fly), genomic survey sequence. ALI03436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="DrosBAC"
/clone="BACN10102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="end : SP6"
                  9
/note="end : T7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL103436.1 GI:5615047
                                                                                                            13.2%;
33.7%;
                  91 c
                                                                                                                              Best Local Similarity 33.7
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fruit fly.
                       Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope
                  419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372
                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS013XE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
```

us-09-698-903b-8.rst

ORIGIN

```
egaagaaatecatgtaaageageagggggeaceatggttteaagtattatatatataa 207
                                                                                                                                                                                                             319 AATATATTTATATATGTATTATATATATATACATGGATAAGGAAAATAAAAA 260
                                                                                                                                                                                                                                                                                                                                                                                                            gtccaagcaaaaacataaatttattgatgcaagtttaaattcagaaatatttcaataact 387
                                                                                                     208 ttataattatggtaggatgtacatggccgataagaaaaggcaatttgtagatgttaattc
                                                                                                                                                                                                                                                                  268 ccatcttgaaagaaatatagtttaaatatttattgataaaataacaagtcaggtattata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 gattatat 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 AATATTAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                     148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                             328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS0182A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                  ò
                                                                                                  a
                                                                                                                                                       δ
                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Junichi Watanabe
Institute of Medical Science
Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokaneda, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5378
Fax: 81-3-5449-5419
Email: Jwatanab@menage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched colva library Gene 200 (1-2), 149-156 (1997).
                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU087444 5Ugano Melaria cDNA library Plasmodium falciparum cDNA clone XPFn4669, mRNA sequence.
                                                                                                                                                             551 TKAAAATTATWAAKAWAAAKATKWKKTWTTDTKWWKWTAWKAAAAAAHAAWATAAATWAT 610
                                                                                                                                                                                                                                                                     146 agcgaagaaatccatgtaaagcagcagggggcaccatggtttcaagtattatataattat 205
                                                                                                                                                                                                                                                                                                         eattataattatggtaggatgtacatggccgataagaaaaggcaatttgtagatgttaat 265
                                                                                                                                                                                                                                                                                                                                                                                                                            tocoatottgaaagaaatatagtttaaatatttattgataaaataacaagtcaggtatta 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | : : :|| ||| ||| || :||: :| :|||||:|| | :| | | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 tagtocaagcaaaacataaatttattgatgcaagtttaaattcagaaatattcaataa 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malaria paragite P. falciparum.
Bukaryota; Alveolarum
Eukaryota; Alveolaru, Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 500;
                                                                   Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S. FULL-malaria: a database for a full-length enriched from human malaria parasite, Plasmodium falciparum Nucleic Acids Res. 29 (1), 70-71 (2001)
                                                                                                             57; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.3%; Pred. No. 0.57;
Matches 155; Conservative 0; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5833"
/clone="xpFn4669"
/clone_lib="sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .500
/organism="Plasmodium falciparum"
                                                                   DB 13;
                                                                Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU087444
AU087444.1 GI:12389585
                                                             13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="3D7
                                               Query Match
Best Local Similarity 34.78
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
AU087444/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                             206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

970 bp

CNS0182A

```
Genoscope.

Direct Submission
Submitted (23.JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                               Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - ihttp://www.edgp.ebl.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
Drosophila melanogaster genome survey sequence T7 end of BAC BACN37C16 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL108796
G1:5629100
                                                                                                                                                                           Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tataaatatatgtacattatacgtatatacacgtatacaaaatagtagcgaagaaatcc 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 caccattacatattgaaactcttacggatgagaacaactcacaagcattaatcatgttca 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
_
_
_ = = _ _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/plasmid="pBeloBaCil"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.9%; Score 53.4; DB 42.6%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="DrosBAC"
/clone="BACN37C16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lone="BACN37C16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                       fruit fly.
Plasmid Dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

Search completed: February 25, 2002, 17:21:06 Job time: 16159 sec

THIS PAGE BLANK (USPTO)

```
February 25, 2002, 12:03:22 ; Search time 1457.19 Seconds (without alignments) 4698.309 Million cell updates/sec
                                                                                                   US-09-698-903B-8
415
1 gtcgagtttggtgttcatga......cagctggtacattgccgtag 415
                                                                                                                                                                                                   2944280
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                             1472140 segs, 8248589755 residues
                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     OM nucleic - nucleic search, using sw model
                                                                                                                                             IDENTITY_NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_un: *
em_v1: *
em_v1: *
em_htgo_hum: *
em_htgo_rod: *
em_htg_hum: *
em_htg_hum: *
em_htg_rod: *
em_htg_rod: *
                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                      9b_ba: *
9b_htg: *
9b_on: *
9b_on: *
9b_ov: *
9b_ph: *
9b_pr: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_hum: *
em_in: *
em_om: *
em_or: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_ro:*
em_sts:*
em_sy:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_ov:*
em_pat:*
em_ph:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_pl:*
                                                                                                                                                                                                                                                                                               GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                             Searched:
                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX127755 Sequence AX127757 Sequence	. e	3 Sequen	Mutated	A76916 Sequence 2	8 Sequen	Mutated b	I44104 Sequence 23	AX172441 Sequence	A76915 Sequence 1	AR098307 Sequence	AX172440 Sequence	A60112 Sequence 5	AR098311 Sequence	A24783 plasmid pPS	AR074388 Sequence	A24/82 plasmid pub	A10942 Nucleotide	A10939 Nucleotide	A10943 Nucleotide	144103 Sequence 22	AJ251013 Transform	Algorous Transform Algora DNA used as	AR095107 Sequence	AR098313 Sequence AX012338 Sequence	149886 Sequence 2	I82374 Sequence 2	V00090 Agrobacteri	X00431 Agrobacteri	E00404 Ti plasmid	00546 DN F242881	x05579		15-MAY-2001	1				producing same			elite event MS-B2"
																																		PAT					IOL			ou of
, QI	AX127755 AX127757	AX127748	AX063413	E31991	A76916	AR098308	E31990 AR078675	144104	AX172441	A76915	AR098307	AX172440 A71437	A60112	AR098311	A24783	AR074388	A24/82 AD074387	A10942	A10939	A10943 AX172463	I44103	TBI251013	TB1251014 A18051	AR095107	AR098313 AX012338	149886	I82374 HINHYGDNA	ATTRN7	ATTDNA	E00404	46 28	ARG	ALIGNMENTS	ă	nt WO0131042.	402		eleer, M	р <u>га</u> , 03 v	alifiers	<pre>-"synthetic construct" taxon:32630"</pre>	order flanking region
DB	99																					2 0	V				C			9	9 -	12		od od	ater		ict.	15) Beuc	12-A		Sm="E	ž,
Length	415	5865	7599	6539	6548	6548	7811	3200	4832	4946	4946	5349	5560	5560	7566	7566	7639	1037	1085	1160	3201	2476	1186	1186	1186	1186	12095		~	. 4	24595 194140	,		415	fro	. GI:14134	construct	cial sequence. ses 1 to 415) ,B. and de Beuck	rile brassi WO 0131042-	Location/Qua	organ db_xr	note=":
Query Match	100.0		٠.			٠. س	, ic		'n.	 M	δ.	വ		r C	. n	ις.	ນີ້ນ	. 4	÷.	4.~		· .		6	ی ن						35.2			27755	Sequence 8	27755.1	thetic	druitciai 1 (bases 1 Weston, B. a	e-steri ent: WC	L L	' ` `	. `
Score	415	6	5	20 20	3 8	8	£ 6	8	188.4	8	8	£ 6	8	88	38	8	ž č	56	8	8 6	. –	155	153	153	153	153	153	146	146	146	146 146	116		1	_		SM	ലഗ		ă)	
esult No.	77	m	41	n u	۰,	& (ν <u>C</u>	11	17	14	15	17	18	19	21	22	2 6	25	56	27	23	30	37 37	33	3.4 5.4	36	37	36	40	42	43	45		RESULT AX127755 LOCUS	DEFINITION	VERSION KEYWORDS	OURCE	REFERENCE AUTHORS	TTLE OURNAL	FEATURES		
Res	Ú	O	Ç.	o c	v	υ	υ	υ							O	O	o c	ט ט	υ	ပ	υ		O	O	0 0	O	o c	υ	U			ပ		RESUL AX1277	DEF	VER	Sou	REF	нБ	FEA		

```
tacattgccgtag 415
|||||||||||||||
TACATTGCCGTAG 5621
                                                                                                                                                                                                                                                                                                                                                                                                                             Ø
                                                                                                                                                                                                                                                                                                                                                                                                                            1849
                                                                                                                                                                                                                                                             AX127748/C
                      601
                                                      349
                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                        ORGANISM
                                      67
                                                                                                                                          246
                                                                                                                                                                                                            366
                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403
                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5633
                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                      LOCUS
                  Db
                                                     g
                                     ŏ
                                                                                     ΩD
                                                                      οy
                                                                                                        ò
                                                                                                                       g
                                                                                                                                        δ
                                                                                                                                                        q
                                                                                                                                                                          ŏ
                                                                                                                                                                                          a
                                                                                                                                                                                                            ð
                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                          240
                                                                                                                                             tacggatgagaacaactcacaagcattaatcatgttcatataaatatatgtacattatac 120
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elite event MS-B2"
                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2001
                                                                                                 1 gtcgagtttggtgttcatgattttggttttgactcttcaccattacatattgaaactct
                                                                                                                                                                                                    181 atggtttcaagtattatatattatattataattataattatggtaggatgtacatggccgataa
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 416)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing Patent: WO 0131042-A 10 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                  tttaaattcagaaatattcaataactgattatatcagctggtacattgccgtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416;
                                                                    Length 415;
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oţ
                                                                                                                                                                                                                                                                                                                                                                       PAT
                                                                  Score 415; DB 6;
Pred. No. 2.2e-64;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 380.8; DB 6;
Pred. No. 2.5e-58;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:32630"
/note="3' border flanking region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .416
/organism="synthetic construct"
                                   ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ų
                                   136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152
                                                                                                                                                                                                                                                                                                                                                                     DNA
WO0131042.
                                   б
1. .234
/note="plant DNA"
235. .415
/note="T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194. .416
/note="plant DNA"
a 72 c 54 g
                                  70
                                                                Query Match
100.0%; Sc
Best Local Similarity 100.0%; P1
Matches 415; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                             AX127757 416 bp
Sequence 10 from Patent
AX127757
                                                                                                                                                                                                                                                                                                                                                                                             AX127757.1 GI:14134404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.8%;
98.5%;
                                55 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.5
Matches 404; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .193
                                154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
misc_feature
                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                  RESULT 2
AX127757/C
LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                  දු
                                                                                                  8
                                                                                                                                   õ
                                                                                                                                                q
                                                                                                                                                                   õ
                                                                                                                                                                                  q
                                                                                                                                                                                                                   g
                                                                                                                                                                                                   à
                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                      g
```

```
ö
125
                                                                                                        185
                                                                                                                                                         245
                                                                                                                                                                                                           305
                                                                                                                                                                                   171
                                                                                                                                                                                                                 5634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-2001
                                                              ggcaatttgtagatgttaattcccatcttgaaagaaatatagtttaaattttattgata
                                                 tgagaacaactcacaagcattaatcatgttcatataaatatatgtacattatac-gtata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methods for producing same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5753 TATAGTTTAAATATTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 tatagitiaaatatitatigataaaataacaagicaggiatiatagiccaagcaaaaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                        attcagaaatatttcaataactgattatatcagctggtacattgccgtag 415
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
46.1%; Score 191.4; DB 6;
Best Local Similarity 99.5%; Pred. No. 5.7e-25;
Matches 192; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="synthetic construct"
/db_xref="taxon:32630"
/note="T-DNA of plasmid pc0113"
1 1095 c 1149 g 1772 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic construct.

synthetic construct
artificial sequence.

1 (bases 1 to 5865)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methc
Patent: WO 0131042-A 1 03-MAY-2001;
Aventis Cropscience N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                             AX127748 5865 bp DNA
Sequence 1 from Patent W00131042.
AX127748
AX127748.1 GI:14134395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .5865
```

```
Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      î (bases 1 to 6548)
De,B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A60109.1 GI:3715125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.0
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                           Plasmid PTS172.
Plasmid PTS172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acattgccgtag 415
             source
                                                                                           1755 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1756 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmids.
FT
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
A60109/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                   Ω
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                              synthetic construct.

ISM synthetic construct

ISM synthetic construct

Ism synthetic construct

In (bases 1 to 7599)

IORS Hoffmann, B., Mollier, P. and Pelletier, G.

Is Promoter expressed specifically in the cells of plant roots,

recombinant vectors and host cells comprising same and transgenic

plants obtained

URNAL Patent: WO 0100833-A S 04-JAN-2001;

INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR)

INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR)

Location/Qualifiers

Source /organism="synthetic construct"

/db_xref="texon:32630"
/note="ADN-T de PGKB5"

/note="ADN-T de PGKB5"
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAZUYUKI HAMADA, FUMIO NAKAKIDO
C12N15/09, A01H5/00, C12N5/10, C12N9/22//(C12N5/10, C12R1:91), PC
                                                                                                                                                                                                                                                                                                                                                                                                                              283 tatagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaaca 342
                                       24-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                           DB_6; Length 7599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mittated barnass gene and transgenic plant thereof
Patent: JP 2000041682-A 4 15-FEB-2000;
JAPAN TOBACCO INC
OS ESCHATCHIA COLI LE392
PN JP 2000041682-A/4
PD 15-FEB-2000
PF 04-AUG-1998 JP 1998220060
PR KAZUTUKI HAMADA, FUMIO NAKAKIDO
PC C12N15/09, A01H5/00,C12N5/10,C12N9/22//(C12N5/10,C12N15/00)
CC C12N15/00, (C12N5/00,C12R1:91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E31991 6539 bp DNA PAT
Mutated barnase gene and transgenic plant thereof.
E31991
                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                        Query Match

46.1%; Score 191.4; DB 6
Best Local Similarity 99.5%; Pred. No. 5.6e-25;
Matches 192; Conservative 0; Mismatches 1
                                    AX063413 7599 bp DNA
Sequence 5 from Patent W00100833.
AX063413
AX063413.1 GI:12541201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E31991.1 GI:13021588
JP 2000041682-A/4.
unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 6539)
Kazuyuki, H.F.N.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6591 TACATTGCCGTAG 6579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified unclassified.
                                  LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
          RESULT 4
AX063413/c
                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403
                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
E31991/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                             284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacat 343
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                        ö
                       organism='Escherichia coli LE392'
                                                                                                                                   DB 6; Length 6539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 6548;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic transformation using a PARP inhibitor
Patent: WO 9706267-A 2 20-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
                                                                                                                                                                                                                                                                                                                                                                                                AOU109 6548 bp DNA circular PAT
Sequence 2 from Patent WO9706267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%; Score 188.8; DB 6;
99.0%; Pred. No. 1.6e-24;
Live 0; Mismatches 2;
                                                                                                                                Score 188.8; DB 6;
Pred. No. 1.6e-24;
0; Mismatches 2;
Location/Qualifiers
1. .6539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. 6548
/organism="Plasmid PTS172"
/db_xref="taxon:106340"
a 1579 c 1523 g 1690 t
                                Location/Qualifiers
1. 6539
/organism="unidentified"
/db_xref="taxon:32644"
a 1578 c 1519 g 1687
                                                                                 1687
```

07-FEB-2001

g

RESULT 7
A76916/C
LCCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

source

EATURES

BASE COUNT

셤 à g

AUTHORS TITLE

JOURNAL

REFERENCE

```
PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
PC C12N15/09, A0145/00, C12N5/10, C12N9/22//(C12N5/10, C12R1:91), PC C12N15/00, (C12N5/00, C12R1:91)
CC C12N5/00, (C12N5/00, C12R1:91)
FF Key
FT Source
FT
                                                                                                                                                             284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacat
                                                                                                   284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coation/Qualifiers
To 5548
Octanism*'Escherichia coli LE392'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Toases | To 6548 |
| Kazuyuki, H.F.N.N. |
| Mutated barnase gene and transgenic plant thereof Putated barnase gene and transgenic plant thereof Data |
| Patent: JP 2000041682-A 3 15-FEB-2000; JAPAN TOBACCO INC |
| OS Escherichia coli LE392 |
| PN JP 2000041682-A/3 |
| PD 15-FEB-2000 |
| PF 04-AUG-1998 JP 1998220060 |
| PRAUG-1998 JP 199822000 |
| PRAUG-1998 JP 1998
                                                                                                                                                                                                                                                                                                                                                                                                E31990 6548 bp DNA PAT
Mutated barnase gene and transgenic plant thereof.
E31990.1 GI:13021587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 188.8; DB 6;
Pred. No. 1.6e-24;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1690 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .6548
/organism="unidentified"
/db_xref="taxon:32644"
1 1579 c 1523 g 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.5%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP 2000041682-A/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 190; Conservative
                                                                                                                                                                                                                                                                         404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                           6362
                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6362
                                                                                                                                                                                                                                                                                                                                                                               E31990/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                           ŏ
                                                                                                                   g
                                                                                                                                                             δ
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.5%; Score 188.8; DB 6; Length 6548; Best Local Similarity 99.0%; Pred. No. 1.6e-24; Matches 190; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                 GENETIC TRANSFORMATION USING A PARP INHIBITOR PACENT: EP 0757102-A 2 05-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
LOCALION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetic transformation using a PARP inhibitor Patent: US 6074876-A 2 13-JUN-2000;
Location/Qualifiers
                                                                                          A/6916 6548 bp DNA circular PAT
Sequence 2 from Patent EP0757102.
A76916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%; Score 188.8; DB 6;
99.0%; Pred. No. 1.6e-24;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Plasmid PTS172"
/db_xref="taxon:106340"
1579 c 1523 g 1690 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
1579 c 1523 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR098308 6548 bp DNA
Sequence 2 from patent US 60
AR098308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR098308.1 GI:12807565
                                                                                                                                                                                                                                                              1 (bases 1 to 6548)
De, B.M.
                                                                                                                                                                   A76916.1 GI:6088713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
1 (bases 1 to 6548)
De Block, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.0
Matches 190; Conservative
                                                                                                                                                                                                             Plasmid PTS172.
Plasmid PTS172
plasmids.
6362 ACATTGCCGTAG 6351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1756
```

ö

Gaps

ö

Indels

Length 6548;

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS source

BASE COUNT

ORIGIN

ð

JOURNAL FEATURES

TITLE

RESULT 8 AR098308/c LOCUS

6362

8

à

g

ð

S

```
Genetic transformation using a PARP inhibitor Patent: WO 9706267-A 1 20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT
                                                                                                                                                            PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 188.4; DB 6;
Pred. No. 2e-24;
0; Mismatches 1;
                                                                                                                                                           Sequence 2 from Patent WOO141558. AXI72441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4946 bp DNA
Sequence 1 from Patent W09706267
A60108
A60108.1 GI:3715124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transformation vector pTHW107.
Transformation vector pTHW107
artificial sequence; vectors.
1 (bases 1 to 4946)
De, B.M.
                                                                                                                                                                                                                                                                                                        Aventis CropScience N.V. (BE Location/Qualifiers
                                                                                                                                                                                              AX172441.1 GI:14597553
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.4%;
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 ATTGCCGTAG 243
                                                                        406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                         1528
                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                    RESULT 12
AX172441
                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
A60108
                                                                                                                                                                                                                      SOURCE
                                                                                                                                                            LOCUS
   a
                                                g
                                                                       ŏ
                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                         ò
                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 3200)

Cornelissen,M., Soetaert,P., Stam,M. and Dockx,J.

Cornelissen,M., Soetaert,P., Stam,M. and Dockx,J.

Modified Bacillus thuringlensis insecticidal-crystal protein genes and their expression in plant cells

Patent: US 5633446-A 23 27-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3141 GTACAFGGFCGAFAAGAAAAGGCAATTTGTAGAFGTTAAATTCCCATCTTGAAAGAAATAT 3082
                                                                                                                                                                                                                                                                                           286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa 345
                                                                                                                                                                                                                                                                        Gaps
             31-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-0CT-1997
                                                                                                         1 (bases 1 to 7811)
Cornellisen,M., Reynaerts,A., Gossele,V. and Van Aarssen,R.
Marker gene
Patent: US 5962768-A 5 05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                               DB 6; Length 7811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
             PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                             / Match 45.5%; Score 188.8; DB 6 Local Similarity 99.0%; Pred. No. 1.6e-24; les 190; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 188.4; DB
Pred. No. 2e-24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5633446.
                        5962768.
                                                                                                                                                                               /organism="unknown"
1906 c 1873 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
710 c 720 g
                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as
          AR078675 7811 bp DN
Sequence 5 from patent US
AR078675
AR078675.1 GI:10005421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 from patent 144104
144104 GI:2469202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3200 bp
                                                                                                                                                                    .7811
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 đ
                                                                                                                                                                                              1950 a
                                                                     Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144104
                                                                                                                                                                                                                                             Query Match
Best Local S
                     DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                   ORGANISM
                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
144104/c
LOCUS
                                                                                                                       AUTHORS
                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                          KEYWORDS
SOURCE
                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AR078675
                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
3081 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACATAA 3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                      03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAR-1998
                                                                                                                                                                                                                                                                                                                     synthetic construct.
synthetic construct
synthetical sequence.
1 (bases 1 to 4832)
de Both, G. and de Beuckeleer, M.
Hybrid winter oilseed rape and methods for producing same Patent: WO 0141558-A 2 14-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .4832
/organism="synthetic construct"
/db_aref="taxon:32630"
/note="T-DNA of plasmid pTHW118"
1883. .4065
/note="Hpal restriction fragment"
on a 883 c 932 g 1488 t 1 c
```

```
RESULT 15
AR098307
LOCUS
DEFINITION
                                                                                                   ORGANISM
                                                                                                                               AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                             BASE COUNT
                                                        ACCESSION
VERSION
                                                                             KEYWORDS
SOURCE
                                                                                                                       REFERENCE
                                                                                                                                                                FEATURES
                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                  agtttamatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-OCT-1999
                                                                                                                    .;
0
                                                                                              DB 6; Length 4946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4946;
                 1. .4946
/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
a 891 c 963 g 1523 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .4946
/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
1 891 c 963 g 1523 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENETIC TRANSFORMATION USING A PARP INHIBITOR Patent: EP 0757102-A 1 05-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                       PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.4%; Score 188.4; DB 6; Best Local Similarity 99.5%; Pred. No. 2e-24; Matches 189; Conservative 0; Mismatches 1;
                                                                                          Quary Match
45.4%; Score 188.4; DB
Best Local Similarity 99.5%; Pred. No. 2e-24;
Matches 189; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                              A/6915 4946 bp DNA
Sequence 1 from Patent EP0757102.
A76915
                                                                                                                                                                                                                                                                                                                                                                                   Transformation vector pTHW107 artificial sequence; vectors. I (bases 1 to 4946)
            Location/Qualifiers
PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                 A76915.1 GI:6088712
                                                                                                                                                                                                                                                                          234 ATTGCCGTAG 243
                                                                                                                                                                                                                                                           406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111111111
234 ATTGCCGTAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                  1569
                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                           286
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                               RESULT
A76915
                                                                                                                                                                           à
                                                                                                                                                                                            g
                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
```

```
286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
            14-FEB-2001
                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                            Length 4946;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                          1 (bases 1 to 4946)
De Block,M.
Genetic transformation using a PARP inhibitor
Patent: US 6074876-A 1 13-JUN-2000;
Location/Qualifiers
1. .4946
                                                                                                                                                                                                                                                          ;
9
                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                         Score 188.4; DB
Pred. No. 2e-24;
0; Mismatches
                                                                                                                                                                                                       1523
акиувзо7 4946 bp DNA
Sequence 1 from patent US 6074876.
AR098307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 25, 2002, 12:51:36
Job time: 2894 sec
                                                                                                                                                                                      /organism-"unknown"
891 c 963 g
                                              AR098307.1 GI:12807564
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                   Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 ATTGCCGTAG 243
                                                                                                                                                                                                     1569 a
                                                                       Unknown.
```

THIS PAGE BLANK (USPTO)

Nucleotide sequenc T-DNA of pTTS24. Plasmid pTC0113 T-Chimeric T-DNA of

Plasmid pPS0212 co Plasmid pJD884 con USP-Promoter-casse

Plasmid pTS88 (Eco pPS029 Bt ICP codi Nucleotide sequenc T-DNA of plasmid p

OM nucleic

Run on:

Searched:

Database

10 9 10 10

0000000000

٠ ي Result

```
elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to plant DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                   AAN50182
AAF58252
AAF58254
AAF58257
AAF58259
AAF58255
AAF58255
                                                                                AAD06990
AAQ42160
AAQ42159
AAQ04705
AAQ04703
AAQ04706
                                                                                                                                                                 AAQ15144
AAQ25707
AAZ29122
AAZ29121
AAZ29124
AAZ29123
                                                                                                                                                                                                                                                                                                                                              AAF58254
AAF58257
AAF58259
AAF58262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1.234
/*tag= a
/note= "Corresponds to
235..415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AVET ) AVENTIS CROPSCIENCE NV
AAD06997 standard; DNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Agrobacterium sp.
Chimeric - Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                  4946
4946
5349
5864
5865
7566
7639
1037
1085
                                                                                                                                                                  3201
1186
3153
3336
3694
3877
                                                                                                                                                                                                                                         24593
24596
936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     male-sterility gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
 WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2001.
                                                                                                                                                                                                                                                   146
107.6
107.6
                                                                                                                                                                                                                                                                                      107.6
107.6
107.6
106.4
106.4
106.4
106.4
AAD06997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MS-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD06997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                               00000
                                                                                                                                                          000000
                                                                                                                                                                                                                                                                  000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric T-DNA of
Nucleotide sequenc
Plasmid pTS172delt
E. coli plasmid pT
Plasmid pTS174 use
Plasmid pTS172. C
E. coli plasmid pT
Plasmid pTS172. C
                                                                                             (without alignments)
2488.912 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Right (5') border
Left (3') border f
Plasmid pTC0113 T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                               February 25, 2002, 12:03:22 ; Search time 142.95 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                      1 gtcgagtttggtgttcatga......cagctggtacattgccgtag
                                                                                                                                                                                                                                                                                                                                                       **Singsy_decodata/geneseqn/Nal980.DAT:**
**Singsy_gedata/geneseq/geneseqn/Nal981.DAT:**
**Singsy_gedata/geneseq/geneseqn/Nal981.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal981.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal981.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal981.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal981.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal981.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal980.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal980.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal981.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal991.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal991.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal991.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal992.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal992.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal995.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal995.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal995.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal995.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal995.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal995.DAT:**
**Singsy_gedata/geneseqy_geneseqn/Nal999.DAT:**
**Singsy_geneseqy_geneseqy_geneseqn/Nal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                930621 segs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT39339
AAD06990
AAF25320
AAF86439
AAT39336
AAT61394
AAZ91096
AAF86441
                                                         - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD06997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06999
                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                              US-09-698-903B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416
5864
5865
7599
5228
6539
6548
6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0
91.8
46.1
46.1
46.1
45.5
45.5
45.5
45.5
                                                                                                                                                                                                                                                                                                                                                                                                        22009: ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380.8
191.4
191.4
191.4
1188.8
1188.8
1188.8
1188.8
1188.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                           Perfect score:
Sequence:
                                                                                                                                                                               Scoring table:
```

Legumin-signalpept USP-signalpeptide Right flanking reg pVB36 Bt ICP codin Chimeric neo gene Plasmid DV131 comp Plasmid DV131 used Plasmid DV132 used Sequence of opine Complete nucleotide Oligonucleotide DI Oligonucleotide DI

```
원
                                                                                                                                                                                                                                                                                                               ö
                                                                                                              The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the Hybrid seed from the transgenic Brassica plant.

The present sequence is right (5') border flanking region of ellte event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                gtatatacacgtatacaaatagtagcgaagaaatccatgtaaagcaggggggcacc 180
                                                                                                                                                                                                                                                                                                                                                                               tacggatgagaacaactcacaagcattaatcatgttcatataaatatatgtacattatac 120
                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360
                                                                                                                                                                                                                                                                                                                                             gtcgagtttggtgttcatgattttgggttttgactcttcaccattacattgaaactct 60
                                              Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MS B2 elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 gtatatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcaggggggcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 atggtttcaagtattatatatattatattataattataattatggtaggatgtacatggccgataa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgataaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                       Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Left (3') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                           Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 415; DB 22;
Best Local Similarity 100.0%; Pred. No. 3.5e-76;
Matches 415; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                             Claim 11; Page 51; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD06999/c
ID AAD06999 standard; DNA; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Agrobacterium sp.
- Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
  Beuckeleer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         male-sterility gene; ds
                       WPI; 2001-300517/31
  Se
De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2001
 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric
Chimeric
 Weston
                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Кеу
à
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
elite event
                                                                                                                                                                                                                                                                                                      The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
                                                                                                                                                                                                                                             by
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 TIGGGIGTICATGATITIGGGITITIGACICTICACCATIACATATIGAAACTCTTACGGA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaa 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                      Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tttggtgttcatgattttgggttttgactcttcaccattacatattgaaactcttacgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 tgagaacaactcacaagcattaatcatgttcatataaatatgtacattatac-gtata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 tatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggggcaccatggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttcaagtattatatatatattataattatagtatggtaggatgtacatggccgataagaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                     /note= "Corresponds to plant DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 380.8; DB 22;
Pred. No. 3.2e-69;
1; Mismatches 3;
                          to T-DNA
1..193
/*tag= a
/note= "Corresponds to
194..416
                                                                                                                                                                                                                                                                                   Claim 11; Page 52; 53pp; English.
                                                                                                                                                                      ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.8%;
98.5%;
                                                                                                                                                                     (AVET ) AVENTIS CROPSCIENCE
                                                                                                                         26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                            De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.5
Matches 404; Conservative
                                              /*tag=
                                                                                                                                                                                                                WPI; 2001-300517/31.
                                                                             WO200131042-A2
 misc_feature
                                  misc_feature
                                                                                                                                               29-OCT-1999;
                                                                                                  03-MAY-2001
                                                                                                                                                                                            Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                  4S-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366
 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

ä

m

Page

```
/note= "region containing polyA signal of nopaline
synthase gene of Agrobacterium T-DNA"
complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Bacillus amyloliquefaciens barnase coding region"
                                                                                                                                                                                                                                           /note= "region containing polyA signal of gene 7 of Agrobacterium T-DNA" complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "region containing polyA signal of gene 7 of Agrobacterium T-DNA" complement (5840..5864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                 Plasmid pTCO113 T-DNA used to obtain male sterile oilseed rape.
                                                                                                      Plasmid pTCO113; male sterile; barnase; ribonuclease; barstar; transgenic plant; oilssed rape; canole; Brassica napus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                    /note "promoter of Arabidopsis Rubisco small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "promoter of nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "region coding for barstar of Bacillus
    amyloliquefaciens"
                                                                                                                                                                                                 /note= "right border of Agrobacterium T-DNA" complement (98..330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "left border of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                             /note- "region coding for phosphinothricin
acetyltransferase"
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "promoter of stamen-specific TA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                              subunit gene"
complement (2659..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (3368..4877)
                                                                                                                                                          Location/Qualifiers complement (1..25)
                   AAT39339 standard; DNA; 5864 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Barstar
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Barnase
                                                                                                                                                                                                                                                                                                                                                                                       /*tag= e
/label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- PTA29
                                                                                                                                                                                                                                                                                                                                          /label- Pssu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= h
/label= Pnos
                                                                                                                                                                                                                         /*tag= b
/label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= 3'g7
                                                                                                                                                                                                                                                                                      /label- bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1924..5216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5490..5765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= k
/label= LB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5217..5489
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                    misc_feature
                                                                                                                                                                                                              polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9626283-A1
                                                                                                                                                                                                                                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyA_signal
                                                             22-JAN-1997
                                                                                                                                     Synthetic
                                         AAT39339;
                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
RESULT 3
                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
```

29-AUG-1996

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-DNA; plasmid pTCO113; transgenic Brassica plant; transformation event; male-sterility gene; chimeric; tobacco; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 tatagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaca 342
                                                                                                                                                                                                                                                              plasmid pTCO113 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-regulatory) agene under control of the Pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterium-mediated transformation using PTCO113 were male sterile. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.1%; Score 191.4; DB 17; Length 5864; 99.5%; Pred. No. 1.4e-30; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;
                                                                                                                                                                                                                                     Example 3; Page 33-3743-47; 56pp; English.
                                                                                                   Cornelissen M, Michiels F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Streptomyces hygroscopicus. Chimeric - Arabidopsis thaliana. Chimeric - Bacillus amyloliquefaciens. Chimeric - Nicotiana tabacum. Chimeric - Agrobacterium tumefaciens. Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric T-DNA of plasmid pTCO113.
                                                                       Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD06990 standard; DNA; 5865 BP
                                                                      (PLBZ ) PLANT GENETIC SYSTEMS
                                        95EP-0400364.
            96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5632 TACATTGCCGTAG 5620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                              WPI; 1996-402373/40.
                                                                                                   Botterman J,
            21-FEB-1996;
                                        21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD06990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD06990/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
/note- "TaqI fragment from the 3' untranslated end of the nopaline synthase gene (3'nos) from the T-DNA of prim37 and containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                   /*tag= g/note= "Promoter from the atSlA ribulose-1,5-biphosphate
carboxylase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= o
//note= "Promoter of the nopaline synthase gene from the
T-DNA of pTiT37 of Agrobacterium tumefaciens"
5216..5217
                                                                                                                                                                                                                                                                                                                                                                                                                                       /nors- Abrose The 3' untranslated region downstream from the barnase coding sequence of Bacillus amyloliquefactens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= m
hote= "Promoter region of the anther-specific gene
17429 from Nicotiana tabacum"
                                                                                                                                                                                                                          /product = "Protein encoded by bialaphos resistance
gene (bar) of Streptomyces hygroscopicus"
884..2609
 1.25
/*tag= a
/note= "Right border repeat from the TL-DNA from
                                                                                            /*tag= c
/note= "Residual sequence from the TL-DNA at the
right border repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οį
                                                                                                                                     ...ce= The 3' untranslated end from the TL-DNA gene 7 (3'97) of pTiB6S3" 310..331
                                                        /*tag= b
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "The 3' untranslated end from the TL-DNA
                                                                                                                                                                                     /*tag= e
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                               /*tag= h
2/60ce "Synthetic polylinker derived sequence"
2/60c. 2920
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= j
/note= "Synthetic polylinker derived sequence"
2937..3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= n
/note= "Synthetic polylinker derived sequence"
4925..5215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cas - Sequence from the 3' untranslated end varstar gene from Bacillus amyloliquefaciens" 5531..5554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **tag= p
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= s
note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= q
/product= "protein encoded by barstar gene of
Baillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product "Protein encoded by barnase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus amyloliquefaciens"
3369..4878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5218..5490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5491..5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5766
                                                                                                                                                                                                            ..883
                                                                                                                           98..309
                                                                                                                                                                                                                                                                                                                                                  /*tag=
   misc_feature
                                                misc_feature
                                                                                misc_feature
                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                            3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                           3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3'UTR
                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
```

```
The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic Diant with a male-fertile Brassica plant and harvesting the transgenic Diant with a male-fertile Brassica plant and harvesting the transgenic Brassica plant. The present sequence is chimeric T-DNA of plasmid probli3. This sequence comprises right border repeat, left border repeat and 3' untranslated comprises right border repeat, left border repeat and 3' untranslated coding regions of blalaphos resistance gene (bar) from Streptomyces hygroscopicus, barnase gene from Bacillus amyloliquefaciens and barstar gene from manipulates small subunit gene from Arabidopsis thallana, the anther-specific gene TA29 from Arabidopsis thallana, the anther-specific gene from the T-DNA of pills?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οť
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                             /*tag= v
/note= "Residual sequence from the TL-DNA at the
                                                                                                                                                                                          /*tag= x
/note= "Left border repeat from the TL-DNA from
gene 7 (3'97) of pTiB6S3"
5767..5773
/*tag= u
//tag= "Synthetic polylinker derived sequence"
5774..5810
                                                                                                                                              /*tag= w
/note= "Synthetic polylinker derived sequence"
5841..5865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.1%; Score 191.4; DB 2; Best Local Similarity 99.5%; Pred. No. 1.4e-30; Matches 192; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 47-49; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                    (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                      26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                        99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                      De Beuckeleer M;
                                                                                                                             811..5840
                                                                                                                                                                                                                          pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-300517/31.
                                                                                                                                                                                                                                                      WO200131042-A2
                  misc_feature
                                                                                                                                                                                                                                                                                                                                                      29-OCT-1999;
                                                               misc_feature
                                                                                                                             misc_feature
                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                        03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                      Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
AAZ91097,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
           9
                   AAF86439/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                    Plant promoter; root cell; root-specific expression; parasite resistance; nematode resistance; fungal resistance; water stress; salt stress; sugar content; nitrogen transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a plasmid PCKB5. The plasmid contains a plant promoter that directs expression of a selected sequence in root cells at all stages of development of a plant. The plant promoter is used to control expression of genes in a root-specific manner, especially genes that provide resistance to parasites, pests (nematodes or fungi), water and salt stress, or alter sugar content or nitrogen transport. Fragments of the promoter are useful as probes or primers to detect or amplify at least part of the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tatagittiaaatattiattigataaaataacaagicaggiattatagiccaagcaaaaaca 342
                                                                                                                                                                                                                                                                                                                                                             New constitutive plant promoter active specifically in roots, useful for controlling expression of pest or drought resistance genes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          taaatttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.1%; Score 191.4; DB 22; Length 7599; 99.5%; Pred. No. 1.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7599 BP; 1972 A; 1938 C; 1937 G; 1752 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                Nucleotide sequence of a plasmid PGKB5,
                                                                                                                                                                                                                                                                                                                     Pelletier G;
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 9; 92pp; French.
                                                                    AAF25320 standard; DNA; 7599 BP
                                                                                                                                                                                                                                                       23-JUN-2000; 2000WO-FR01768
                                                                                                                                                                                                                                                                           99FR-0008185
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  related transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                     Mollier P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5633 TACATTGCCGTAG 5621
403 tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tacattgccgtag 415
                                                                                                                                                                                                                                                                                                (INRG ) INRA INST NAT
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-102893/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                               WO200100833-A1.
                                                                                                                                                                                                                                                                            25-JUN-1999;
                                                                                                            30-APR-2001
                                                                                                                                                                                                                                                                                                                    Hoffmann B,
                                                                                                                                                                                                                                   04-JAN-2001
                                                                                                                                                                                            Synthetic.
                                                                                        AAF25320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403
                                                           AAF25320/
                                                RESULT
                   a
                                                                                        g
 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
```

```
The present invention relates to a method for producing male sterile plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 aaatttattgatgcaagtttaaattcagaaatatttcaataactgattatatatcagctggt 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 atagittaaatatitatigataaaataacaagicaggiatiatagiccaagcaaaaacat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                        ds.
                                                                                                                                                                        Male sterile plant; RNAase inhibitor; plasmid pTS172delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5228 BP; 1384 A; 1307 C; 1263 G; 1274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 188.8; DB 22;
Pred. No. 4.6e-30;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 14-17; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
AAF86439 standard; DNA; 5228 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6239
                                                                                                                                                                                                                                                                                                                                              .2-SEP-2000; 2000WO-JP06222
                                                                                                                                                                                                                                                                                                                                                                                      99JP-0279307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2000 (first entry)
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamada K, Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5042 ACATTGCCGTAG 5031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                             Plasmid pTS172delta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-266212/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ91097 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 acattgccgtag
                                                                                                                                                                                                                                                         WO200124616-A1.
                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1999;
                                                                                                                                                                                                                  Unidentified
                                                                                   25-JUN-2001
                                                                                                                                                                                                                                                                                                   12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DXXXX
```

9

us-09-698-903b-8_1.rng

```
ö
                                                                                                                                                                                                                                                                                                     Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undesirable characters by specifically expressing the gene alone in anther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pTS174; male sterile; barnase; ribonuclease; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AA291095) for expression specifically in the anther of a plant. This sequence represents the E. coli/Agrobacterium shuttle vector plasmid prS172 which contains the mutated barnase gene (AA291095) under control of the cauliflower mosaic virus 355 promoter. The vector also contains a region of the Agrobacterium T-DNA gene? The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell. The transformed plant is used in plant breeding.
                                        Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 6539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6539 BP; 1755 A; 1578 C; 1519 G; 1687 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.5%; Score 188.8; DB 21; Length
99.0%; Pred. No..4.7e-30;
Live 0; Mismatches 2; Indels
             coli plasmid pTS431 containing mutant barnase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pTS174 used to obtain male sterile rice.
                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 23-27; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT39336 standard; DNA; 6548
                                                                                                                                                                    99WO-JP04167
                                                                                                                                                                                             98JP-0220060
                                                                                                                                                                                                                        (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.0°
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                   Hamada K, Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6353 ACATTGCCGTAG 6342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 acattgccgtag 415
                                                                                                                                                                                                                                                                            WPI; 2000-195581/17.
                                                                                                          WO200008176-A1.
                                                                                                                                                                  03-AUG-1999;
                                                                                                                                                                                             04-AUG-1998;
                                                                                                                                      17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JAN-1997
                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT39336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT39336/C
ID AAT3933
XX AC AAT393:
XX DT 22-JAN
XX DE Plasmir
XX FW Plasmir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

```
Plasmid pTS174 (AAT39336) contains Bacillus barnase DNA under control of the stamen-specific PEI promoter. Embryogenic callus from rice cv. Kochinbiriti was transformed with pTS174 alone or with pTS88 (see also AAT39337), a plasmid control, barstar DNA under control of a 35S promoter. With pTS174 alone, 1 male sterile line was recovered from 40 electroporation cuvettes. With both plasmids, 7 normal male sterile lines were recovered from 40 cuvettes. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low
                                                                                                                                                                                                                                                                                                                                                   function= 35S promoter of cauliflower mosaic virus 711..6262
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'function= region containing polyadenylation signal
                                                                                                                                                                                                                                                                                         El gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodn. of male sterile plants by transforming with a chimaeric construct. - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                          polyadenylation signal gene of Agrobacterium
                                                                                                                                                                                                                  /label= Barnase
/product= Bacillus amyloliquefaciens barnase
complement (2625..4313)
                                                                                                                                                                                                                                                                                                                                                                                                  /product- phosphinothricin acetyltransferase
                                                                                                                                                                                                                                                                                   /function- promoter of the stamen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6548 BP; 1757 A; 1578 C; 1523 G; 1690 T; 0 other;
                                                                                                        vector sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             level expression of barnase in non-stamen tissue.
                                                                                                                                                    /note= "region containing
nopaline synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botterman J, Cornelissen M, Michiels F;
                                                                                    /loces vector
/note= "pUC19 derived vecomplement (2019..2283)
                                                                                                                                                                                              complement (2284..2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 33-37; 56pp; English.
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                   of rice
 rice; Oryza sativa; ds; cyclic
                                                                                                                                             sou,
                                                                                                                                                                                   T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                         /*tag= e
/label= P35S
                                                                                                                                                                                                                                                                                                                                                                                                                                /label= 3/g7
                                                                                                                                                                                                                                                             - d
1- PE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95EP-0400364,
                                                                                                                                                                                                                                                                                                                                                                           /*tag= f
/label= bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-EP00722
                                                                                                                                                                                                                                                                                                            1336..5710
                                                                                                                                /*tag= b
/label= 3'
                                                               .2003
                                                                                                                                                                                                                                                                          /labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-402373/40.
                                                               misc_feature
                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                            polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1996
                         Synthetic.
                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                            CDS
```

Length 6548;

DB 17;

45.5%; Score 188.8;

Query Match

_

95EP-0401844

```
06-JUN-2000
       04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                  AAZ91096;
                                                                                                                                                                                   copies
                                                                                                                                                                                                                                                                                                                                                               AAZ91096,
                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                  g
       ö
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                    /note= "35S promoter region of cauliflower mosaic virus"
                                                                                                                                                                                                                                                                                /note= "3' untranslated region contg. the poly-A signal of Agrobacterium T-DNA nopaline synthase gene" complement (2289.2624)
                                                                                                                                                                                                                                                                                                                                                                                                                              '3' untranslated region contg. the poly-A signal of gene 7 of Agrobacterium T-DNA"
                                                                                                                                                                                               Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP; niacinamide; Agrobacterium; T-DNA; male sterile; barnase; ribonuclease; RNase; cereal; wheat; Triticum aestivum;
       ;
                                                                                                                                                                                                                                                                                                                                                                                                    'note= "phosphinothricin acetyltransferase"
      Indels
                                                                                                                                                                                                                                                                                                                                            gene"
                                                                                                                                                                                                                                                                                                                                           /note= "promoter region of rice El
complement (4336..5710)
99.0%; Pred. No. 4.7e-30; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                              complement (2019..2288)
                                                                                                                                                                                                                                                                                                                 /product= barnase
complement (2625..4313)
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                              Chimeric Agrobacterium sp.;
Chimeric Oryza sativa;
Chimeric cauliflower mosaic virus.
                                                                                                                                            BP.
                                                                                                                                                                                                                                                                            3'nos
                                                                                                                                                                                                                                                                                                                                                              P35S
                                                                                                                                            AAT61394 standard; DNA; 6548
                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                     /label- PE1
                                                                                                                                                                                                                                                                                                                                                                                             /label- Bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95EP-0401844.
                                                                                                                                                                                                                                                                                                                                                                                                                       /label= 3'g
/note= "3'
                                                                                                                                                                                                                                                                                                                                                                                                           6243..6496
                                                                                                                                                                                                                                                                                                                                                                                 5711..6262
                                                                                                                                                                      (first entry)
      Conservative
                                                                                                                                                                                                                                                                     /*tag= //label= :
                                                                                                                                                                                                                                                                                                                                                         /*tag= (
/label= 1
                                                                                                      6362 ACATTGCCGTAG 6351
                                                                                               acattgccgtag 415
190; Conserv
                                                                                                                                                                                                                  plasmid pTS172; ds.
                                                                                                                                                                                   Plasmid pTS172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1995;
                                                                                                                                                                     07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                EP757102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1997
                                                                                                                                                         AAT61394;
                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                 promoter
Local
                                                                                                                                                                                                                                                        Key
3'UTR
                                                                                                                                     AAT61394/c
                                                                                                                                                                                                                                                                                                                                                                                                          3'UTR
                                                                                               404
                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                 CDS
                              a
                                                        셤
                                                                                g
                                                                                              ö
                                                                                                           a
                                                                                                                                                         à
                                                                     ð
```

```
Plasmid pTS172 (AAT61394) contains the barnase coding sequence under control of the rice El gene stamen-specific promoter and a phosphiothricin acetyltransferase coding sequence under control of the CaWW 355 promoter. Brassing pTS172 and plasmid pTS772 (see also AAT61395) were used to transform wheat Spring variety Pavon calli via particle bombardment. Some calli were treated with the poly-(ADP-ribose) polymerase inhibitor niacinamide before, or before and after, bombardment. Healthy, male sterile plants were regenerated only from bombarded calli that were treated with niacinamide. This was believed to be due to more faithful expression characteristics of the integrated stamen-selective batnase gene in these calli and regenerated shoots. For plants transformed with pTS172, foreign DNA was stably incorporated in the wheat genome in 2-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
                                                                                                                                                                                               Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 45.5%; Score 188.8; DB 18; Length Best Local Similarity 99.0%; Pred. No. 4.7e-30; Matches 190; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli plasmid pTS172 containing synthetic barnase gene.
                                                                                                                                                                                                                                                                                                                                   Example 2; Page 17-20; 25pp; English.
(PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ91096 standard; DNA; 6548 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-111050/11.
                                                                                                                                                                                                                                                                 reduces metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200008176-A1.
```

æ

```
22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PolyA_signal
                   Hamada K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                             AAT39337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
          ð
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                      á
                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                           The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AAZ91095) for expression specifically in the anther of a plant. This sequence represents the E. coli/Agrobacterium shuttle vector plasmid pTS172 which contains the synthetic barnase gene (AAZ91094) under control of the cauliflower mosalc virus 35s promoter. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell.
                                                                                                                                                                                                                                                                                               Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undestrable characters by specifically expressing the gene alone in anther
                                                                                                                                                                                                                                                                                                                                             6363
                                                                                                                                                                                                                                                                                                                                    284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacat 343
                                                                                                                                                                                                                                                                                                                                                                              403
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                       344 aaatttattgatgcaagtttaaattcagaaatatttcaataactgattatcagctggt
                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 6548;
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                  Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                            Query Match
45.5%; Score 188.8; DB 21; Length
Best Local Similarity 99.0%; Pred. No. 4.7e-30;
Matches 190; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Male sterile plant; RNAase inhibitor; plasmid pTS346; ds.
                                                                                                                          Example 3; Page 19-23; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
AAF86441/c
ID AAF86441 standard; DNA; 7492
                   98JP-0220060.
 99WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2000; 2000WO-JP06222
                                    (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0279307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NISB ) JAPAN TOBACCO INC.
                                                     Hamada K, Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                           6362 ACATTGCCGTAG 6351
                                                                                                                                                                                                                                                                                                                                                                                                           acattgccgtag 415
                                                                      WPI; 2000-195581/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pTS346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200124616-A1.
03-AUG-1999;
                  04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF86441;
                                                                                                                                                                                                                                                                                                                                                                                                           404
ð
                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
ö
                                                                                                                                                                              The present invention relates to a method for producing male sterile plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                           Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function= 35S promoter of cauliflower mosaic virus strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 atagtttaaatattattgataaaataacaagtcaggtattatagtccaagcaaaacat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/label= barstar
/product= Bacillus amyloliquefaciens barstar
968..1287
/*tag= d
                                                                                                                                                                                                                                                                                                                                           Sequence 7492 BP; 1987 A; 1801 C; 1752 G; 1952 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 188.8; DB 22;
Pred. No. 4.7e-30;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= pGEM2
/note= "polylinker of pGEM2"
                                                                                                                                       Disclosure; Page 19-23; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT39337/c
ID AAT39337 standard; DNA; 1303 BP.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/label= P35s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695..967
Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36..694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7306 ACATTGCCGTAG 7295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                    WPI; 2001-266212/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 acattgccgtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
```

g

```
"n" in the sequence refers to not known nucleotides. pPS029 is identical to pVE36 (AAQ15144), but carries both the terminal modification and the internal modification of the Bt
                                                                                                                                                                                                                                            Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
               Bacillus thuringiensis; insecticidal crystal protein; ICP;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3201 BP; 880 A; 710 C; 720 G; 886 T; 5 other;
                                                                                                                                                                                                                                                                                             Disclosure; Fig 6(c); 78pp; English
                                                                                                                                                                                                                                                                                                                                                                     See also AAQ14529, AAQ15142-44.
                                                                                                                                                90EP-0401055
                                                                                                                                                                                              Soetaert P,
                                                                                                                                                                        GENETIC SYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                      WPI; 1991-339820/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 attgccgtag 415
                                                                                                                                                                                              Cornelissen M,
                                                                                                                                                                        PLAN-) PLANT
                          deletion; ss
                                                                                                                                                18-APR-1990;
                                                                         W09116432-A
                                                                                                 31-0CT-1991
                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH25423;
                                                                                                                                                                                                                                                                                                                                                          coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1167 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATATCAGCTGGTAC 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gion containing polyadenylation signal gene 7 og Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                               barstar DNA under control of a 355 promoter. The plasmid was used with pTS174 (see also AAT39336) contg. barnase DNA under control of the stamen-specific promoter El to produce male sterile rice cv. Kochihhbiki transgenic plants, and with plasmid pVB136 (see also AAT39338) contg. barnase DNA under control of the stamen-specific PCA55 promoter to produce male sterile maize plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible low level expression of barnase DNA in non-stamen tissue.
                                                                                                                                                                                                                                                                   Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac
                                                                                                                                                                                                                                                                                                                                                       The HindIII-EcoRI fragment (AAT3937) of plasmid pTS88 contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.4%; Score 188.4; DB 17; Length 1303;
1larity 99.5%; Pred. No. 5e-30;
Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
                                                                        pGEM2
                                                                                                                                                                                                                      Michiels F;
                                                /*tag= e
/label= pGEM2
/note= "polylinker of
               region
                                                                                                                                                                                                                                                                                                                               Example 1; Page 38; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA014529 standard; DNA; 3201 BP
                          of
                                                                                                                                                                                              GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pPS029 Bt ICP coding sequence.
                                                                                                                                                                                                                     Cornelissen M,
/label= 3'g7
                                                                                                                                              96WO-EP00722
                                                                                                                                                                      95EP-0400364
               /function=
                                    1288..1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGCCGTAG 1098
                                                                                                                                                                                                                                            WPI; 1996-402373/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                              (PLBZ ) PLANT
                                                                                                                                                                                                                      Botterman J,
                                    misc_feature
                                                                                              WO9626283-A1
                                                                                                                                              21-FEB-1996;
                                                                                                                                                                     21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-1992
                                                                                                                      29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ14529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1:
AAQ14529/
  BXBXGXB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

amino-ICP

Dockx J;

Stam M,

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene; fertility restorer gene; barstar gene; ss.
                                                                                                                                                                                          3022
                                                                          405
                                          Gaps
                                                                                                                                                                            286 agtttaaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa
                                                                                                                                                                                                                                 atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac
  Length 3201;
                                        ö
Score 188.4; DB 12; Length
Pred. No. 5.3e-30;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of plasmid pTHW118.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH25423 standard; DNA; 4832 BP
  Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces hygroscopicus.
Arabidopsis thaliana.
Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2001 (first entry)
```

```
07-MAY-1997
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             AAT59531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_RNA
                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                    286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'UTR
                                                                                                                                                                                                                                                                                                                                                                                    AAT59531
         ð
                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                    ο
                                                                                                                                                                                                                                                                                                                                                   셤
                                    /*tag~ a
/note= "right border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                   /note= "atSIA ribulose-1,5-biphosphate carboxylase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= p
/note= "left border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                    /*tag= j
/note= "Tag1 fragment from 3' UTR of nopaline
synthase gene from T-DNA of pTiT37 and
containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                           /note= "downstream of Bacillus amyloliquefaciens barstar coding region" complement (2981..3253)
                                                                                                                                                                                                                                                                                                                                                                                            /noce= "Barstar gene coding region from Bacillus amyloliquefaciens" complement (3254.4762)
                                                                                                                                                                  /*tag= f
//tag= synthetic polylinker derived sequences"
complement (331..882)
                                                          /*tag= b
/note= "synthetic polylinker derived sequences"
                                                                                                                          /*tag= c
/note= "residual sequence from TL-DNA at right
border repeat"
                                                                                                                                                                                                                                                                                                                              *tag= k
/note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "anther-specific gene TA29 promoter from Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= o
/note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                   /noce- "synthetic polylinker derived sequences complement (2659.2919)
                                                                                                                                            /*tag= e
/note= "3' UTR from TL-DNA gene 7 of pTiB6S3"
                                                                                                                                                                                            /*tag= g
/note= "Streptomyces hygroscopicus bialaphos
resistance (bar) gene"
complement (883..2608)
                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2000; 2000WO-EP12872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0457037
                                                                                                                                                                                                                                                     2609..2658
                                                                                                                                                                                                                                                                                                                                              ..2980
                                                                                                                                                                                                                                                                                                                                                                                                                                              4763..4807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4808. 4832
                                                                                                                                                             310.330
                            ...25
'*tag≔
                                                                           54..90
/*tag=
                                                                                                                                                                                                                                                                                                                                                       *tag=
 Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40200141558-A1
                          misc_feature
                                                  misc_feature
                                                                         misc_feature
                                                                                                         misc_feature
                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Both G,
                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                                  3'UTR
                                                                                                                                                                                                                                                                           3'UTR
                                                                                                                                                                                                                                                                                                                                            3'UTR
                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                            CDS
```

```
ô
                                                                                                               The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is seed have agronomic performance, genetic stability and adaptability to seed have gronomic performance, genetic stability and adaptability to plasmid pFWW18. This plasmid comprises the barstar gene, which acts as fertility restorer gene. The plasmid is used to create transgenic
Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP; niacinamide; Agrobacterium; T-DNA; male sterile; barnase; ribonuclease; RNase; cereal; wheat; ollseed rape; Brassica napus;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 188.4; DB 22; Length 4832;
Pred. No. 5.5e-30;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    '3' untranslated region contg. the poly-A signal of gene-7 of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                          Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/label= RB
/note= "T-DNA right border"
complement (97..330)
                                                                              Example 1; Page 80-82; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (1..25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT59531 standard; DNA; 4946 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Agrobacterium sp.;
Chimeric Arabidopsis thaliana;
Chimeric Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/label= 3'g7
/note= "3' un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-DNA of plasmid pTHW107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 attgccgtag 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid pTHW107; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 attgccgtag 415
```

```
οy
                                                             g
                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid pTHW107 is a vector carrying T-DNA (AAT59531) comprising a barnase coding sequence under control of the tobacco TA29 gene stamen-specific promoter and a phosphinothricin acetyltransferase coding sequence under control of an Arabidopsis Rubisco small subunit gene promoter. Oilseed rape hypocotyl explants were infected with Agrobacterium tumefaciens C58ClRif carrying vector pTHW107 and helper T1 plasmid pMP60. In some treatments, the hypocotyls were treated with the poly-(ADP-ribose) polymerase inhibitor niacinamide (250 mg/l) 4 days prior to infection. Plants regenerated from niacinamide-treated transformed calli
                                                                 /*tag= d
/label= PSSU
/note= "promoter region of Rubisco small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and
                                                                                                                                                            /note= "3'untranslated region contg. the poly-A signal of the nopaline-synthase gene of Agrobacterium T-DNA" complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.4%; Score 188.4; DB 18; Length 4946; 99.5%; Pred. No. 5.5e-30;
                                                                                                                                                                                                                                                                                                  /note= "promoter region of tobacco TA29 gene" complement (4822..4946)
                                /product- phosphinothricin acetyltransferase complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               had a low copy number and displayed less variation in the expression profile of the transgenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;
                                                                                                         gene of Arabidopsis thaliana" complement (2658..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      /note= "T-DNA left border"
                                                                                                                                                                                                                                                          complement (3368..4876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 13-16; 25pp; English.
complement (331..882)
                                                                                                                                                                                                                                                /product= barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ž
                                                                                                                                                                                                                   /*tag= f
/label= Barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENETIC SYSTEMS
                                                                                                                                                  3'nos
                                                                                                                                                                                                                                                                                   /label- PTA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                               95EP-0401844.
                         /label- Bar
                                                                                                                                                                                                                                                                                                                                                                                                                                      95EP-0401844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 189; Conservative
                                                                                                                                     /*tag= (/label= :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-111050/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reduces metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PLBZ ) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                 EP757102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De Block M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                      promoter
                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                misc_RNA
                                                                                                                      3'UTR
                                                                                                                                                                                                     CDS
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

Search completed: February 25, 2002, 12:55:46 Job time: 3144 sec

13, Appli 1, Appli 1, Appli 1, Appli 45, Appli 1, Appli 1, Appli 5428147

Tue Feb

```
Sequence 595, App
Sequence 1137, Ap
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appli
Sequence 8, Appli
                                                                                                                                                                                         Sequence 1,
Sequence 1,
Patent No. 5
                                                                                                                                                                                                                                                                   Sequence 3,
                           Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: T-DNA OTHER INFORMATION: plasmid pTCO113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rubisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08894440
Patent No. 6025546
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: Copplement((98)..(330))
OCTHER INFORMATION: region containing polyadenylation
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οį
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene
OTHER INFORMATION: Arabidopsis (Pssu)
US-08-920-828-6
US-08-751-359-21
US-08-487-8268-13
US-08-446-855A-1
US-09-150-141-1
US-08-871-924A-1
US-08-673-768-1
US-08-673-768-1
5428147-1
US-09-078-485-1
US-08-998-416-595
US-08-998-416-595
US-08-998-416-758-1
US-07-991-8678-32
US-08-108-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
    8654

8654

19124

19124

8920

8920

1316

1588

15397

24595

8659

660

660

660

660

660
  RESULT 1
US-08-894-440-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5864
                                                                                                                                                           444
444
43.6
42.6
42.6
42.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
    υ
                                                                                                                                               ပပ
                                                                                                                                                                                                00000
                                                                                                                                                                                         (without alignments)
1165.530 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5, Appli
4, Appli
5428147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Appl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                February 25, 2002, 12:03:22; Search time 80.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5,
Sequence 4,
Sequence 6,
Sequence 6,
Sequence 6,
Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                          1 gtcgagtttggtgttcatga......cagctggtacattgccgtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sednence
Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             702406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/ina/5A_COMB.seg:*
/cgn2_6/ptodata/2/ina/5B_COMB.seg:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-549-680A-5
US-08-894-440-2
US-08-694-804-23
US-08-694-814-23
US-08-817-188-1
US-08-817-188-5
US-08-232-016-23
US-08-232-016-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-894-440-4
US-08-453-104-22
US-08-694-824-22
US-08-064-121-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-920-812-6
US-08-920-827-6
US-08-921-177-6
US-08-362-577C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-478-015-2
US-08-475-975-2
US-09-084-889-2
US-09-080-625-3
US-09-080-625-2
US-09-080-625-4
                                                                                                                                                                                                                                                                                                                                                                                                                            351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                                                                              US-09-698-903B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5864
65848
1303
3200
1303
3200
7556
7556
7556
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
11186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . . . .
```

Score

Result Š

000

191.4 1188.8 1188.8 1188.6 1188.4 1188.4 1188.4 1188.4 1188.4 1188.4 1188.4 1188.4 1188.4 1188.4

000

0000000000

υυ

sed

0B 0B

Minimum Maximum Database

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

gene

of

ō

```
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-817-188-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                 AME/KEY: misc_feature
LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene of
OTHER INFORMATION: promoter of nopaline synthase gene of
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (517)..(5489)
OTHER INFORMATION: amyloliquefaciens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((5840)..(5864))
OTHER INFORMATION: left border of Agrobacterium T-DNA
OTHER INFORMATION: left border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: Complement((3368)...(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana OTHER INFORMATION: tabacum (PTA29)
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.1%; Score 191.4; DB 3; Length 5864; 99.5%; Pred. No. 2.7e-37; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NNSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILIGO DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (1).(2003)
OTHER INFORMATION: pUC19 derived vector sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              % Sequence 1, Application US/08894440; Sequence 1, Application US/08894440; Patent No. 6025546; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.5
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5632 TACATTGCCGTAG 5620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 tacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
```

```
COTHER INFORMATION: Complement(12625)..(4313))

OTHER INFORMATION: promoter of the stamen-specific El gene of rice of the INFORMATION: (PEI)

FEATURE:
FAME/KEY: misc_feature
LOCATION: (4336)..(5710)

OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
FEATURE:
FEATURE:
OTHER INFORMATION: region coding for phosphinothricin acetyl
FEATURE:
NAME/KEY: misc_feature
FEATURE:
NAME/KEY: misc_feature
COCATION: (5262)
OTHER INFORMATION: region containing polyadenylation signal fo gene 7

OTHER INFORMATION: region containing polyadenylation signal fo gene 7

US-08-894-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: plasmid PTS172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REPERENCE: 2121-0127P
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PO7-31
EARLIER PELING DATE: 1996-07-31
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VEY. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                     Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
45.5%; Score 188.8; DB 3;
Best Local Similarity 99.0%; Pred. No. 1.1e-36;
Matches 190; Conservative 0; Mismatches 2;
                                        NAME/KEY: misc_feature
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08817188 Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
```

```
NAME/KEY: misc_feature LOCATION: 3001..3023
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_recomb
LOCATION: 1..7811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATTGCCGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                         CTHER INFORMATION: PEL: promoter region of El gene of rice
FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: PEL: promoter region of El gene of rice
FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: p35S: 35S promoter region of Cauliflower Mosaic
COTHER INFORMATION: p35S: 35S promoter region of Cauliflower Mosaic
COTHER INFORMATION: p35S: 35S promoter region of Cauliflower Mosaic
COTHER INFORMATION: p1cs
COTHER INFORMATION: acetyltransferase
COTHER INFORMATION: acetyltransferase
COTHER INFORMATION: acetyltransferase
COTHER INFORMATION: acetyltransferase
COTHER INFORMATION: 3/37: 3' untranslated region containing the
COTHER INFORMATION: p0lyadenylation signal of gene 7 of Agrobacterium
US-08-817-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 atagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacat 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 aaatttattgatgcaagtttaaattcagaaatatttcaataactgattatatacagctggt 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
LOCATION: Complement((2019)..(2288))
OTHER INFORMATION: 3' nots: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of the nopaline synthase OTHER INFORMATION: gene of Agrobacterium T-DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.5%; Score 188.8; DB 3; Length 6548; 99.0%; Pred. No. 1.1e-36; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CORNELISSEN, MARCUS
APPLICANT: REYNAERTS, ARLETTE
APPLICANT: COSSELE, VERONIQUE
APPLICANT: VAN ARRSEN, ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2289)..(2624))
OTHER INFORMATION: barnase: region coding for barnase
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08549680A Patent No. 5962768 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.0°
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 acattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
344 aaatttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggt 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 484..684
COTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Verson #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 194..218
OTHER INFORMATION: /note= "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: complement (729..1340)
OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.5%; Score 188.8; DB 2; Best Local Similarity 99.0%; Pred. No. 1.2e-36; Matches 190; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "T-DNA left border OTHER INFORMATION: sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1../811
OTHER INFORMATION: /label= vector pTRVA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEGNARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-0111P
TELECAMIONICATION INFORMATION:
TELEPAX: (703) 205-8050
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                       APPLICATION NUMBER: US/08/549,680A FILING DATE: 16 JANUARY 1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular MOLECULE TYPE: DNA (synthetic)
```

```
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3081 AGTITAAAIATITATIGATAAAAAAAGAGGGGGGTATIATATAGTCCAAGCAAAAACAIAA 3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 agtttaaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.4%; Score 188.4; DB 1; Length 99.5%; Pred. No. 1.3e-36; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
US-08-453-104-23
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFTCATION: 800
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY,AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRENCE/DOCKET NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
SEQUENCE CHRACATERICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-08-694-824-23/C
Sequence 23, Application US/08694824
Facent No. 5877306
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                   STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111111111
2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI
CTHER INFORMATION: fragment of pTS88
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(35)
COTHER INFORMATION: polylinker of pGEM2 (pGEM2)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (36)..(694)
COTHER INFORMATION: 355 promoter of Cauliflower Mosaic Virus strain
FEATURE:
NAME/KEY: misc_feature
LOCATION: (36)..(967)
COTHER INFORMATION: region coding for barstar of Bacillus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (695)..(367)
COTHER INFORMATION: amyloliquefaciens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (968)..(1287)
CTHER INFORMATION: of Agrobacterium T-DNA (3'97)
CTHER INFORMATION: region containing polyadenylation signal of gene 7
FEATURE:
NAME/KEY: misc_feature
LOCATION: (368)..(1287)
CTHER INFORMATION: of Agrobacterium T-DNA (3'97)
CTHER INFORMATION: Of Agrobacterium T-DNA (3'97)
COTHER INFORMATION: polylinker of pGEM2
USCATION: (1288)..(1303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 atttattgatgcaagtttaaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
45.4%; Score 188.4; DB 3; Length 1303;
Best Local Similarity 99.5%; Pred. No. 1.1e-36;
Matches 189; Conservative 0; Mismatches 1; Indels 0;
                                                 GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
TITLE OF INVENTION: Method to obtain male sterile plants
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
CURRENT FILING DATE: 1997-11-12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
ERNOTH: 1303
         Sequence 2, Application US/08894440 Patent No. 6025546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/08453104
Patent No. 5633446
GENERAL INFORMATION:
APPLICANY: CORNELISSEN, Marc
APPLICANY: SOETAERY, Piet
APPLICANY: STAM, Maike
                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1107 ATTGCCGTAG 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-453-104-23/c
                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

S

```
LOCATION: Complement((97)..(330))
OTHER INFORMATION: 3'97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4876))
OTHER INFORMATION: tabacum
OTHER INFORMATION: tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: Complement((2658)..(3031))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of the nopaline synthase OTHER INFORMATION: gene of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter region of Rubisco small subunit gene
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                   GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1997-05-15
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((311)..(882))
OTHER INFORMATION: Legion coding for phosphinotricin acetyl
OTHER INFORMATION: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 188.4; DB 3;
Pred. No. 1.4e-36;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((4922)..(4946))
OTHER INFORMATION: LB: T-DNA left border
                                            Sequence 1, Application US/08817188 Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: Complement((8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement(()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-817-188-1
                        US-08-817-188-1
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
              APPLICANT: CORNELISSEN, Marc
APPLICANT: SOFFAERT, Piet
APPLICANT: SOFFAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: IN SECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                              ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                               COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "Nucleotides 2078-2082 OTHER INFORMATION: wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.4%; Score 188.4; DB 2
99.5%; Pred. No. 1.3e-36;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TORNEY/AGENT INCOLLESS S
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 3200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 2078..2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

οţ

ö

Gaps

ö

Length 4946; Indels 9

```
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
agittaaatatitatigataaaataacaagicaggiattatagiccaagcaaaaaataa 345
                        atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac 405
                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW142
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1). (25)
OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from OTHER INFORMATION: prib653
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DE BLOCK, MARC

TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICANTON NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 5560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (84)..(296)
OTHER INFORMATION: 3' g7: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (4483)..(4671)
OTHER INFORMATION: IV2: region corresponding to the second intron of OTHER INFORMATION: the ST-LS1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU: promoter region of Rubisco small subunit
OTHER INFORMATION: gene of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (3059)..(5056)
OTHER INFORMATION: uidA: region coding for beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (318)..(869)
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08817188 Patent No. 6074876 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                   234 attgccgtag 243
                                                                                                                                                                406 attgccgtag 415
                                                                                                                                                                                                                                                                       RESULT 9
US-08-817-188-5
                                                                              346
                                   요
                                                                          à
                                                                                                             요
                                                                                                                                                           à
                                                                                                                                                                                            g
```

```
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (5533)..(5560)
OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
OTHER INFORMATION: pTIB6S3
                                                                                                                                                                                                                           ç
                                                                                                                                                                                                                                                                      NAME/KET: misc_feature
| IOCATION: (5077)..(5078)
| OCHER INFORMATION: region with unknown sequence (may contain up to OTHER INFORMATION: nucleotides)
| FEATURE: | NAME/KEY: misc_feature | LOCATION: (3476)..(5479) | OTHER INFORMATION: region with unknown sequence (may contain up to US-08-817-188-5
                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (5058)..(5059)
OTHER INFORMATION: region with unknown sequence (may contain up OTHER INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SOCRAELISEN, MAIC
APPLICANT: SOCRAERT, Piet
APPLICANT: SOCRAERT, Piet
APPLICANT: STAM, MAIKE
APPLICANT: STAM, MAIKE
APPLICANT: STAM, MAIKE
APPLICANT: STAM, MAIKE
APPLICANT: VAN AARSEN, Roel
ITILE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STREET: Virginia
COUNTY: United States
INFE: Virginia
COUNTY: United States
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                             of CaMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
45.4%; Score 188.4; DB 3;
Best Local Similarity 99.5%; Pred. No. 1.4e-36;
Matches 189; Conservative 0; Mismatches 1;
iON: (5067)..(5502)
INFORMATION: P35S: 35S promoter region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/08232016
Patent No. 5952547
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 attgccgtag 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-016-23/C
```

```
LOCATION: 1.1869
OTHER INFORMATION: /note= "Coding region of a
OTHER INFORMATION: truncated bt2 (cryIAb) gene, also designated as the bt884
                                                          2070 GTACATGGTCGATAAGAAAAGGCAATTTGTAGATGTTAATTCCCATCTTGAAGAAATAT 2011
                                                                                                                                                                           346 atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: VAN ARSSEN, Roel
APPLICANT: VAN ARSSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: FF 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION NUMBER: GB 92400820.4
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: plasmid DNA designated as pJD884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MGGOWAN, MAICOIM K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMNUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 7639 base pairs
LENGTH: 7639 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/08232016 Patent No. 5952547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: CORNELISSEN, MArc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                 1890 ATTGCCGTAG 1881
                                                                                                                                                                                                                                                     406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-08-232-016-22/c
                                                                                                     g
                                                                                                                                                                                                  qq
                                                          Qγ
                                                                                                                                                       ò
                                                                                                                                                                                                                                                     δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
COTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
CACATION: 3582..4407
CTHER INFORMATION: Anote= "3' regulatory sequence
OTHER INFORMATION: Containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Coding region of a truncated modified bt2 (cryIAb) gene, also designated as the truncated modified bt2 (cryIAb) gene, also designated as the \ensuremath{\mathsf{L}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to nt No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.4%; Score 188.4; DB 2; Length 7566; Best Local Similarity 99.5%; Pred. No. 1.5e-36; Matches 189; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 2922.3581
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 2396..2921
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: plasmid DNA designated as pPS0212
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MR-1992
ATTONNEY/AGENT INFORMATION:
NAME: MGGOWAN, MALCOLM K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECHONE: (703) 836-620
TELECHONE: (703) 836-620
TELEPHONE: (703) 836-2021
INFORMATION FOR SED ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7566 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  crylAb6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 5600..6457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.1785
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
; OTHER INFORMATION:
US-08-232-016-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
```

NAME/KEY: misc_feature

226

```
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 agtttaaatattattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATION: Complement((2659)..(3031))
COTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA OTHER INFORMATION: (3'nos)
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                    LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5864;
                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (5217)...(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                        LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; LOCATION: Complement((5840))..(5864)); OTHER INFORMATION: left border of Agrobacterium T-DNAUS-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.0%; Score 186.8; DB 3;
98.9%; Pred. No. 3.4e-36;
.lve 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (4924)...(5216)
OTHER INFORMATION: promoter of nopaline synthase
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
                    INFORMATION: plasmid prc0113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.9
Matches 188; Conservative
                                                                                                                                                  NAME/KEY: misc_feature
                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                  OTHER INFORMATION: /note= "3' regulatory sequence OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
                                                                                                                                                                                                                                                                                                                                              LOCATION: 3666..4491
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2154 GTACATGGTCGATAAGAAAAGGCAATTTGTAGATGTTAATTCCCATCTTGAAGAAAATT 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2094 AGTTTAAATATTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAAACATAA 2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 agittaaatatitatigataaaataacaagicaggiattatagiccaagcaaaaacataa 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                      LOCATION: 3006..3665
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenical acetyl transferase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                        LOCATION: 2480..3005
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 7639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08894440
| Patent No. 6025546
| GENERAL INFORMATION:
| TITLE OF INVENTION: Method to obtain male sterile plants
| FILE REPERENCE: NMGOOR
| CURRENT APPLICATION NUMBER: US/08/894,440
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 4
| ENGTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature

1.CCATION: 7155..7639

2.OTHER INFORMATION: /note= "TR1' and TR2' promoter

3.0THER INFORMATION: derived from Agrobacterium T-DNA."

US-08-232-016-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 5684..6541
OTHER INFORMATION: /note= "Sequence complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.4%; Score 188.4; DB 2
99.5%; Pred. No. 1.5e-36;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 3666..4491
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 5684..6541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.5:
Matches 189; Conservative
1877..2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1974 ATTGCCGTAG 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 attgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
TITLE OF INVENTION: IN PLANT CELLS
TORRESPONDENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 attgataaaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgca 358
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
CLASSIFICATION: 536
PROOF APPLICATION NUMBER:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
CLING DATE: 16-DEC-1992
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 2151.2155
OTHER INFORMATION: /note-"Nucleotides 2151-2155
OTHER INFORMATION: wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
42.7%; Score 177; DB 2;
Best Local Similarity 100.0%; Pred. No. 6.5e-34;
Matches 177; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               Sequence 22, Application US/08694824 Patent No. 5877306 GENERAL INFORMATION:
                                                                                                                                                                                                                     APPLICANT: CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Rea, Teresa S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11.
MOLECULE TYPE:
                                                                                                         RESULT 14
US-08-694-824-22/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-694-824-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                          APPLICANT: CORNELISSEN, MARC
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "Nucleotides 2151-2155 OTHER INFORMATION: wherein N is not known." US-08-453-104-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States
ZIP: 22313-1404
MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.7%; Score 177; DB 1; L. Best Local Similarity 100.0%; Pred. No. 6.5e-34; Matches 177; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 94401055.0
FILING DATE: 18-APR-1990
ATTORNEY, AGGNT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
FELECHOMENICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
                                                                                                                                               Sequence 22, Application US/08453104
Patent No. 5633446
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 2151..2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 800
406 attgccgtag 415
               234 attgccgtag 243
                                                                                                                           US-08-453-104-22/c
                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

us-09-698-903b-8_1.rni

```
õ
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 791.1186
OTHER INFORMATION: /Label= 3'97
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                          APPLICANT: D'HALLOIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BLING, DOGNE, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandia
STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,121
FILING DATE: 24-MAY-1993
CLASSIFICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 30-NOV-1991
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/TOCKET NUMBER: 36,113
REGUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
LENGTH: 1186 base pairs
LENGTH: 1186 cacid
STRANDEDNESS: double
                                                                                                                                                                         Sequence 2, Application US/08064121
Patent No. 5641664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
FEATURE:
NAME/KEY:
LOCATION: 1.8
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11nea
MOLECULE TYPE: DN
HYPOTHETICAL: NO
                                                                                                                          RESULT 15
US-08-064-121-2/c
     à
                                            g
```

```
Gaps
                                                                              ö
                                             Query Match 36.9%; Score 153; DB 1; Length 1186; Best Local Similarity 100.0%; Pred. No. 2.8e-28; Matches 153; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                          Search completed: February 25, 2002, 12:53:10 Job time: 2988 sec
; OTHER INFORMATION: T-DNA gene 7" US-08-064-121-2
```

THIS PAGE BLANK (USPTO)

OM nucleic

Run on:

Searched:

Minimum Maximum Database

000000

Result 8 0 N

Sequence:

```
AU087444 AU087444
ALIO8796 Drosophil
ALIO895 Drosophil
ALIO895 Drosophil
ALIO895 Drosophil
ALO75824 Drosophil
ALO75824 Drosophil
ALO75824 Drosophil
ALO71865 Drosophil
ALO71865 Drosophil
ALO71865 Drosophil
ALO71865 Drosophil
ALO71865 Drosophil
ALO71865 Drosophil
ALO73234 Tetraodon
ALIO3735 Drosophil
ALO63784 Drosophil
ALO6378 Drosophil
ALO6376 ALS66565
ALO6408 Drosophil
ALO6576 Drosophil
ALO6706 Drosophil
ALO6706 Drosophil
ALO6706 Drosophil
ALO6706 Drosophil
ALO6706 Drosophil
ALO6708 Drosophil
ALO6708 Drosophil
ALO6708 Drosophil
ALO6708 Drosophil
ALO6708 Drosophil
ALO64089 Drosophil
BE71264 BRAC-201
ALO64089 Drosophil
BE12664 BRAC-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence T7 end of BAC BACOVALLO of DrosBAC library from Drosophila melanogaster (fruit AL099163
                                                                                                                                                                                                                                                                                                                                                                                                               fruit fly.
Plasmid Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. 734
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACNO4L20"
                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                         CNSO0J7I
CNSO0EPO
CNSO1U9O
CNSO0FUH
                                                                                                                                                        CNS009G1
CNS02A0C
CNS01400
CNS00EVL
                                                                                                                                                                                                                     CNS0022U
AQ272964
CNS003BB
CNS016CO
                                                                                                                                                                                                                                                               AQ326762
BH126604
CNS014PQ
               CNS0182A
CNS0155H
CNS0106X
                                                                                            CNS038CX
CNS00DKY
CNS0039G
CNS00FMC
CNS0562R
CNS0145P
CNS01607
                                                                                                                                                                                            BF274512
AL566565
CNS00CYH
                                                                                                                                                                                                                                                                                                                                                                                                AL099163.1 GI:5610774
pBeloBAC11
Genoscope.
                                                 23
                                                                                                                                                                                                                                                                                                                                                     LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                    RESULT
CNS010MP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
υυ
                                                                                                                                                                                                ပပ
                                                                   (without alignments)
3191.557 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL099163 Drosophil
AL238491 Terraodon
AL038491 Terraodon
AL065632 Drosophil
AL06866 Drosophil
AL06896 Drosophil
AL064091 Drosophil
AL064091 Drosophil
AL067032 Drosophil
AL067032 Drosophil
AL067032 Drosophil
AL067034 Drosophil
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                          ; Search time 1397.28 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                            1 gtcgagtttggtgttcatga......cagctggtacattgccgtag
                                                                                                                                                                           22703874
        4.5
Compugen Ltd.
                                                                                                                                                        11351937 seqs, 5372889281 residues
                                                                                                                                                                         hits satisfying chosen parameters:
        GenCore version
Copyright (c) 1993 - 2000
                                                         February 25, 2002, 12:03:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                      summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS0042W
CNS03D01
CNS00B8
CNS00238
CNS016L1
AQ506817
CNS003BD
CNS003BD
CNS00GUL
CNS00GUL
                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS010MP
                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                            em_gss_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                em_gss_pro:*
em_gss_rod:*
em_gss_vrt:*
                                                                                                                                                                                          DB seq length: 0
DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                       em_gss_hum:*
em_gss_inv:*
                                                                                            US-09-698-903B-8
                                                                                                                                                                                                                                                                                                                                                                      gb_gss:*
em_gss_fun:*
                                                                                                                                                                                                                                                                                                                                                                                                        em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1333333333333
                                                                                                                                                                                                                                                               em_estfun:*
em_esthum:*
                                                                                                                                                                                                                                                                                em_estin:*
em_estom:*
em_estpl:*
em_estba:*
em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length DB
                                                                                                                                                                                                                                                                                                                                  em_htc:*
gb_est1:*
gb_est2:*
gb_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          734
1101
1101
1101
1101
1101
537
987
1101
893
                                                                                                                                                                                                                                                       EST: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115.2
113.2
113.2
113.2
113.2
113.2
113.2
                                                                                                                                                                                                                                                                                          Potal number of
                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                               Scoring table:
```

```
Best Local Similarity
Matches 149; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS03D0I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS03D01/c
                                                                                                                                                                                                                                928
                                                                                                                                                                                                                                                                                                                                                                                                     313
                                                                                                                                                                                                                                                                 194
                                                                                                                                                                                                                                                                                                                                   253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                           g
                                                                                                                              δ
                                                                                                                                                           g
                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                               쉽
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ulrect submission.

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Wab. :www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Droscophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Droscophila melanogaster genome using these BACs: For further information please see http://www.fruifily.org The BDGP Droscophila melanogaster BAC ilbrary was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, ECORI digestion of Droscophila DNA provided by the BDGP from the 180genic strain y2: on bw spy, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Localing/Qualifiers

Source Genetic Center can be Conce. The Conce of Center can be Localing/Qualifiers

Found at http://bacpac.med.buffalo.edu/droscophila_bac.htm.
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSO04ZW 1101 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR11E08 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                189 aagtattatataaattataattataattatggtaggatgtacatggccgataagaaaggc 248
                                                                                                                                                                    249 mattigtagatgitaatteceatetigaaagaaatatagittaaatattattgataaaa 308
                                                                                                                                                                                                                                    309 taacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaaatt 368
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                           ö
                                                                                       Length 734;
                   171 others
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"

    5; Score 63; DB 13; L.
    5; Pred. No. 0.0079;
    43; Mismatches 79;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253
                211 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                        233 AWAMAATATWWMAAAAMWWWWWTAT 259
                                                                                                                                                                                                                                                                                                                                                        cagaaatatttcaataactgattatat 395
                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone-"BACR11E08"
                N
/note-"end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL055440.1 GI:4932241
                                                                                  Query Match
Best Local Similarity 41.1%;
Matches 85; Conservative 4:
                62 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
              288 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
CNS0042W/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                    369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                  ð
                                                                                                                                                                             g
                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                   g
```

Length 1101;

DB 13;

Score 61;

14.78;

Query Match

```
GSS; genome survey sequence.

GSS; genome survey sequence.

Tetraodon ingroviridis

Tetraodon ingroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

E 1 (bases 1 to 844)

S Roest-Crollius, H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetler,F., Saurin,W., Bernot,A. and Weissenbach,J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 844)
bost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                            Tetracdon nigroviridis genome survey sequence PUC-Ori end of clc 015L14 of library G from Tetracdon nigroviridis, genomic survey sequence.
                                                                                                                                                                                                134 tatacaaatagtagcgaagaaatccatgtaaagcagcagggggcaccatggtttcaagta 193
                                                                                                                                                                                                                                                                                                                                         TATWAATAWAATHWTAAWATAAAAAAWTAWAAAWATATAWTAAAWATTTTAWTTATTK 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaaattcaga 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                            ttcatgattttgggttttgactcttcaccattacatattgaaactcttacggatgagaac 73
                                                                                                                                                                                                                           ttatataaattat-aattataattatggtaggatgtacatggccgataagaaaaggcaatt
                                                          ij
                       Pred. No. 0.018;
1; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           718 AATMTAAWAMTGTKTATATATTH 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 aatatttcaataactgattatatc 396
38.8%; Pic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL238491
AL238491.1 GI:7897626
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
```

```
228
   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS00Z38/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EWR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecost digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO00BB 1101 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR01A24 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                            actettacggatgagaacaacteacaagcattaateatgtteatataaatatatgtacat 115
                                                                                                                                                                                                                                                                                                    tatacgtatatatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggg 175
                                                                                                                                                                                                                                                                                                                                       235
                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AAAAAAAAAAAAAAATTAAATWAAAACMTAAATGATAAAAAAAAAAAAAATTAAAAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 tttattgataaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgat 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AAAAAAAAAAAAAATATACAMATAAAAATAAAAAAAGAATAAAAAAATATAACTTAWC 188
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophija melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                 /clone_lib="G"
/note="Genoscope sequence ID : C0BG015DF07SP1-end
PUC-Or1"
                                                                                                                                                                                                                                                                                                                                                                             176 gcaccatggtttcaagtattatatataattataattataattatggtaggatgtacatggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                 Length 844;
                                                                           others
                                                                                                                                                                                        Indels
                                                                           40
                                                                                                                                                 Query Match 13.8%; Score 57.2; DB 13; Best Local Similarity 47.0%; Pred. No. 0.099; Matches 155; Conservative 6; Mismatches 169;
                                                                         ų
                                                                         484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 gcaagtttaaattcagaaatatttcaataa 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey sequence. AL063632
                                                                           6
                                                                         89
/clone="015L14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL063632.1 GI:4938680
                                                                         79 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit fly.
                                                                           ه
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNS000B8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                              487
                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                    116
                                                                                                                                                                                                                                                                                                                                                                                                                                                         236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                         ORIGIN
                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -, This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence SP6 end of BAC BACNOIA24 of DrosBAC library from Drosophila melanogaster (fruit AL097166
                                                                                                                                                                                                                                                                                                                                                                             1087 AWAAWAAATTAAATTTTWWAAAAAAAAAAAATTATAAAWIWATWTWTWAWAWTAATA-A 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               849
                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 tatagtttaaat---atttattgataaaataacaagtcaggtattatagtccaagcaaaa 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 aatatatgtacattatacgtatatatacacgtatacaaatagtagcgaagaaatccatgt 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 acataaatttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagc 399
                                                                                                                                                                                                                                                                                                                            43 attacatattgaaactcttacggatgagaacaactcacaagcattaatcatgttcatata 102
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterrygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilldae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 aaagcagcaggggggggcaccatggtttcaagtattatataattataattataattatggtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                           Length 1101;
                                                                                                                             others
                                                                                                                                                                                                                                                                             Indels
/organism="Drosophila melanogaster"
/db_xref="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR01A24"
                                                                                                                          137
                                                                                                                                                                                                                        ; Score 57.2; DB 13;
; Pred. No. 0.094;
56; Mismatches 165;
                                                                                                                             ų
                                                                                                                          512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .1101
                                                                                                /note="end : TET3"
114 c 110 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL097166.1 GI:5608777
                                                                                                                                                                                                                           13.8%;
39.5%;
                                                                                                                                                                                                                                                                             Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 tggtacattgcc 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 AATTAWATTHCM 717
                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope.
```

us-09-698-903b-8_1.rst

Conservative

```
96;
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
AQ506817/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                        43
                                                                                                                                                                                                                                                                  283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                               g
                                                                                             ð
                                                                                                                        d
                                                                                                                                                                             qq
                                                                                                                                                   à
                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre Drosophila du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence T7 end of BAC BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                      186 ttcaagtattatataattataattataattataggtaggatgtacatggccgataagaaaa 245
                                                                                                                                                                                                                 anataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagttaa 365
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila, Genoscope.
                                                                                                                                                                            ö
                                                                                                                                                Length 1101;
                                                                                          others
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .1101
/organism-"brosophila melanogaster"
/plasmid-"pBeloBAC11"
/db_xref-"taxon:7227"
/clone_llb-"brosBAC"
/clone="BACM16D22"
/note="end:17"
/organism="Drosophila melanogaster"
/plasmid="pbeloBAC11"
/db_xref="taxon:7227"
/clone_lib="brosBAC"
/clone="BACN01A24"
                                                                                         93
                                                                                                                                                 2;
0.094;
85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436
                                                                                                                                              DB 13;
                                                                                         Ļ
                                                                                                                                                      Bost Local Similarity 41.4%; Pred. No. 0.09
Matches 87; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      u
                                                                                       386
                                                                                                                                             13.8%; Score 57.2; 41.4%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158
                                                                                                                                                                                                                                                                                                                                                                                      366 attcagaaatatttcaataactgattatat 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid Drosophila melanogaster
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL106896.1 GI:5624374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS016LI
                                                                                    308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                             306
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS016LI/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                              g
```

Score 55.4; DB 13; Length 1101; Pred. No. 0.21;

Best Local Similarity

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ506817 537 bp DNA GSS 29-APR-1999
RPCI-11-281J17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-281J17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 537)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)
Other_GSSS: RPCI-11-281U17.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
                                        attacatattgaaactcttacggatgagaacaactcacaagcattaatcatgttcatata 102
                                                                                                                                aatatatgtacattatacgtatatacacgtatacaaatagtagcgaagaaatccatgt 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
1 1 c 30 g 280 t
                                                                  282
                                                                                                                                                                                                                                                                                                                                                                                                     tatagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaca 342
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                          163 aaagcagcagggggcaccatggtttcaagtattatataattataattataattatggtag
                                                                                                                                                                                                                                                      ;
0
    Indels
    138;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .537
/organism="Homo sapiens"
/db_xref="GDB:7607752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="RPCI-11-281J17"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ506817.1 GI:4711564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 taaatttattgat 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     750 ATMANTITITIWI 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ50681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
```

g ò g

ద ð a

à

g à g

ò

ö

ö

```
Web: www.genoscope.cns.fr.n.

- Web: www.genoscope.cns.fr.n.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org rhe BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI disection of Drosophila DNA provided by the BDGP from the isogenic strain y2: on by sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K08 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                          184 gtttcaagtattatataattataattataattatggtaggatgtacatggccgataagaa 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaggcaatttgtagatgttaattoccatottgaaagaaatatagtttaaatatttattga 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tatatacacgtatacaaatagtagcgaagaaatccatgtaaagcagcagggggcaccatg 183
                                                                                                                                                                                                                                                                                                            710 TWTTTTTTTTTAAWAAAAWWAAAWAAAWTWTTAAWATWWTTTAAAGAAAWTTATAAA 769
                                                                                                                                                                                                                                                                                                                                                                                                       taaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagttt 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 ggatgagaacaactcacaagcattaatcatgttcatataaatatatgtacattatacgta 123
                                                                       gagtttggtgttcatgattttgggttttgactcttcaccattacatattgaaactcttac 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                   590 RRBKKBNKKKKKKKKKTKTTTTTTKAYMWCTBKCCCCCCCCCMMMAMAAMAAWM
                                                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="Laxon:7227"
/clone_lb="RPCI-98"
/clone="BACROBRO8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
                           182;
       Pred. No. 0.27:
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fly), genomic survey sequence. AL064091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaattcagaaatatttcaataactg 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WWWWWTTTTTTTTTKAWKTTKNKG 974
                        103; Conservative 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL064091.1 GI:4941847
    26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1101 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope.
Direct Submission
       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS003BD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               950
                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
CNS003BD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                 g
                                                                                                                                                               ò
                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                         å
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                   ,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   When years of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etudé du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN12P22 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                           tatatgtacat-tatacgtatatacacgtatacaaatagtagcgaagaatccatgta 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                      280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214
                                                                                                                                                                                                                                                                                                         aagcagcaggggggcaccat---ggtttcaagtattatatatattataattataattatggt 220
                                                                                                                                                                                                                                                                                                                                                                                                    333 TATCCATATATATAAATATATACATATATATAAATATATATAAATATATAAATATATATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacatattgaaactcttacggatgagaacaactcacaagcattaatcatgttcatataaa 104
                                                                                                                                                                                                            453 ТАТАТАТАААТАТАТАТАТАТАТАТАТАСАТАТАТААТАТАТАТАТАТАТАТАТАТАТАТАТА 394
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthrópoda; Tracheata; Hexapoda; Insecta; Pterryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      aggatgtacatggccgataagaaaaggcaatttgtagatgttaattcccatcttgaaaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 aatatagtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 cataaatttattgatgcaagtttaaattcagaaatatttcaaataactgattatat 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54.8; DB.13; Length 987;
                                                                       DB 13; Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    others
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
                                                                                             Pred. No. 0.28;
0; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 t
                                                                       Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN12P22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL104456.1 GI:5616067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.28;
                                                                    13.3%;
51.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            987 .bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 c
                                                                  Query Match 13.39
Best Local Similarity 51.0°
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNS014PQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                        164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                               45
                                                                                                                                                                                                                                                           105
                                                                                                                                                                                                                                                                                                                                                                                                                                                   221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
CNS014PQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
ORIGIN
```

of a

```
Query Match
```

us-09-698-903b-8_1.rst

à g ö 8

g ð

à q à g

g à

à g

```
Query Match
Best Local Simi
Matches 100;
                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSOOEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
- Dlease see http://www.fruitfly.org The BDGP Drosophila
- Maron Mammoser in Pleter de Jong's laboratory in the Department of Aaron Mammoser in Pleter de Jong's laboratory in the Department of NY. The library is named RPCI-gB and was constructed by partial
- EcoRI digestion of Drosophila DNA provided by the BDGP from the
- Blogenic strain y2; cn bw sp, the same strain used for the BDGP's
- A more detailed description of the library and how to order individual BAC clones, the entire library, or
- filters for hybridization from the BACPAC Resource Center can be
- found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome survey sequence T7 end of BAC: BACRSBJ18 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                   607
                                                                                                                                                                                                                                           207
                                                                                                                                                                                                                                                                                                                                           208 ttataattatggtaggatgtacatggccgataagaaaaggcaatttgtagatgttaattc 267
                                                                                                                                                                                                                                                                                                                                                                                                                             728 TATATAWIWITITAWAAATATATTAAAAAAWATAWITITTATITATATAAAAATATWATW 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccatcttgaaagaaatatagtttaaatatttattgataaaataacaagtcaggtattata 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        788 ATTTATATATATWWATAWTTWTTWATAWTTWAATWTWAATWTTAAATWTWAWA 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             giccaagcaaaaacataaatitatigaigcaagiiitaaaiicagaaataiiicaataaci 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophija melanogaster
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                    28 ttttgactcttcaccattacatattgaaactcttacggatgagaacaactcacaagcatt
                                                                                                                                                                                          148 cgaagaaatccatgtaaagcagcaggggggcaccatggtttcaagtattataattataa
                                                                                                                                             ö
                                                                                                       Length 1101;
                               149 others
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS
                                                                                      DB 13;
                                                                                                                     ; Pred. No. 0.27;
32; Mismatches 189;
                           334 t
                                                                                                  13.2%; Score 54.8; 39.8%; Pred. No. 0.
/note="end : TET3"
120 c 103 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL076232.1 GI:4955810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     980 bp
                                                                                                                                 Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                   Similarity
                       395 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gattata 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       908 AAAAAA 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS00JG1
                                                                                              Query Match
                                                                                                                 Local
                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
CNS00JG1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
```

```
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the ISCORI digestion of Drosophila DNA provided by the BDGP from the ISCORI digestion of Drosophila DNA provided by the BDGP from the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Quallifiers

Location/Quallifiers
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope.

Direct Submission
Submitted (02-JDW-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNSOOEVL 1101 bp DNA GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                        181 atggtttcaagtattatatatatatataattataattatggtaggatgtacatggccgataa 240
                                                                                                                                                                                                                                                                                                                                                                                                        tgataaaataacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaag 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pteryota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                     Length 980;
                                                                                                                                                                                                                                                                                                                                     Indels
                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/dboalib="RRCI-98"
/clone="PaACR88118"
/note="end : 17"
                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29823"
                                                                                                                                                                                                                                                                                                                                95;
                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tttaaattcagaaatatttcaataactgattatat 395
                                                                                                                                                                                                                                                                                                        Pred. No. 0.3;
20; Mismatches
                                                                                                                                                                                297
                                                                                                                                                                                                                                                                             13.2%; Score 54.6; 46.5%; Pred. No. 0.
Location/Qualifiers
1. .980
                                                                                                                                                                          102 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL069706.1 GI:4949849
                                                                                                                                                                          112 c
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly.
                                                                                                                                                                          400
```

us-09-698-903b-8_1.rst

```
Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
CNSOOKHX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                           g
                                                                                                                                            δy
                                                                                                                                                                            a
                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNSO13XE 893 bp DNA GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN101010 of Drossbac library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        69 agaacaactcacaagcattaatcatgttcatataaatatatgtacattatacgtatatat 128
                                                                                                                                                           129 acacgtatacaaatagtagcgaagaaatccatgtaaagcagcaggggggcaccatggtttc 188
                                                                                                                                                                                                                                                                          aagtattatataaattataattataattatggtaggatgtacatggccgataagaaaaggc 248
                                                                                                                                                                                                                                                                                         249 aatttgtagatgttaattcccatcttgaaagaaatatagtttaaattttattgataaaa 308
                                                                                                                                                                                                                                                                                                                                                                                                        taacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaaatt 368
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 893)
                                                                                                                                                                                                                             ;
                                                                              Length 1101;
                  others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 others
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/plasmid="pbeloBAC11"
/db_xref="Laxon:7227"
/clone_lib="DrosBAC"
/clone="BACN10102"
/note="end : SP6"
                232
                                                                           13.2%; Score 54.6; DB 13;
33.7%; Pred. No. 0.29;
.1ve 62; Mismatches 156;
                ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 t
                299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1031 WIAATATWATAWWWIAWATATAWAWWA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 cagaaatatttcaataactgattatatca 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                  9
               9
: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL103436.1 GI:5615047
/note="end
                                                                                            Best Local Simitation
Matches 111; Conservative
               91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                                                                                                                      309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS013XE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

```
Direct Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Bringle 191006 Evric cans. fr. Parker edex - FRANCE (E-mail : seqref@genoscope.cns.fr. - Web : www.genoscope.cns.fr. Parker edex - FRANCE (E-mail : seqref@genoscope.cns.fr. - Web : www.genoscope.cns.fr. - Gollaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcokI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://www.institalo.com.du.disio.order.pub.
                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence T7 end of BAC:
BACRI7N06 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL077798
                                                                                                                                                                                                                                                      129 acacgtatacaaatagtagcgaagaaatccatgtaaagcagcaggggggacccatggtttc 188
                                                                                                                                                                                                                                                                                                                                                                                          304 AMAMTMTMMATTTTAAAMMAAMATANNTNTAAAAMTATNTTNAMTAAMAAAAAMTATMM 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 taacaagtcaggtattatagtccaagcaaaaacataaatttattgatgcaagtttaaatt 368
                                                                                                            agaacaactcacaagcattaatcatgttcatataaatatatgtacattatacgtatatat 128
                                                                                                                                                              124 АММИААМАТТАТАААААТТМАМТТААТТТМАТТТАТАМААТТАМАТТТАТАМААТТА 183
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-1999
                                                                                                                                                                                                                                                                                                                                     189 aagtattatataattataattataattatggtaggatgtacatggccgataagaaaaggc
                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 others
Length
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
DB 13;
                                                    26; Mismatches 169;
Score 54.4; DB Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 cagaaatatttcaataactgattatatcagc 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-98"
/clone="BACR17N06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:4957174
13.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  905 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 c
                                                    Matches 136; Conservative
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL077798.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS00KHX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
```

ŏ g δ g

208 ttataattatggtaggatgtacatggccgataagaaaggcaatttgtagatgttaattc

319 AATATTTTTATATATGATTATATATATATACATGGATAAGGAAAATAAAAAA 260 giccaagcaaaaacataaatttattgatgcaagtttaaattcagaaatatttcaataact 387

388 gattatat 395

328

δ g ò

qq à

268 ccatcttgaaagaaatatagtttaaatatttattgataaaataacaagtcaggtattata

œ

ORIGIN

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata: Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 500)
Watanabe,J., Sasaki,M., Suzuki,Y. and Sugano,S.
FULL-malaria: a database for a full-length enriched cDNA library
from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                    AU087444 500 bp mRNA EST 27-JAN-2001
AU087444 Sugano Malaria cDNA library Plasmodium falciparum cDNA
clone xPFn4669, mRNA sequence.
                                                        agogaagaaatocatgtaaagoagoaggagggcaccatggtttcaagtattatataattat 205
                                                                                                                                          206 aattataattatggtaggatgtacatggccgataagaaaaggcaatttgtagatgttaat 265
                                                                                                                                                                                                      266 tcccatcttgaaagaaatatagtttaaaatatttattgataaaataacaagtcaggtatta 325
                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shizokanedal, Minatoku, Tokyo 108-8639, Japan.
Fax: 81-3-5449-5378
       Length 905;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53.4; DB 10; Length
Pred. No. 0.57;
0; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:5833"
/clone="xppn4669"
/clone_libb="Sugano Malaria cDNA library"
                               57; Mismatches 139;
       DB 13;
0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 500
/organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="erythrocytic stage"
36 c 24 g 227 t
      Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20574754
Contact: Junichi Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU087444.1 GI:12389585
Query Match
Best Local Similarity 34.7%;
Matches 104; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
12.9%;
Best Local Similarity 50.3%;
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                      AU087444/c
                                                                                                                   146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                          ð
                                                                                  g
                                                                                                                à
                                                                                                                                          g
                                                                                                                                                                          ð
                                                                                                                                                                                                   g
                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
```

```
Submitted (23-7UL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.cbi.ac.uk - . This Drosophila melanogaster BAC http://www.edgp.cbi.ac.uk - y his Drosophila at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                       Drosophila melanogaster genome survey sequence T7 end of BAC BACN37C16 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                             Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Epiydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 caccattacatattgaaactcttacggatgagaacaactcacaagcattaatcatgttca 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.9%; Score 53.4; DB 13; 42.6%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="DrosBAC"/clone="BACN37C16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"end : T7'
                                                                                                                                                                                          AL108796.1 GI:5629100
                                                                                                   970 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 c
                                                                                                                                                                                                                                                                                                                                          Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
     AATATTAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                   CNS0182A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                         LOCUS
                                                                                                                                                                                                                                             ORGANISM
 199
                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                      ACCESSION
                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                             CNS0182A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

Search completed: February 25, 2002, 12:26:59 Job time: 1417 sec

THIS PAGE BLANK (USPTO)

Title: Perfect score: Sequence:

Scoring table:

Searched:

OM nucleic - nucleic search, using sw model

Run on:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

GenCore version	Result No.	Score	Query Match L	Length DB	3 ID			Description	
Copyright (c) 1993 - 2000 Compugen Ltd.	; ; ;	24	100.0	•		AX127756	! ! !	X127756 Sequenc	
cleic search, using sw model	2 60	2 2 2	100.0			1431 7282 304			
February 25, 2002, 18:00:20; Search time 2331.3 Seconds (without alignments) 169.833 Willion cell undates/sec		7 7 7 7	100.0			AZ1284 BABARSTA A71435 AROO7527		AZIZB4 AFTIIICIAI X15545 Bacillus am A71435 Sequence 5 AR007527 Sequence	
	. co o	24	100.0			084093 172441		AR084093 Sequence AX172441 Sequence	
24 1 tcagaagtatcagcgacctccacc 24		222	100.0			127748 007512		AX127748 Sequence AR007512 Sequence	
IDENTITY_NUC Gapop 10.0 , Gapext 1.0		24 20.8 20.8	100.0 86.7 86.7			084078 1433 1436		AR084078 Sequence A71433 Sequence 3 A71436 Sequence 6	
1472140 seqs, 8248589755 residues		20.8	86.7			1437 1440		A71437 Sequence 7 A71440 Sequence 10	
hits satisfying chosen parameters: 2944280	C 18	18.2	75.8			008007 062270 005330		AF062270 Homo sapi	
length: 0 length: 2000000000	c 20	18.27	75.8 1			023320 434P1 015713		297056 Human DNA s AC015713 Homo sapi	
: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	C 23 23 25 25 25 25 25 25 25 25 25 25 25 25 25	18.2 17.8 17.8 17.8	75.8 2 74.2 74.2 1 74.2 2	234131 1905 173846 238737	8 4 C C C C C C C C C C C C C C C C C C	AC093357 COXCYTSYN AC087781 AC084073			
		17.6	73.3			HSDCTN08 AX015400		AF086933 Homo sapi AX015400 Sequence	
4 4 4	0 0 5 0 0 5 0 0 0	17.6	73.3			HSDYNACTN HSDCTN1A3			
		17.6 17.6	73.3			AE006198 AVU49859		AE006198 Pasteurel U49859 Anabaena va	
	c 32	17.6	73.3			U00066 SPBC530		U00066 Caenorhabdi AL023634 S.pombe c	
		17.6	73.3			HSA494016 HS27C10		AL117328 Human DNA AL031803 Human DNA	
	c 36	17.6	73.3			AC012680 AC013430		AC012680 Arabidops AC013430 Genomic s	
	38	17.6	73.3 1			008854 002525		Homo sar	
		17.6	73.3			023898		Mus mu	
		17.6	73.3 1			073354		HOMO	
16: em_fun:* 17: em_hum:*	C 43	17.6	73.3 1			063966 026322		AC026326 Homo sapi AC026322 Homo sapi	
18: em_in:* 19: em_om:*		17.6	73.3 1			055714		Ношо	
em_or									
						ALIGNMENTS			
23: em_ph:* 24: em pl:*	RESULT	-							
	AX127756	ŀ	77766		٤		E	15-WAY-2001	
	DEFINITION		6	from Pat	ent v	from Patent W00131042.	164	1007 199 61	
	ACCESSION VERSION	7	AX127756 AX127756.1	GI:14134403	34403				
	KEYWORDS		1						
	SOURCE		synthetic consynthetic con	construct	.i				
33: em_htg_hum:* 34: em_htg_ioy:*	NEGREGA		tificial	sequence	o,				
35: em_htg_rod:* 36: em_htg_other:*	AUTHORS		ston, B. a le-steril	nd de Be e brassi	eucke] [ca_p]	Weston, B. and de Beuckeleer, M. Male-sterile brassica plants and methods for producing	for pr	oducing same	
sults predi o the score	JOURNAL FEATURES	ıı	Patent: WO Aventis Cro Lo	WO 0131042-A 9 03-M CropScience N.V. (B Location/Qualifier	-A 9 (N.V =	03-MAY-2001; . (BE) fiers			
rived by analysis of the total score distribution.	301	source	9	.24 rganism=	"syn1	thetic construct"			
SUMMARIES 8			₹5	/db_xref="taxon:32630' /note="primer MDB8"	taxor Lmer 1	n:32630" MDB8"			

Pred. No. is the number of results predicted by chascore greater than or equal to the score of the reand is derived by analysis of the total score dist

```
/codon_start=1
/product="barstark"
/protein_id="camega71.1"
/db xref="c1:6736048"
/vranslation="MKKAVINGEQIRSISDLHQTLKKELALPEYVCENLDALWDCLTG
WVEYPLVLEWROFEGSKQLTENGAESVLQVFREAKAEGCDITIILS"

69 c 87 g 69 t
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BABARSTA 474 bp DNA BCT 23-JUN-1996
X15545
X15545
X15546.1 GI:1155006
Barstar; ribonuclease inhibitor.
Bacillus amyloliquefaciens.
SM Bacillus amyloliquefaciens.
Bacillus amyloliquefaciens.
Bacillus amyloliquefaciens.
Bacillus Abcillus amyloliquefaciens.
Bacillus Abcillus amyloliquefaciens.
Bacillus Abcillus Abcillus.
Bacillus Abcillus Abcillus.
Bacillus Abcillus.
Bacillus Abcillus.
Bacillus Abcillus.
Bacillus Abcillus.
Barnase and barstar. Expression of its cloned inhibitor permits expression of a cloned ribonuclease
B 89012012
B 89012012
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                           31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                     Score 24; DB 6; Length 323;
Pred. No. 0.096;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 24; DB 6; Length 340; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified.

unidentified
unidentified
unclassified.
1 (bases 1 to 340)
Mariani.C., Leemans,J. and De Greef,W.
Plants with modified flowers
Patent: EP 0412911-A 2 13-FEB-1991;
PLANT GENETIC SYSTEMS, N.V.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unidentified"
/db_xref="taxon:32644"
13 c 92 g 69
                       db_xref="taxon:32644"
                                                                                                                                                                                                                                                         1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                            32 TCAGAAGTATCAGCGACCTCCACC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 TCAGAAGTATCAGCGACCTCCACC 65
                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                              A21284 340 bp
Artificial barstar gene.
A21284
                                                                                                                                                                                                   ch 100.0%;
l Similarity 100.0%;
24; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                            A21284.1 GI:514151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 474)
Hartley, R.
Direct Submission
                                                                                                                                                                                                               Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                            ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۵
                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106
                                                                                                                                                                                                   Query Match
                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BABARSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                RESULT
A21284
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
//transl_trable=11
//transl_trable=11
/product="Paksays"
/product="Paksays"
/product="A775045"
/translation="kravingEQTRSISDLHQTLKKELALPEYYGENLDALWDCLTG
WVEYPLVLEWROFEQGKQLTENGAESVLQVFREARAEGCDITILLS"

58 c 74 g 58 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                     Gaps
                                                                                                                                                                                                                                     07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2000
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                               Bacillus amyloliquefaciens.

**Bacillus amyloliquefaciens
Bacillus, Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococus group; Bacillus.

**I (bases 1 to 270)
Michiels, F. and Williams, M.
IMPROVED BARSTAR GENE

**D. Patent: WO 9610081-A 1 12-MAR-1998;
MICHIELS FRANK (BE)
                                                                       Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 24; DB 6; Length 270; 100.0%; Pred. No. 0.095; 1ve 0; Mismatches 0; Indels
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .270
/organism="Bacillus amyloliquefaciens"
/db_xref="taxon:1390"
1. .>270
                                                                                                                                                                                                                                     PAT
                                                     Score 24; DB 6; Le
Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases I to 323)
Hutther, E. and Betzner, A.S.
PROFIN COMPLEMENTATION IN TRANSGENIC PLANTS
PAtent: WO 9837211-A 7 27-Aug-1998;
GENE SHEARS PTY LTD (AU): HUTTINER ERIC (AU)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .>z/u
/function="INHIBITOR OF BARNASE"
                                                        Query Match 100.0%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                             A71431 270 bp DNA
Sequence 1 from Patent W09810081.
A71431.1 GI:4775044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A87282 323 bp DNA
Sequence 7 from Patent W09837211.
A87282.1 GI:6736047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"unidentified"
           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
                                                                                                                   1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified.
unidentified
unclassified.
       æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A87282
                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                            RESULT
A71431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
A87282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                      õ
                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

m

ö

Gaps

ö

others

01-SEP-2000

PAT

```
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 4832)
de Both,G. and de Beuckeleer,M.
Hybrid winter oilseed rape and methods for producing same Patent: WO 0141558-A 2 14-JUN-2001;
Aventis Cropscience NV. (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                Query Match 100.0%; Score 24; DB 6; Length 4808; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 24; DB 6; Length 4808; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
                                                            Unclassified.

1 (bases 1 to 4808)
Williams,M. and Leemans,J.
Waintenance of male-sterile plants
Patent: US 5750867-A 17 12-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 4808)
Williams,M. and Leemans,J.
Maintenance of male-sterile plants
Patent: US 5977433-A 17 02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 from patent US 5977433.
AR084093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AXI72441 4832 bp DNA
Sequence 2 from Patent WO0141558.
AXI72441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
1063 c 1038 g
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                       /organism="unknown"
1063 c 1038 g
                                                                                                                                                                                                                                                                                                                              2529 TCAGAAGTATCAGCGACCTCCACC 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2529 TCAGAAGTATCAGCGACCTCCACC 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                             1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX172441.1 GI:14597553
    GI:3967011
                                                                                                                                                          1. .4808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
Unclassified.
    AR007527.1
                                                                                                                                                                                       1370 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1370 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
                                 Unknown
                                                   Unknown
                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
AR084093/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                   ORGANISM
                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                          TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX172441/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
   VERSION
KEYWORDS
                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                   SOURCE
                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                           /transl_table=11
/protein_id="CAA33551.1"
/protein_id="CIA33551.1"
/db_xref="GI:39312"
/db_xref="SWISS-PROF:P11540"
/translation="MKKAVINCEQIRSISDLHQTLKKELALPEYYGENLDALWDCLTG
WVEYPLVLEWRQFEGSKQLFENGAESVLQVFREAKABGCDITIILS"
a 104 c 123 g 93 t
Submitted (14-JAN-1996) R.Hartley, LCDB/NIDDK, NIH, Bethesda, 20892 USA, email:hartleyrêhelix.nih.gov
Revised by author
On Jan 15, 1996 this sequence version replaced gi:39311.
See also acc# x12871.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4032;
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 24; DB 1; Length 474; 100.0%; Pred. No. 0.098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                    /organism="Bacillus amyloliquefaciens"
/db_xref="taxon:1390"
/clone="pWT311"
                                                                                                                                       94..99
/note="-10 region"
119..119
/note="pot. ribosome binding site"
124..396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A71435 4032 bp DNA circular PAT Sequence 5 from Patent WO9810081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24; DB 6;
Pred. No. 0.11;
Mismatches 0
                                                                                                                                                                                                                  124. .396
/note="barstar (AA 1 - 90)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1029 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 4032)
Michiels,F. and Williams,M.
IMPROVED BARSTAR GENE
Patent: WO 9810081-A 5 12-MAR-1998;
MICHIELS FRANK (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 4032
/organism="unidentified"
/db_xref="taxon:32644"
a 968 c 963 g 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               аки07527 4808 bp DNA
Sequence 17 from patent US 5750867.
AR007527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3435 TCAGAAGTATCAGCGACCTCCACC 3458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 TCAGAAGTATCAGCGACCTCCACC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
100.0%;
                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A71435
A71435.1 GI:4775048
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Conservative
                                                                                            1. .474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                          154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1072
                                                                                                                                                         promoter
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR007527/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                     RBS
                                                                                                                                                                                                                    CDS
                                 REMARK
                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
A71435
                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
```

COCUS

ð a ö

Gaps

; 0

others

03-JUL-2001

PAT

ò 셤

Gaps

ö

```
07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                        6; Length 6555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 20.8; DB 6; Length 273; 91.7%; Pred. No. 4.6; Live 0; Mismatches 2; Indels
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                  PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .>273
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 24; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 24; Conservative 0; Mismatches
                        Mismatches
                                                                                                                                                                                                                                                   1 (bases 1 to 6555)
Williams, M. and Leemans, J.
Maintenance of male-sterile plants
Patent: US 5977433-A 2 02-NOV-1999;
Location/Qualifiers
1. 6555
                                                                                                                                      AR084078 6555 bp DNA
Sequence 2 from patent US 5977433.
AR084078 GI:10010849
                                                                                                                                                                                                                                                                                                                                                    1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 273)
Michiels,F. and Williams,M.
IMPROVED BARSTAR GENE
Patent: WO 9810081-A 3 12-MAR-1998;
MICHIELS FRANK (BE)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A71433 273 bp DNA
Sequence 3 from Patent W09810081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .273
/organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                /organism="unknown"
1 1611 c 1584 g
                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A71433.1 GI:4775046
                  24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.77
Best Local Similarity 91.77
Matches 22; Conservative
                                                                                                                                                                                                                          Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                              1690 a
                                                                                                                                                                                                            Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                            RESULT 12
AR084078/c
                                                                                                                                                                                                                                                                                                                      source
                 Matches
                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                   ACCESSION
                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
A71433
                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                       synthetic construct.
SM synthetic construct
synthetic construct
stiffial sequence.
E 1 (bases 1 to 5865)
SS Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing same Male-sterile brassica plants and methods for producing same Aventis CropScience N.V. (BE)
S Location/Qualifiers
I . 5865
//organism="synthetic construct"
//db_xref="taxon:32630"
//note="T-DNA of plasmid pcoll3"
//note="T-DNA of plasmid pcoll3"
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                      15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
0
                                                                                                        Query Match
100.0%; Score 24; DB 6; Length 4832;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 24; DB 6; Length 5865; 100.0%; Pred. No. 0.11; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 24; DB 6; Length 6555; 100.0%; Pred. No. 0.11;
                                                               1 others
                                                                                                                                                                                                                                                                     PAT
/db_xref="taxon:32630"
/note="T-DNA of plasmid pTHW118"
1883. .4065
/note="Hpal restriction fragment"
a 883 c 932 g 1488 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR007512 6555 bp DNA
Sequence 2 from patent US 5750867.
AR007512 1 GI:3966996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 6555)
Williams.M. and Leemans.J.
Maintenance of male-sterile plants
Patent: US 5750867-A 2 12-MAY-1998;
Location/Qualifiers
1. 6555
                                                                                                                                                                                                                                                          AX127748 5865 bp DNA
Sequence 1 from Patent W00131042.
AX127748 GI:14134395
                                                                                                                                                                                  Db 3222 TCAGAAGTATCAGCGACCTCCACC 3199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
1611 c 1584 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 5249 TCAGAAGTATCAGGGACCTCCACC 5272
                                                                                                                                                              1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100. Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified
                                                       1528 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                             RESULT 10
AX127748
LOCUS
DEFINITION
ACCESSION
VERSION
                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
AR007512/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

ö

Gaps

ö

ô

Gaps

35 TCAGGAGCATCAGCGACCTCCACC 58

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                  07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 86.7%; Score 20.8; DB 6; Length 5349; Best Local Similarity 91.7%; Pred. No. 5.3; Matches 22; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match

86.7%; Score 20.8; DB 6; Length 563;
Best Local Similarity 91.7%; Pred. No. 4.8;
Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT
                                                                  PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michiels, F. and Williams, M.
Michiels, F. and Williams, M.
IMPROVED BARSTAR GENE
PATENT: WO 9810081-A 712-MAR-1998;
MICHIELS FRANK (BE)
Location/Qualifiers
ce /organism="unidentified"
/db_xref="taxon:32644"
T 1339 a 1233 c 1290 g 1487 t
                                                                                                                                                                                                                                                                                                                  | Chases 1 to 563 |
| Michiels, F. and Williams, M. IMPROVED BARSTAR GENE |
| PACHIELS FRANK (BE) |
| Location/Qualiflers |
| Location/Qualifled |
| Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 t
                                                     A71436 563 bp DNA
Sequence 6 from Patent WO9810081.
A71436
A71436.1 GI:4775049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A71437 5349 bp DNA
Sequence 7 from Patent W09810081.
A71437.1 GI:4775050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: February 25, 2002, 18:00:23 Job time: 18431 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                        unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
A71437
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                           LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
RESULT 14
A71436
                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

THIS PAGE BLANK (USPTO)

Nuclectide sequence plasmid prc0113 T-Chimeric T-DNA of Plasmid pVE144 use Plasmid pVE144 use Part of plasmid pr5346. U Syntheric barstar Plasmid pr7834. Plasmid pLH48. Sy Probe #20868 used truman polynuclecti Human polynuclecti Human polynuclecti Human polynuclecti Human polynuclecti Probe #10885 for ge Probe #1672 used throbe #1673 used throbe #1673

score:

Title: Perfect so Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

03 03

Minimum Maximum Database

```
PCR primer MDB251 to generate the flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MS-B2 elite event; transgenic Brassica plant; transformation event; male-sterility gene; PCR primer; thermal asymmetric interlaced;
                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                  AAV23242
AAI52182
AAI39127
AAZ41289
AAI59601
                                                                                                                                                         AAI57815
AAI20952
AAI46196
                                                                                                                                                                                                                 AAI33046
AAI01667
                                                                                                                                                                                                                                       AAC34918
AAC50006
AAV52206
AAD02697
AAC83227
AAC83227
AAC832424
AAAB9494
AAH67560
AAH67560
AAD08025
                      AAT39339
AAD06990
                                                                                                                                                                                                                                                                                                                                                                  AAF33121
AAT41492
                                             AAQ53874
                                                                                                                                                                                           AAI06663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AVET ) AVENTIS CROPSCIENCE
 26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                         469
3534
4721
4753
384
 4896
4896
5864
5865
6555
7492
7492
273
563
563
5611
245
                                                                                                                                                                                                                                                                                               3831
154
609
1239
1292
1371
1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD06998 standard;
WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2001.
                                                                                                                                                                                                                                                                                               00000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAIL; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06998;
                                                                                                                                                                                                                                                                                                100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD06998
  RESULT
                                                                                                                Barstar coding seq
Clai-Hindii fragme
Plasmid pr388 (Eco
Oligonuclectide #1
pr5200 contg. P355
Nuclectide sequenc
Plasmid pWy1. Sy
Restriction fragme
Nuclectide sequenc
                                                                                          (without alignments)
28.715 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer MDB251
Wild type barstar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                             ; Search time 716.55 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                        **SIDSZ/gcgdata/geneseq_/geneseqn_NA1980_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1981_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1981_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1981_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1981_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1986_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1986_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1980_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1980_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1980_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1980_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1980_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1991_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1999_DAT:**

**SIDSZ/gcgdata/geneseq_/geneseqn_NA1
           4.5
Compugen Ltd
                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                      930621 segs, 428662619 residues
                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
           GenCore version
Copyright (c) 1993 - 2000
                                                                             February 25, 2002, 18:17:34
                                                                                                                        US-09-698-903B-9
24
1 tcagaagtatcagcgacctccacc
                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV23236
AAV60977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ10460
AAT39337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD06998
                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                 N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323
340
1303
2275
3544
3544
4032
4808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11000.0
11000.0
11000.0
11000.0
11000.0
11000.0
```

C glutamicum codin Rat EM-3 coding se Rat G-protein coup Rat G-protein coup Human secreted pro DNA encoding MAGE-

 $_{
m of}^{
m by}$

Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -

AAT17246 AAX15632 AAV23237 AAQ53889 AAH25423

AAF86440

4444444444

4 7 7 7 110 110

000

Score

Result No. WPI; 2001-300517/31.

Streptococcus pneu Cone snail alpha-c

Streptococcus pneu Human glycosyl sul

DNA sequence from

74 G; 58 T; 0 other;

Sequence 270 BP; 80 A; 58 C;

ğ

Query Match

ö

& × 0 0 0 0 0 0 0 0 0 0 0 × 8

ò 음

```
ö
                                                    The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic plant with a male-fertile Brassica plant as useful for producing a hybrid seed by crossing the hybrid seed from the transgenic Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is primary thermal interlaced (TAIL)-PCR primer The present sequence is primary thermal interlaced to left (3') border flanking region of elite event MS-B2. This primer corresponds to position 5249-5272 of plasmid procili3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding an improved barstar protein - used to restore fertility in male-sterile plant lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence was used in the preparation of an improved Bacillus amyloliquefaciens barstar, i.e. barnase inhibitor, which can be used to restore fertility to male-sterile lines.

The DNA sequence encoding the improved barstar, leads to increased barstar production in tapetum cells, due to improved translation, and possibly protein stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 22; Length 24;
Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barstar; barnase inhibitor; fertility restoration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..273
/*tag= a
/product= barstar
/note= "stop codon not given"
                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 7 A; 9 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Pages 34-35; 54pp; English.
Example 3; Page 28; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV23236 standard; DNA; 270 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96EP-0202446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-EP04739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.(
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michiels F, Williams M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              male-sterile line; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wild type barstar DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-193630/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW53344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9810081-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV23236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV23236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
```

```
The present invention describes a pair of parent plants for producing seeds comprising: (a) a first parent plant containing at least 1 gene sequence encoding a polypeptide or protein A, and (b) a second parent blant containing at least 1 gene sequence encoding a polypeptide or protein B; where the polypeptides A and B, when expressed in separate plants, do not form an active enzyme, a regulatory protein or protein which affects the functionality and/or viability and/or the structural integrity of a cell, but when expressed in the same plant do form an active enzyme, regulatory protein, or protein which affects the structural or structural integrity of a cell. Also described is a method for producing a plant having a desired phenotype by virtue of an active enzyme, a regulatory protein or a protein which affects the structural integrity of a cell. Also described is a method for producing a regulatory protein or a protein which affects the structural integrity of a cell. Also described is a method for producing a cell according a first line with a second line where the first line contains one or more gene sequences encoding a polypeptide or the second line plants one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encoding a polypeptide or the second line contains one or more gene sequences encode line and where the contains and where the contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the second line contains one or more gene sequences encoding a polypeptide or protein B which is complementary to the polypeptide or protein A but which line does not have the desired phenotype. The method can be used for producing plants having altered phenotypes, e.g. male-
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnase; barstar; IPCR; inverse polymerase chain reaction; phenotype; transgenic plant; hybrid seed; male sterile plant; active enzyme; regulatory protein; embryoless seed; herbicide resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of transgenic plants having a desired phenotype - by using a pair of parent plants which each produce a polypeptide which complement each other when crossed
                                                           ö
          Length 270;
                                                      Indels
Score 24; DB 19;
Pred. No. 0.048;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "barstar"
                                                                                                                            32 tcagaagtatcagcgacctccacc 55
                                                                                                  24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paul W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 1C; 58pp; English.
                                                      ö
                                                                                                                                                                                                                                                                     AAV60977 standard; DNA; 323 BP
                                                                                          1 tcagaagtatcagcgacctccacc
  100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-GB00542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-0003681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENE SHEARS PTY LID.
                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1998 (first entry)
                                              24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Barstar coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huttner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-467572/40.
                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW71704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9837211-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Betzner AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                      AAV60977;
                                           Matches
                                                                                                                                                                                                                                           AAV60977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                            ò
                                                                                                                                         g
```

ds.

m

```
//label- P35S
/function= 35S promoter of cauliflower mosaic virus
strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                        Plasmid pTS88; male sterile; barstar; barnase; ribonuclease; transgenic plant; rice; Oryza sativa; maize; corn; Zea mays;
                                                                                                                                                                                                                                       /*tag= c
/labbl= barstar
/product= Bacillus amyloliquefaciens barstar
968..1287
                                                                                                                                            /note= "polylinker of pGEM2"
                                                                                                                                                                                                                                                                                                                                         /*tag= e
/label= pGEM2
/note= "polylinker of pGEM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cornelissen M, Michiels F;
                                   Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 38; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                         1..35
/*tag= a
/label= pGEM2
                                                                                                                                                                                                                                                                                              'label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                                                       95EP-0400364
                                                                                                                                                                                                                                                                                                        /function=
                                                                                                                                                                                                                                                                                                                             1288..1303
               (first entry)
                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-402373/40.
                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botterman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-1995;
                                                                                                                                                                                                                                                                         polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                    WO9626283-A1
            22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1996
                                                                                         Synthetic.
                                                                                                                                                                       promoter
                                                                                                                                                                                                                            CDS
    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The barstar gene encodes and inhibitor of barnase, which degrades RNA molecules by hybridising the bond after a quantine residue. The gene is used, in a chimaeric sequence, to restore fertility in plants transformed with the gene. The promoter cassette PTA29
sterility, embryoless seeds, altered biochemical (e.g. fatty acid) composition or herbicide resistance. The present sequence encodes barstar which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell of fertility restored plant – in which nuclear genome in transformed with foreign DNA sequence neutralising activity of
                                                                                                                                                                                                                                                                                           Inhibitor; extracellular ribonuclease; barnase; fertility; ss.
                                                                           Query Match 100.0%; Score 24; DB 19; Length 323; Best Local Similarity 100.0%; Pred. No. 0.049; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 12; Length 340; Pred. No. 0.05;
                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EP-401194) is fused in frame with the initiating ATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 340 BP; 106 A; 73 C; 92 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                            Sequence 323 BP; 98 A; 69 C; 87 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                     ClaI-HindII fragment contg barstar gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Greef W;
                                                                                                                       Disclosure; Fig 2; 25pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 tcagaagtatcagcgacctccacc 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT39337 standard; DNA; 1303 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcagaagtatcagcgacctccacc
                                                                                                                                                                                                   AAQ10460 standard; DNA; 340
                                                                                                                                                                                                                                                                                                                                                                                    90EP-0402281
                                                                                                                                                                                                                                                                                                                                                                                                                               (PLAN-) PLANT GENETIC SYST.
                                                                                                                                                                                                                                                                                                                  Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martani C, Leemans J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-046026/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        another prod.
                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-1989;
                                                                                                                                                                                                                                                16-APR-1991
                                                                                                                                                                                                                                                                                                                                                              13-FEB-1991
                                                                                                                                                                                                                                                                                                                                        EP412911-A
                                                                                                                                                                                                                          AAQ10460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT39337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT39337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                              SX B
 8 \times 3 \times 3 \times 3
                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

jion containing polyadenylation signal gene 7 og Agrobacterium T-DNA

region of gene

```
Gaps
The HindIII-ECORI fragment (AAT39337) of plasmid prS88 contains barstar DNA under control of a 35S promoter. The plasmid was used with prS174 (see also AAT39336) contg. barnase DNA under control of the stamen-specific promoter El to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pvE136 (see also AAT39338) contg. barnase DNA under control of the stamen-specific PCA55 promoter to produce male sterile maize plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible low level expression of barnase DNA in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 24; DB 17; Length 1303; Best Local Similarity 100.0%; Pred. No. 0.059; Matches 24; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
```

Socation/Qualifiers

us-09-698-903b-9.rng

```
Key
misc_signal
                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                            06-JUN-1994;
                                                                                                                                                                                                                                                                                                                       21-DEC-1995,
                                                                                                                                                                                                                                         misc_signal
                                                                                                                                                                                                                                                                                                                                                                                               Krebbers E,
                                                                                                                      promoter
                                                                                                                                                          promoter
                                                                         CDS
                                                                                                                                                                                            CDS
        ö
                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for producing male sterile plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is an oligonucleotide used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                     Wethod for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C1, C1-S; transgenic plant; male sterility; colour-linked restorer;
anthocyanin; aleurone; B-peru; bar; barstar; bar*; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 100.0%; Score 24; DB 22; Length 2275; Similarity 100.0%; Pred. No. 0.063; Score 24; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2275 BP; 604 A; 496 C; 496 G; 679 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pTS200 contg. P35S-bar-3'nos and PCA55-barstar-3'nos.
                                                                                                                                      Male sterile plant; RNAase inhibitor; ds.
                                                                                                                                                                                                                                                                                                                               Disclosure; Page 17-19; 29pp; Japanese.
1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AT17246/c
ID AAT17246 standard; DNA; 3544 BP
XX
AT AT17246;
XX
DX 12-AUG-1996 (first entry)
XX
DE PTS200 contg. P35S-bar-3'nos an
XX
KW C1; C1-S; transgenic plant; mal
XX
XX
Synthetic.
XX
                                                             AAF86440 standard; DNA; 2275
                                                                                                                                                                                                             12-SEP-2000; 2000WO-JP06222
                                                                                                                                                                                                                                99JP-0279307
                                                                                                  25-JUN-2001 (first entry)
                                                                                                                    Oligonucleotide #1: SEQ ID
                                                                                                                                                                                                                                                 (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                  Hamada K, Nakakido F;
                                                                                                                                                                                                                                                                                    WPI; 2001-266212/27
                                                                                                                                                                          WO200124616-A1.
                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                              30-SEP-1999;
                                                                                                                                                                                            12-APR-2001
                                                                                AAF86440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
Matches 2
                                                    AAF86440/C
ID AAF86
XX
                                                                               셤
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
Shortened forms of anthocyanin (An) regulatory genes (ARG) are easier to manipulate than the complete gene and still provide An prodn. The Cl gene (and the Cl-S gene) can be considerably shortened while still retaining, under appropriate conditions, its capability of conditioning anthocyanin prodn. In the aleurone of seeds of cereal plants such as corn. A pref. shortened Cl gene is comprised in pCoL9 (see AAT08975). The full Cl gene sequence is Arrowspap and presumed sequence = AAT08973, any also be used.

Sequence = AAT08970, may also be used.

Plasmids pTS256 (AAT08976) and pTS200 (AAT17246) were used in the construction of vectors comprising the Cl and B-peru genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             easier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                    /*tag= c
/label= P35s
/note= "35s promoter of Cauliflower Mosaic Virus"
complement (626.1803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic plants contg, male sterility and colour-linked restorer genotypes - used for prodn. of male sterile seeds identifiable frotheir colour, also new truncated anthocyanin regulatory genes and aleurone specific promoters
                                              /note= "3' regulatory sequence contg. the polyadenylation signal of the nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= f
//label= 3'nos
/note= "3' regulatory sequence contg, the
polyadenylation signla of the nopaline
synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
100.0%; Score 24; DB 17; Length 3544;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 24; Conservative 0; Mismatches 0; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                /*tåg= d
/label= PCA55
/note= "promoter of CA55 gene of Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "coding region of baratar gene
Bacillus amyloliquefaciens"
complement (30.352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3544 BP; 1011 A; 847 C; 767 G; 919 T; 0 other;
                                                                                                                                                                                                                     /note- "coding region of bar gene of
Streptomyces hygroscopicus"
1841..2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 72-74; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (353..625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leemans J, Williams M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/label= barstar
/*tag= a
/label= 3'nos
                                                                                                                                                                      /*tag= b
/label= bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-EP02157
                                                                                                                                      1675..3226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-049664/05.
```

S

ò g

```
DNA encoding an improved barstar protein - used to restore fertility in male-sterile plant lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "region containing 3' unstranslated end of
the nopaline synthase gene of Agrobacterium
T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence was used in the preparation of an improved Bacillus amyloliquefaciens barstar, i.e. barnase inhibitor, which can be used to restore fertility to male-sterile lines.
The DNA sequence encoding the improved barstar, leads to increased barstar production in tapetum cells, due to improved translation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maintainer gene; sterile; sterility; homogenous population; hybrid; seed; fertility restorer gene; pollen lethality gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Restriction fragment of construct carrying plant maintainer gene.
                                                                                                                                                                                                                                                                                                                                 a
"promoter region of rice actin gene
contains an intron in the leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4032 BP; 1072 A; 968 C; 963 G; 1029 T; 0 other;
                                                                                                                  Barstar; barnase inhibitor; fertility restoration; male-sterile line; plasmid pMV71; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 24; DB 19; Similarity 100.0%; Pred. No. 0.068; 24; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Pages 37-39; 54pp; English.
                                                                                                                                                                                                                                                           Location/Qualifiers
1999.3400
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3435 tcagaagtatcagcgacctccacc 3458
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/product= barstar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and possibly protein stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 tcagaagtatcagcgacctccacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            889/c
AAQ53889 standard; DNA; 4808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96EP-0202446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3677..4003
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-EP04739
                                                                                                                                                                                                                                                                                                                                                                                                                       3401..3676
17-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Michiels F, Williams M;
                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-193630/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PLBZ ) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9810081-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1998.
                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ53889;
                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ53889,
NAME OF THE PROOF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECORI Thindill fragment of plasmid pr2556, comprising the chimeric gene PCA55-barstar-3'nos. It is used in the course of the invention. The specification describes a process for maintaining a male-sterile corn line, using male sterile parent plants lacking a functional gene for anthoryanin production, and a maintainer corn line comprising male fertile parent plants containing foreign DNA comprising a restorer gene and an active requiatory protein gene. By using the anthoryanin gene, the colour of the male-sterile plants will differ from that of the male fertile plants. This will enable the seeds harvested from the plants to be easily separated into those that will grow into male-fertile plants and those that will grow into male-sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of an EcoRI-HindIII fragment of plasmid pTS256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Process for maintaining a male-sterile corn line - using male sterile plants lacking functional regulatory gene for anthocyanin production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cl gene; maize; male-sterile corn line; anthocyanin production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 24; DB 20; Length 3544;
.larity 100.0%; Pred. No. 0.067;
Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence represents the nucleotide sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3544 BP; 1011 A; 847 C; 767 G; 919 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Columns 37-40; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leemans J, Williams
                         1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV23237 standard; DNA; 4032 BP
                                                                                                                                                                                                                                 AAX15632 standard; DNA; 3544 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0485139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0485139.
94US-0254776.
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-204053/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PLBZ ) PLANT
```

06-JUN-1994;

Krebbers E,

The

07-JUN-1995; 07-JUN-1995;

US5880331-A.

pTS256; ds. Synthetic. 09-MAR-1999

07-MAY-1999

AAX15632;

ö

Gaps

ö

Indels

Query Match

Best Loc Matches

AAV23237

AXXX

σ

q

AAV23237 RESULT

Length 4032;

9

us-09-698-903b-9.rng

```
Synthetic.
                                                                                                                                                                                        AAH25423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                                          RESULT 11
AAH25423/c
                                                                                                                                                                                                                                                                                                                                                                                                                    3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
           88888888%8
                                                                                                                    δ
                                                                                                                                   g
                                                                                                                                                                                        /note= "3' regulatory sequence containing the polybadenylation site derived from Agrobacterium T-DNA nopaline synthase gene.
                                                                                                                                                                                                                                                                                   35S3" promoter sequence derived from cauliflower mosaic virus isolate CabbB-JI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A maintainer gene of plants, pref. a foreign chimeric gene, comprises (a) a ferility restorer gene which comprises a fertility restorer DNA and (ii) a restorer promoter capable of directing the expression of the fertility restorer DNA and (b) a pollen lethality gene that is selectively expressed in microspores and/or pollen of the plant to prevent the production of functional pollen and which comprises (i) a pollen lethality DNA and (ii) a
                                                                                                                                                Zea
                                                                                                                                             the Zm 13 gene of
                                                                                                          õ
                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                               /note= "Coding region of the phoshinothricin
                                                                                                                                                                                                                                            /note= "Promoter region of the TA29 gene of Nicotiana tabacum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maintainer gene for maintenance of male-sterile plants -comprises fertility-restorer gene and pollen-lethality gene
                                                                                                                                                                                                      /note= "Coding region of the barstar gene
Bacillus amyloliquefaciens."
complement (2555.3099)
                                                                                                  /note- "Coding region of the barnase
Bacillus amyloliquefaciens."
complement (738. 1944)
                                                                                                                           /*tag= c
/label= P2M13.
/note= "Promoter region of
                                                                                                                                                                      /label= 3' nos.
complement (2282..2554)
                                                                                                                                                         complement (1945..2281)
                        Location/Qualifiers
complement (18..401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 73-75; 87pp; English.
                                                                                                                                                                                       /*tag= e
/label= Barstar.
                                                                                               Barnase.
                                                                                                                                                                                                                                                                                                                                                                                                                                (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                 /note- "3553"
                                                                                                                                                                                                                                                                                                                                        /*tag= i
/label= 3' nos
                                                                                                                                                                                                                                     /label- PTA29
                                                                                                                                                   mays
                                                                                                                                                                                                                                                                           /label= 35S3
                                                                                                                                                                                                                                                                                                                                                                                                          92US-0899072.
                                                                                      /*tag= b
/label= Ba
                                                                                                                                                                                                                                                                                                                                                                                            93WO-EP01489
                                                                                                                                                                                                                                                          3100..3932
                                                                                                                                                                                                                                                                                                3933..4484
                                        /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                               Leemans J, Williams M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-007552/01.
                       Key
misc_signal
                                                                                                                                                        misc_signal
                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                          L2-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1992;
         Synthetic.
                                                                                                                                                                                                                                                                                                                                                            WO9325695-A
                                                                                                                                                                                                                                                                                                                              misc_signal
                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1993
                                                                                                                   promoter
                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                          promoter
                                                                            CDS
                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                               CDS
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene;
fertility restorer gene; barstar gene; ss.
                                                                                                                                                                                                                                                             Gaps
pollen specific promoter capable of directing expression of the pollen lethality DNA. Plants transformed with this DNA (maintainer plants) can be used to maintain a homogenous population of male sterile plants for the production of hybrid seed. This sequence is an EcoRI-HindIII restriction fragment of the construct designated pTS218 and comprises the maintainer gene described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
"right border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag- h
/note= "atSlA ribulose-1,5-biphosphate carboxylase
small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= d
/note= "synthetic polylinker derived sequences"
complement (98..309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /w.c.
/wtag- c
/note- "residual sequence from TL-DNA at right
border repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "synthetic polylinker derived sequences"
complement (331..882)
                                                                                                                                                                                                            Score 24; DB 15; Length 4808;
Pred. No. 0.069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= i
/note= "synthetic polylinker derived sequences"
coplement (2659.2919)
/*tag= j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "raq1 fragment from 3' UTR of nopaline synthase gene from T-DNA of prim37 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
/note= "3' UTR from TL-DNA gene 7 of pTiB6S3"
                                                                                                                                         Sequence 4808 BP; 1370 A; 1064 C; 1037 G; 1333 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= g
/note= "Streptomyces hygroscopicus bialaphos
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resistance (bar) gene"
complement (883,.2608)
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of plasmid pTHW118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                   2529 TCAGAAGTATCAGCGACCTCCACC 2506
                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                              1 tcagaagtatcagcgacctccacc
                                                                                                                                                                                                  Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 24; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                 AAH25423 standard; DNA; 4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces hygroscopicus.
Arabidopsis thaliana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus amyloliquefaciens. Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310..330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..25
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
```

colour-linked restorer;

Cauliflower Mosaic Virus"

tabacum"

, nos

```
/note= "3' regulatory sequence contg. the polyadenylation signal of the nopaline synthase gene of Agrobacterium T-DNA" complement (318.86)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "3' regulatory sequence contg. the polyadenylation signla of the nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                        /note= "promoter of TA29 gene of Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "coding region of barstar gene of
Bacillus amyloliquefaciens"
                                                           C1; C1-S; transgenic plant; male sterility; colour-lin
anthocyanin; aleurone; B-peru; bar; barstar; bar*; ds
                                    PTS256 contg. P35S-bar-3'nos and PTA29-barstar-3'nos.
                                                                                                                                                                                                                                             /note= "coding region of bar gene of
Streptomyces hygroscopicus"
complement (870..1702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..38
/*tag=
//label= pUC19
/note= "pUC19 derived sequence"
                                                                                                                                                                                                                                                                                            /label= P35S
/note= "35S promoter of
complement (1740..2284)
                                                                                                                      Location/Qualifiers
complement (39..317)
                                                                                                                                                                                                                                                                                                                                                                                             /*tag= e
/label= barstar
                                                                                                                                                                                                                                                                                                                                  /*tag= d
/label= PTA29
                                                                                                                                                           /label- 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= puc19
                                                                                                                                                                                                                                  label- bar
                                                                                                                                                                                                                                                                                                                                                                                                                                           2558..2879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4986
             12-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                2285..2557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-049664/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krebbers E,
                                                                                                                        Key
misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9534634-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_signal
                                                                                                 Synthetic
                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_RNA
                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                 CDS
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. The present sequence represents plasmid primylls. This plasmid comprises the barstar gene, which acts as a fertility restorer gene. The plasmid is used to create transgenic plants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                               /*tag= p
/note= "left border repeat from TL-DNA from pTiB6S3"
 containing plant polyadenylation signals
                                                                      /note= "downstream of Bacillus amyloliquefaciens
barstar coding region"
complement (2981..3253)
                                                                                                                      /note= "Barstar gene coding region from Bacillus amyloliquefaciens" complement (3254..4762)
                                                                                                                                                                      /note= "anther-specific gene TA29 promoter from Nicotiana tabacum"
                                                                                                                                                                                                         /*tag= o
/note= "synthetic polylinker derived sequences"
4808..4832
                                     sednences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB 22; Length 4832;
Pred. No. 0.069;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
                         /*tag= k
/note= "synthetic polylinker derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 80-82; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3222 TCAGAAGTATCAGCGACCTCCACC 3199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT08976 standard; DNA; 4896 BP
                                                                                                                                                                                                                                                                                                                                                                              (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 24; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                        De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                06-DEC-2000; 2000WO-EP12872.
            2920..2940
                                              2941..298Ô
                                                                                                                                                                                             4763..4807
                                                                                                              /*tag=
                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-381419/40.
                                                                                                                                                                                                                                                                                  WO200141558-A1
             misc_feature
                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                        08-DEC-1999;
                                                                                                                                                                                                                                                                                                       14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                        De Both G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT08976;
                                                                                                                                                promoter
                                                3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT08976
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
```

```
Shortened forms of anthocyanin (An) regulatory genes (ARG) are easier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plants contg. male sterility and colour-linked restorer genotypes - used for prodm. of male sterile seeds identifiable from their colour, also new truncated anthocyanin regulatory genes and aleurone specific promoters
/note= "pUC19 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 68-71; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leemans J, Williams M;
                                                                                                                                                                                                                                                                                                                                                                                                                 (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                       95WO-EP02157
```

Sequence 4896 BP; 1251 A; 1147 C; 1186 G; 1312 T; 0 other;

œ

```
ö
C to manipulate than the complete gene and still provide An prodn.
C The C1 gene (and the C1-S gene) can be considerably shortened
While still retaining, under appropriate conditions, its
capability of conditioning anthocyanin prodn. In the aleurone
of seeds of cereal plants such as corn. A pref. shortened C1 gene
of seeds of cereal plants such as corn. A pref. shortened C1 gene
of seeds of cereal plants such as corn. A pref. shortened C1 gene
of seeds of cereal plants such as corn. A pref. shortened C1 gene
of sequence = AAT08973.
A truncated B-peru gene (presumed sequence - AAT08674; actual
plants and service (and prs200 (AAT17246) were used in the
construction of vectors comprising the C1 and B-peru genes
as well as male-sterility gene and a selectable marker gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the nucleotide sequence of plasmid describes a process for maintaining a male-sterile corn line, using male describes a process for maintaining a male-sterile corn line, using male production, and a maintainer corn line comprising male fertile parent plants leave corn line comprising male fertile parent requiatory protein gene. By using the anthocyanin gene, the colour of the male-sterile plants will differ from that of the male fertile easily separated into those that will grow into male-fertile plants to be those that will grow into male-fertile plants and
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Process for maintaining a male-sterile corn line - using male sterile plants lacking functional regulatory gene for anthocyanin production
                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                maize; male-sterile corn line; anthocyanin production;
                                                                                                                                                                                                                                                         Score 24; DB 17; Length 4896;
Pred. No. 0.069;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                      Sequence 4896 BP; 1252 A; 1146 C; 1186 G; 1312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Columns 31-36; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of plasmid pTS256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leemans J, Williams M;
                                                                                                                                                                                                                                                                                                                                   2316 tcagaagtatcagcgacctccacc 2339
                                                                                                                                                                                                                                                                                                                         74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                               1 tcagaagtatcagcgacctccacc
                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAX15631 standard; DNA; 4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0485139,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0485139.
94US-0254776.
                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-204053/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5880331-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cl gene; ma
pTS256; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krebbers E,
                                                                                                                                                                                                                                                    Query Match
Best Local S1
Matches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX15631;
                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AAX15631
ID AAX
    8$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= region containing polyA signal of nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Barnase
/note- "bacillus amyloliquefaciens barnase coding
                                 ö
                                                                                                                                                                       Plasmid pTC0113 T-DNA used to obtain male sterile oilseed rape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag- g
/label- PTA29
/note- "promoter of stamen-specific TA29 gene of
Nicotiana tabacum"
                                                                                                                                                                                          Plasmid pTCO113; male sterile; barnase; ribonuclease; barstar;
transgenic plant; oilssed rape; canole; Brassica napus; ds.
                                                                                                                                                                                                                                                                                                                             /note= "region containing polyA signal of gene of Agrobacterium T-DNA" complement (331.882)
            Length 4896;
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= promoter of Arabidopsis Rubisco small subunit gene" complement (2659.3031)
                                                                                                                                                                                                                                                                          /label- RB
/note- "right border of Agrobacterium T-DNA"
complement (98..330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "promoter of nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "region coding for barstar of Bacillus amyloliquefaciens" 5490..5765
                                                                                                                                                                                                                                                                                                                                                                             /note= "region coding for phosphinothricin
acetyltransferase"
complement (883..2608)
                               Indels
Query Match
100.0%; Score 24; DB 20;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3368..4877)
                                                                                                                                                                                                                                               Location/Qualifiers complement (1..25)
                                                   2317 tcagaagtatcagcgacctccacc 2340
                                         1 tcagaagtatcagcgacctccacc 24
                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= i
/label= Barstar
                                                                                                            AAT39339 standard; DNA; 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
                                                                                                                                                                                                                                                                                                                    /label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Pssu
                                                                                                                                                                                                                                                                                                                                                                      /label= bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= h
/label= Pnos
                                                                                                                                                  22-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/label= 3'
                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                               PolyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                polyA_signal
                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PolyA_signal
                                                                                                                                 AAT39339;
                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                     AAT39339
                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                         ð
```

σ

```
/*tag= i
/note= "TagI fragment from the 3' untranslated end of the
/note= "TagI fragment from the T-DNA of pT1T37
                                                                                                                                                                                                                                                                                                                                                  /*tag= g
/note= "Promoter from the atSIA ribulose-1,5-biphosphate
narhoxvlase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= k
/note= The 3' untranslated region downstream from the
/note= The 3' untranslated of Bacillus amyloliquefaciens"
3033..3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note "Sequence from the 3' untranslated end of the barstar gene from Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Promoter region of the anther-specific gene
TA29 from Nicotiana tabacum"
4879..4924
                                                                                                                                                                                                                                                                               /product= "Protein encoded by bialaphos resistance
gene (bar) of Streptomyces hygroscopicus"
884..2609
                 a
"Right border repeat from the TL-DNA from
                                                                                                                     /*tag= c
/note= "Residual sequence from the TL-DNA at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product= "Protein encoded by barnase gene from acillus_amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= o
/note= Promoter of the nopaline synthase gene
T-NNA of pTiT37 of Agrobacterium tumefaciens"
5216..5217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "The 3' untranslated end from the TL-DNA
                                                                                                                                                                                                TL-DNA
                                                                         b
"Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                            /*tag= e
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                **tag= h
'note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Synthetic polylinker derived sequence"
2937..3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= n
/note= "Synthetic polylinker derived sequence"
4925..5215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= p
/note= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and containing plant polyadenylation signals"
2921..2936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rag= q //product= "Protein encoded by barstar gene Bacillus amyloliquefaciens" | 541.5530
                                                                                                                                                                                                end from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nopaline synthase gene (3'nos)
                                                                                                                                                                                /*tag= d
/note= "The 3' untranslated
gene 7 (3'g7) of pTiB6S3"
310..331
                                                                                                                                                                                                                                                                                                                                                                                  carboxylase small subunit
2610..2659
                                                                                                                                                   right border repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3369..4878
/*tag= m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5555..5766
                                                                                                                                                                                                                                                                                                                                                                                                                                           660..2920
                              /note= "R
pTiB6S3"
                                                                                                                                                                                                                                                                         32..883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus
                                                                       /*tag=
/note= '
54..90
1..25
/*tag=
                                                                                                                                                                     98..309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tad=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
 misc_feature
                                                            misc_feature
                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter
                                                                                                                                                                  3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-DNA; plasmid pTCO113; transgenic Brassica plant; transformation event; male-sterility gene; chimeric; tobacco; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid prcoll3 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-regulatory) gene under control of the Pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterlum-mediated transformation using prcoll3 were male sterile. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                  Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                         /note= "region containing polyA signal of gene of Agrobacterium T-DNA" complement (5840..5864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 17; Length 5864; Pred. No. 0.071;
                                                                                                    /note= "left border of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 33-3743-47; 56pp; English.
                                                                                                                                                                                                                                                                                         Cornelissen M, Michiels F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Bacillus amyloliquefaciens.
Chimeric - Nicotiana tabacum.
Chimeric - Agrobacterium tumefaciens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Streptomyces hygroscopicus.
Chimeric - Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric T-DNA of plasmid pTC0113.
                                                                                                                                                                                                                                                           (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD06990 standard; DNA; 5865 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
/*tag= j
/label= 3'g7
                                                                                                                                                                                                                            95EP-0400364
                                                                                                                                                                                             96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 24; Conservative
                                                                         /*tag=
/label=
                                                                                                                                                                                                                                                                                                                      WPI; 1996-402373/40.
                                                                                                                                                                                                                                                                                         Botterman J,
                                                          misc_feature
                                                                                                                                  WO9626283-A1
                                                                                                                                                                                              21-FEB-1996;
                                                                                                                                                                                                                            21-FEB-1995;
                                                                                                                                                                  29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD06990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD06990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
```

RESULT

g

õ

```
The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic blant with a male-fertile Brassica plant and harvesting the transgenic blant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is chimeric T-DNA of plasmid problish sequence comprises right border repeat, left border repeat and 3' untranslated comprises right border repeat, left border repeat and 3' untranslated company systems of blalaphos resistance gene (bar) from stronger systems systems shygroscopicus, barnase gene from Bacillus amyloliquefaciens and barsatar gene from Arabhosphate carboxylase small subunit gene from Nicotiana tabacum and nopaline synthase gene from the T-DNA of prinz37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                           /*tog.v.
//tog.v.
/notew Residual sequence from the TL-DNA at the right border repeat.
5811.5840
/*tag= w
/note= "Synthetic polylinker derived sequence"
5841.5865
/*tag= x
/note= "Left border repeat from the TL-DNA from priB653"
   gene 7 (3'g7) of prib6S3"
5767..5773
/*tag- u
//orte= "Synthetic polylinker derived sequence"
5774..5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 47-49; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                                                             26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0430497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                     WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1999;
                     misc_feature
                                                                             misc_feature
                                                                                                                                                       misc_feature
                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                           03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weston B,
```

Query Match
100.0%; Score 24; DB 22; Length 5865;
Bost Local Similarity 100.0%; Pred. No. 0.071;
Matches 24; Conservative 0; Mismatches 0; Indels 0

ö

Gaps

· 0

1 tcagaagtatcagcgacctccacc 24 à q

Search completed: February 25, 2002, 18:17:36 Job time: 16694 sec

```
1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
  1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-894-440-2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH:
  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Appliseduence 17, Appliseduence 17, Appliseduence 2, Appliseduence 2, Appliseduence 2, Appliseduence 1, Appliseduence 1, Appliseduence 11, Appliseduence 15, Appliseduence 16, Appliseduence 16, Appliseduence 16, Appliseduence 16, Appliseduence 16, Appliseduence 16, Appliseduence 11, Appliseduence 16, Appliseduence 17, Appli
                                                                                                                                                                                     (without alignments)
18.022 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                          ; Search time 301.6 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                            Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08 687-139-2

US-08 485-139-2

US-08 155-139-3

US-09 1025-583-17

US-08 185-139-2

US-08 185-139-2

US-08 185-139-2

US-08 185-139-2

US-08 185-139-2

US-08 185-139-2

US-08 185-139-1

US-08 185-139-1

US-08 185-139-1

US-09 105-105-105-105

US-09 105-105-105-105

US-09 105-105-105-105

US-09 105-105-105-105

US-09 105-105-105-105

US-09 105-105-105-105

US-09 115-105-105

US-09 115-105-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                          351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                          24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                      GenCore version (c) 1993 - 2000
                                                                                                                                                            February 25, 2002, 18:05:27
                                                                                                                                                                                                                                                                                                          1 tcagaagtatcagcgacctccacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  sw model
                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_NA:*
                                                                                                               nucleic search, using
                                                                                                                                                                                                                                                   US-09-698-903B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1303
3544
4808
4808
4896
4896
6555
6555
6555
1866
1866
1128
1128
11128
11137
11137
                                          Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110000
110000
110000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.6
16.6
16.6
16.6
16.1
16
16
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6
15.6
15.6
15.6
                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                  nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B B
                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum I
Maximum I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š.
```

```
ö
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of gene 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI OTHER INFORMATION: fragment of pTS88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (36)..(694)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
                                    Sequence Sequence
                                                                                                                     Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 24; DB 3; Length 1303; 100.0%; Pred. No. 0.0042; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KET: misc_feature
LOCATION: (695)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVERTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
NUMBER OF FILING DATE: 1997-11-12
SOFTWARE: PATENTING: 2.0
US-08-716-301-5
US-08-231-193A-41
US-08-486-273A-41
US-08-480-474-41
US-08-240-086A-41
US-08-480-474-44
US-08-480-474-44
US-08-231-193A-43
US-08-240-086A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of pGEM2 (pGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08894440 Patent No. 6025546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1288)..(1303)
CHER INDEMATION: polylinker
US-08-894-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(35)
OTHER INFORMATION: polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
            Query Match
Best Local Similarity 100.0
Matches 24; Conservative
                                    2326
2326
2326
2326
3324
3324
3324
3369
3369
4000
4000
4000
4000
4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
```

us-09-698-903b-9.rni

g

```
/label- barstar
/note= "coding region of barstar gene of Bacillus
amyloliquefaciens"
                                                                                                                                                                              complement (30..352)
RMATION: /label= 3'nos
RMATION: /note= "3' regulatory sequence containing the
RMATION: polyadenylation signal of the nopaline synthase
RMATION: gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-YOU-3/-3/C

Sequence 3, Application US/08750357

Patent No. 6008437

GENERAL INFORMATION:
APPLICANT: KEBBERS, Enno
APPLICANT: KEBBERS, Enno
APPLICANT: LEEMANS, MAIN
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
TITLE OF INVENTION: MALE STERILE PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: PO. BOX 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/750,357
FILING DATE: 21-MAR-1997
CLASSIFICATION: 800

**MONTON NUMBER: US/08/750,357
CLASSIFICATION: 800
**MONTON NUMBER: US/08/750,357
CLASSIFICATION: 800
**MONTON NUMBER: US/08/750,357
**MONTON NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 0.0051;

Matches 24; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: ECORI-HindIII region of plasmid pTS200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-MAR-1997
CLASSIFICATION: 800
ATORNEY AGENT INFORMATION:
NAME: MGGOWAN, MAICOLIN K.
REGISTRATION NUMBER: 39,300
TELEPANUNICATION INFORMATION:
TELEPANUNE: (703) 836-6620
TELEPAN: (703) 836-622

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: -
; LOCATION: 3539..3544
; OTHER INFORMATION: /label- Hindili
US-08-485-139-3
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 1..6
OTHER INFORMATION: /label- ECORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 TCAGAAGTATCAGCGACCTCCACC 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3544 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                   FEATURE:
NAME/KEY:
LOCATION:
COMPLEM:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY:
                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-750-357-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: -
NAME/KEY: -
LOCATION: 1841..2674
COTHER INFORMATION: /label= p35S
OTHER INFORMATION: /note= "35S promoter of Cauliflower Mosaic Virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
NAME/KEY:
LOCATION: 2675.3226
OTHER INFORMATION: /label= bar
OTHER INFORMATION: /note= "coding region of bar gene of Streptomyces
OTHER INFORMATION: hygroscopicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08485139;
Sequence 3, Application US/08485139;
Patent No. S8801331
GENERAL INFORMATION:
MAPPLICANT: KREBBERS, Enno
APPLICANT: LIEEMANION:
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
MUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: Alexandria
STREET: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: complement (626..1803)
OTHER INFORMATION: /Label= PCA55
OTHER INFORMATION: /note= "promoter of CA55 gene of Zea mays"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/485,139
FILING DATE: 07-JUN-1995
GLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECCLE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: ECORI-HindIII region of plasmid pTS200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MGGWAN, MAICOLM K.
RECISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 010830-096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 3:
LENGTH: 3544 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
726 tcagaagtatcagcgacctccacc 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: complement (353..625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
```

```
complement (18..401)

RMATION: /label= 3'nos

RMATION: /note= "3' regulatory sequence containing the

RMATION: polydenylation site derived from Agrobacterium

RMATION: T-DNA nopaline synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "promoter region of the 2m13 gene of Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /label- 35S3
OTHER INFORMATION: /note- ""35S3" promoter sequence derived from
OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-JI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (2282..2554)
RMATION: /label-barstar
RMATION: /note-berstar
RMATION: /note-coding region of the barstar gene of
RMATION: Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (402..737)
MAMYION: /label= barnase
RMATION: /lote= "coding region of the barnase gene
RMATION: Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2555..3099)
SNRATION: /label= PTAA29
PRMATION: /note= "promoter region of the TA29
PRMATION: Nicotiana tabacum"
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/351,413 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: ECORI-HindIII fragment of plasmid pTS218
                                                                                  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEGNARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 3121-102PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: -
LOCATION: complement (1945..2281)
OTHER INFORMATION: /label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (738..1944)
RMATION: /label- PZM13
                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248345
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4808 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: -
LOCATION: 3100..3932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -
LOCATION: complement
OTHER INFORMATION: ,
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: -
LOCATION: CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                               OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
OTHER INFORMATION: signal of the nopaline synthase gene of Agrobacterium T-DNA"
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= 3'nos
/note= "3' regulatory sequence containing the polyadenylation
signal of the nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                  OTHER INFORMATION: /label= bar
OTHER INFORMATION: /note= "coding region of bar gene of Streptomyces hygroscopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCATION: 353..625
COTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of barstar gene of Bacillus orner INFORMATION: amyloliquefaciens"
                                                                                                                                                                                                                                                                                       LOCATION: 1841..2674
OTHER INFORMATION: /label- P35S
OTHER INFORMATION: /note- "35S promoter of Cauliflower Mosaic Virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 626..1803
OTHER INFORMATION: /label- PCA55
OTHER INFORMATION: /note- "promoter of CA55 gene of Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-351-413-17/c
Sequence 17, Application US/08351413
Fatent No. 5750867
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 24; DB 3; L. Best Local Similarity 100.0%; Pred. No. 0.0051; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION: 3539..3544

COTHER INFORMATION: /label= HindIII
US-08-750-357-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..6
OTHER INFORMATION: /label= EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 TCAGAAGTATCAGCGACCTCCACC 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                             2675..3226
                                          3227..3504
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: - 626..1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 8110 Gatehou
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353..625
                                                                                                                                                                                                                                                                         NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                              LOCATION:
                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

of

 $^{\rm ot}$

```
INAME/KEY:

LOCATION: complement (18..401)
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: -
LOCATION: 3100.3932
OTHER INFORMATION: /label-35S3
OTHER INFORMATION: /note=""35S3" promoter sequence derived from
OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-JI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
LOCATION: 3933..4484
OTHER INFORMATION: /label= bar
OTHER INFORMATION: /note= "coding region of the phosphinothricin PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement (738..1944)
RMATION: /label= PZM13
RMATION: /note= "promoter region of the Zm13 gene of NRMATION: mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAMECKEY:

LOCATION: complement (2282..2554)

OTHER INFORMATION: /label= barstar

OTHER INFORMATION: /note= "coding region of the barstar gene of

FRATURE:

NAME/KEY:

LOCATION: complement (2555..3099)

OTHER INFORMATION: /label= pra29

OTHER INFORMATION: /note= "promoter region of the TA29 gene of

FEATURE:

COTHER INFORMATION: Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: complement (402..737)
OTHER INFORMATION: /label= barnase
OTHER INFORMATION: /note= "coding region of the barnase gene
OTHER INFORMATION: Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: ECORI-HindIII fragment of plasmid pTS218
                      REGISTRATION NUMBER: 30,330
empropence/DOCKET NUMBER: 2121-102PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: -
LOCATION: 4485..4763
OTHER INFORMATION: /label= 3'nos
                                               REFERENCE/DOCKET NOMBER: 2121
TELECOMUNICATION INFORMATION:
TELERAX: (703) 205-8000
TELERAX: (703) 205-8050
TELERAX: 248345
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
TENTY: 4808 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPLOGY: 1 inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                              NAME/KEY: -
LOCATION: complement (2538..2586)
LOCATION: /label- TA29SBXOL2
OTHER INFORMATION: /note- "region complementary to oligonucleotide
OTHER INFORMATION: TA29SBXOL2
                                                                                                                                                                                       NAME/KEY: -
LOCATION: 2333..2356
OTHER INFORMATION: /label- BXOL2
OTHER INFORMATION: /note- "region corresponding to oligonucleotide FEATURE:
LOCATION: 3933..4484
OTHER INFORMATION: /label= bar
OTHER INFORMATION: /note= "coding region of the phosphinothricin
OTHER INFORMATION: acetyltransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-025-583-17/C
Sequence 17, Application US/0902583
Sequence 17, Application US/0902583
Sequence 17, Application US/0902583
Sequence 17, Application
Sequence 17, Application
Sequence 17, August Mark
APPLICANT: Lemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
OURESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
SITRET: BILO Gatehouse Road, Suite 500 East
SITRET: Use 10 Country
COMPTR: Us.A.
ZIP: 2046
COMPUTER: LEMANS ADDRESS
SOFTWARE: IBM PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIAN Release #1.0, Version #1.25 (EPO)
FILING DATE:
CLASSIFITANTON
CLASSIFITANTON
CLASSIFITANTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 24; DB 1; Length 4808; Best Local Similarity 100.0%; Pred. No. 0.0054; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (2800..2823)
RMATION: /label= PTA290L5
RMATION: /note= "region complementary to part
RMATION: oligonucleotide PTA290L5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
                                                                                                 NAME/KEY: LOCATION: 4485..4763
OTHER INFORMATION: /label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2529 TCAGAAGTATCAGCGACCTCCACC 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
US-08-351-413-17
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

of

us-09-698-903b-9.rni

```
polyadenylation signal of the nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 3004..3009
; OTHER INFORMATION: /label= ECORI
US-08-485-139-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (318..869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-750-357-2; Sequence 2, Application US/08750357; Patent No. 6008437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATURE.
NAME/KEY: - 2558..2879
                                                                                                                                                                                                                                                                    1740..2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2880..4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3004..3009
                                                        NAME/KEY: -
LOCATION: complement
OTHER INFORMATION: /
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 1..38
OTHER INFORMATION:
OTHER INFORMATION:
     OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                          ö
                                                      complement (2538..2586)
RMATION: /label= TA285BXOL2
RMATION: /note= "region complementary to oligonucleotide
RMATION: TA295BXOL2"
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: complement (39..317)
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                NAME/KEY: -
LOCATION: complement (2800..2823)
COTHER INFORMATION: /label= PTA290L5
OTHER INFORMATION: /note= "region complementary to part of OTHER INFORMATION: oligonucleotide PTA290L5"
US-09-025-583-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08485139; Patent No. 588031
GENERAL INFORMATION:
APPLICANT: REBBERS, Enno
APPLICANT: REBBERS, Enno
TITLE OF INVERTION: MALE STERILE PLANTS
ITTLE OF INVERTION: MALE STERILE PLANTS
OWNERS POWDENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker 6 Mathis
STREET: Alexandria
CITT: Alexandria
                                                                                                                                                                                                                                                                                                   Length 4808;
                                                                                                                                                                                                                                                                                                   100.0%; Score 24; DB 2; Length 48
100.0%; Pred. No. 0.0054;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CAPPLICATION NUMBER: US/08/485,139
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: plasmid pTS256, linearized at HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: MCGOWAN, Malcolm K.
REGISTRATION UNBER: 39,300
REFERENCE/DOCKET NUMBER: 010830-096
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 circular
E: DNA (genomic)
   BXOL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 4896 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                   NAME/KEY: --
LOCATION: complemen
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-485-139-2
                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                             õ
```

```
ö
                                                                                        FEATURE:
NAME/KEY:
LOCATION: complement (870..1702)
OTHER INFORMATION: /label= P35S
OTHER INFORMATION: /note= "35S promoter of Cauliflower Mosaic Virus"
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
LOCATION: 2285..2557
COTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of barstar gene of Bacillus
OTHER INFORMATION: amyloliquefaciens"
/label= bar / /note= "coding region of bar gene of Streptomyces hygroscopicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 2558..2879
OTHER INFORMATION: /label-3'nos
OTHER INFORMATION: /note="3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                       LOCATION: 1740..2284
OTHER INFORMATION: /label= PTA29
OTHER INFORMATION: /note= "promoter of TA29 gene of Nicotiana OTHER INFORMATION: tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KREBBERS, Enno
APPLICANT: WILLIAMS, MARK
APPLICANT: WILLIAMS, MARK
APPLICANT: LENGENIN, USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /label= pUC19
OTHER INFORMATION: /note= "pUC19 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= pUC19
/note= "pUC19 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 24; DB 2; I
ilarity 100.0%; Pred. No. 0.0054;
Conservative 0; Mismatches 0;
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene, of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene
FEATURE:
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: Complement((2659)...(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTCO113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                     Query Match
100.0%; Score 24; DB 3; Length 4896;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-894-40-4
Sequence 4, Application US/08894440
Farent No. 6025546
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
CURRENT APPLICATION: UNAGEN:
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphinothricin acetyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KET: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: Complement((3022)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene of
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
                                         ; LOCATION: 3004..3009
; OTHER INFORMATION: /label= ECORI
US-08-750-357-2
                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement(/3
                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 39.317
COCATION: 7]
LOCATION: /label-3/nos
OTHER INFORMATION: /note-"3' regulatory sequence containing the polyadenylation
OTHER INFORMATION: signal of the nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 318.869
OTHER INFORMATION: /label= bar
OTHER INFORMATION: /note= "coding region of bar gene of Streptomyces hygroscopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 2558..2879
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
OTHER INFORMATION: signal of the nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: -
LOCATION: 1740..2284
OTHER INFORMATION: /label- PTA29
OTHER INFORMATION: /note= "promoter of TA29 gene of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
LOCATION: 870..1702
LOCATION: /label- P35S
OTHER INFORMATION: /note- "35S promoter of Cauliflower Mosaic Virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: -
LOCATION: 2285..2557
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of barstar gene of
OTHER INFORMATION: Bacillusamyloliquefacien"
                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,357
FILING DATE: 21-MAR-1997
FILING DATE: 21-MAR-1997
ATORNEY/AGENT INFORMATION:
NAME: MCGOWAN, Malcolm K,
RECISTRATION NUMBER: 39,300
ATORNEY/AGENT INFORMATION:
REPERENCE/DOCKET NUMBER: 39,300
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4896 Dasa Pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: -
LOCATION: 2880..4896
OTHER INFORMATION: /label- pUC19
OTHER INFORMATION: /note- "pUC19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: -
LOCATION: 1.38
OTHER INFORMATION: /label= pUC19
OTHER INFORMATION: /note= "pUC19 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: plasmid pTS256, linearized at HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: CIRCULAR MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
```

```
RESULT 10
US-09-025-583-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
NAME.KEY: misc_feature
LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
FATURE:
NAME.KEY: misc_feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
FEATURE:
NAME.KEY: misc_feature
LOCATION: Complement((5840)..(5864))
OTHER INFORMATION: left border of Agrobacterium T-DNA
US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                    Length 5864;
                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 24; DB 3; Length 58
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INFORMATION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: BILO Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 2046

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 3121-102PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5248 tcagaagtatcagcgacctccacc 5271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08351413
Patent No. 5750867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-351-413-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

```
/note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA octopine synthase gene"
                                                                                                                                             complement (1025..1607)
RMATION: /label= TA29
RMATION: /nce= "promoter derived from the TA29 gene of RMATION: Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1608..2440
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-JI"
FEATURE:
                                                                                                                                                                                                                                                                                            FEATURE:
NAME:
NAME:
NAME:
LOCATION:
COMPLEMENTION:
OTHER INFORMATION:
Dacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: -
LOCATION: 2441..3256
OTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of In5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 24; DB 1; Length 6555; 100.0%; Pred. No. 0.0057; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09025583
Patent No. 5977433
GENERAL INFORMATION: Mark
APPLICANT: Leemans, Jan
TITLE OF INVERTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                     /label= pUC18 /note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /label= pUC18 OTHER INFORMATION: /note= "pUC18 derived sequence" US-08-351-413-2
ORIGINAL SOURCE:
ORGANISM: plasmid pVE144 (replicable in E.coli)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /label= 3'ocs OTHER INFORMATION: /note= "3' req OTHER INFORMATION: polyadenylatic OTHER INFORMATION: T-DNA octopine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 3257..4315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4316..6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: complemen
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                             NAME/KEY:
LOCATION: 1.396
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION: 4
```

```
NAME/KEY: -
LOCATION: complement (397...751)
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: complement (1025..1607)
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /note= "promoter derived from the TA29 gene of CHER INFORMATION: Nicotiana tabacum"
NAME/KEY:
NAME/KEY:
NAME/KEY: 1608..2440
OTHER INFORMATION: /label= 3553
OTHER INFORMATION: /note= "3553 promoter sequence derived from OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-JI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (752..1024)
*RMATION: /label= barstar
*PMATION: /note= "coding region of the barstar gene
*PMATION: Bacillus amyloliquefaciens"
                                                                                                                                                   ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/09/025,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: -
LOCATION: 1..396
OTHER INFORMATION: /label- puc18
OTHER INFORMATION: /note= "puc18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI SENSE: NO ORIGINAL SOURCE: ORGANISM: plasmid pVE144 (replicable in E.coli)
SSEE: BIRCH, STEWART, KOLASCH & BIRCH
T: 8110 Gatehouse Road, Suite 500 East
Falls Church
: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:

APPLICATION NUMBER: US/08/351,413

APPLICATION NUMBER: US 07/899,072

FILING DATE: US-UNN-1992

PRIOR APPLICATION DATE: US 07/970,849

FILING DATE: US 07/970,849

APPLICATION NUMBER: US 07/970,849

ATTORNEY AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 3121-102PCT

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 6555 base pairs

TYPE: NUCLEIC acid

TYPE: NUCLEIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY:
LOCATION:
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: -
                                                                                           STATE: V.
```

```
Sequence 1, Application US/08403388;
Patent No. 5587289;
GENERAL INFORMATION:
FAPLICANT: Lurquin, Christophe; Boon-Falleur, Thierry
TITLE OF INVENTION:
MUMBER OF SEQUENCES: 12
CORESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                              NAME/KEY: -
LOCATION: 3257..4315
LOCATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium FEATURE: INFORMATION: T-DNA octopine synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
NAME/KEY: -
LOCATION: 2441..3256
COTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of Tn5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 24; DB 2; Length 6555;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                             ; LOCATION: 4316..6555
; OTHER INFORMATION: /label- pUC18
; OTHER INFORMATION: /note- "pUC18 derived sequence"
US-09-025-983-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.2%; Score 16.6; D
82.6%; Pred. No. 21;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,388
FILING DATE: 14-MARCH-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: HARSON, NO. 5587289man D.
REGISTARTION NUMBER: LUD 5408
REGISTARTION NUMBER: LUD 5408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFA: (212) 839-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 tcagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1866 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-403-388-1
                                                                                                                                                                                                                                                                                             NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-403-388-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
Length 1866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%; Score 16.6; DB 4; Length 1866; 82.6%; Pred. No. 21; 1:ve 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09056105

Sequence 19, Application US/09056105

Sequence 10, Application US/09056105

Sequence No. 6287569

Sequence No. 6287569

Sequence No. 6287569

TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR

TITLE OF INVENTION: PROCESSING

FILE REFERENCE: 233/221

CURRENT APPLICATION NUMBER: US/09/056,105

CURRENT FILING DATE: 1998-04-06

EARLIER APPLICATION NUMBER: 66/043,467

EARLIER PILING DATE: 1997-04-10

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FASESEQ for Windows Version 3.0

LENGTH: 1866
                                                   Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.6; DE
Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanson, No. 6017705man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5444.1
TELECHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360
COMPUTER: IBM PC-DOS
SOFTWARE: Wordperfect For DOS 6.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,111b
FILING DATE: 25-APRIL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,578
FILING DATE: 5-MAY-1996
PRIOR APPLICATION NUMBER: 08/403,388
FILING DATE: 14-MARCH-1995
ATCHNEY AGENT 114-MARCH-1995
ATCHNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 CAGAAGCCTCAGGGAGCTCCACC 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||| ||||| 498 cagaagcctcagc 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 cagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 cagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.2%;
Best Local Similarity 82.6%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.2
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-09-056-105-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-056-105-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                            APPLICANT: LUTQUIO, Christophe; Brasseur, Francis;
APPLICANT: LUTQUIO, Thierry
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
TITLE OF INVENTION: Members Of The Mage-Xp Family and Uses Thereof
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lurquin, Christophe; Brasseur, Francis;
APPLICANT: Lurquin, Thierry
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
TITLE OF INVENTION: Members Of The Mage-B Family and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.2%; Score 16.6; DB 1; Length 1866; Best Local Similarity 82.6%; Pred. No. 21; Matches 19; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,578
FILING DATE: 5-MAY-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION WHER: 08/403,388
FILING DATE: 14-MARCH-1995
ATORNEY/AGENT INFORMATION:
NAME: HARSON, NO. 5759783man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 10,946
REFERENCE/DOCKET NUMBER: LUD 5444
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-846-111D-1; Sequence 1, Application US/08846111D; Patent No. 6017705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498 CAGAAGCCTCAGGGAGCTCCACC 520
                                                                                                                                                                         Sequence 1, Application US/08658578 Patent No. 5759783 GENERAL INFORMATION:
                                498 CAGAAGCCTCAGGGAGCTCCACC 520
2 cagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 cagaagtatcagcgacctccacc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1866 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                a
```

ö

ö

Gaps

```
Sequence 15. Application US/OBB46111D
SEQUENCE 15. Sequence 15
```

Search completed: February 25, 2002, 18:05:29 Job time: 18577 sec